

FORM PTO-1390 (REV 11-98)	U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTORNEY'S DOCKET NUMBER 47-138 <i>Box 1507</i>
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371		U.S. APPLICATION NO. (If known, see 37 C.F.R. 1.52) 09/581286 <i>Unassigned</i>
INTERNATIONAL APPLICATION NO. PCT/AU98/01023	INTERNATIONAL FILING DATE 10 December 1998	PRIORITY DATE CLAIMED 10 December 1997
TITLE OF INVENTION P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES		
APPLICANT(S) FOR DO/EO/US ROSS et al 523 Rec'd PCT/PTO 12 JUN 2000		

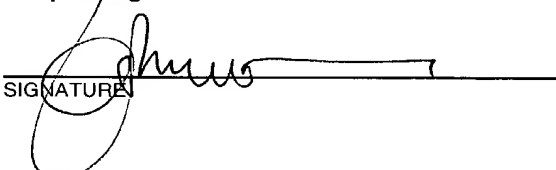
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☐ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. A copy of the International Application as filed (35 U.S.C. 371(c)(2)).
 - a. ☒ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☐ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has **NOT** expired.
 - d. ☐ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (U.S.C. 371(c)(3)).
9. ☐ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. To 16. Below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 C.F.R. 1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. 3.28 and 3.31 is included.
13. ☒ A **FIRST** preliminary amendment.
☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☐ Other items or information.

416 Rec'd PCT/PTO 12 JUN 2000

U.S. APPLICATION NO. (If known, see 37 C.F.R. 1.55) 09/4581286		INTERNATIONAL APPLICATION NO. PCT/AU98/01023		ATTORNEY'S DOCKET NUMBER 47-138	
17. <input checked="" type="checkbox"/> The following fees are submitted:				CALCULATIONS PTO USE ONLY	
BASIC NATIONAL FEE (37 C.F.R. 1.492(a)(1)-(5): -- Neither international preliminary examination fee (37 C.F.R. 1.482) nor international search fee (37 C.F.R. 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO\$970.00 -- International preliminary examination fee (37 C.F.R. 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO\$840.00 -- International preliminary examination fee (37 C.F.R. 1.482) not paid to USPTO but international search fee (37 C.F.R. 1.445(a)(2)) paid to USPTO\$690.00 -- International preliminary examination fee paid to USPTO (37 C.F.R. 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4)\$670.00 -- International preliminary examination fee paid to USPTO (37 C.F.R. 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4)\$96.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$	970.00
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 C.F.R. 1.492(e)).				\$	0.00
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total Claims	34	-20 =	14	X	\$ 18.00
Independent Claims	3	-3 =	0	X	\$ 78.00
MULTIPLE DEPENDENT CLAIMS(S) (if applicable)					\$260.00
TOTAL OF ABOVE CALCULATIONS =				\$	1222.00
Reduction by 1/2 for filing by small entity, if applicable. A Small Entity Statement must also be filed (Note 37 C.F.R. 1.9, 1.27, 1.28).					0.00
SUBTOTAL =				\$	1222.00
Processing fee of \$130.00, for furnishing the English Translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 C.F.R. 1.492(f)).					0.00
TOTAL NATIONAL FEE =				\$	1222.00
Fee for recording the enclosed assignment (37 C.F.R. 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. 3.28, 3.31). \$40.00 per property				+	\$ 0.00
Fee for Petition to Revive Unintentionally Abandoned Application (\$1210.00 - Small Entity = \$605.00)					\$ 0.00
TOTAL FEES ENCLOSED =				\$	1222.00
				Amount to be:	
				refunded	\$
				Charged	\$
a. <input checked="" type="checkbox"/> A check in the amount of \$1222.00 to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. 14-1140 in the amount of \$_____ to cover the above fees. A duplicate copy of this form is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 14-1140. A duplicate copy of this form is enclosed. d. <input type="checkbox"/> The entire content of the foreign application(s), referred to in this application is/are hereby incorporated by reference in this application.					
NOTE: Where an appropriate time limit under 37 C.F.R. 1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. 1.137(a) or (b)) must be filed and granted to restore the application to pending status.					
SEND ALL CORRESPONDENCE TO: NIXON & VANDERHYE P.C. 1100 North Glebe Road, 8 th Floor Arlington, Virginia 22201 Telephone: (703) 816-4000					
				 SIGNATURE	
				Leonard C. Mitchard NAME	
29,009		June 12, 2000			
REGISTRATION NUMBER		Date			

09/581286

416 Rec'd PCT/PTO 1 2 JUN 2000

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of

ROSS et al

Atty. Ref.: 47-138

Serial No. Unassigned

Group:

Filed: June 12, 2000

Examiner:

For: P. GINGIVALIS POLYPEPTIDES AND
NUCLEOTIDES

* * * * *

June 12, 2000

Assistant Commissioner for Patents
Washington, DC 20231

PRELIMINARY AMENDMENT

Sir:

Please amend the above application as follows:

IN THE CLAIMS

Claim 11, lines 2 and 3, delete "any one of claims 1 to 10" and replace by --
claim 1--.

Claim 13, line 2, delete "or claim 12".

Claim 16, line 3, delete "any one of claims 1 to 10" and replace by --claim
1--.

Claim 17, lines 2 and 3, delete "claimed in claim 11 or claim 12" and
replace by --defined above--.

Claim 18, line 1 delete "or claim 17".

Claim 19, lines 2 and 3 delete "any one of claims 16 or 18" and replace by -
-claim 16--.

Claim 22, line 3, delete "or claim 12".

Claim 24, line 2, delete "or claim 23".

Claim 27, lines 1 and 2, delete "any one of claims 1 to 10" and replace by --
claim 1--.

Claim 30, lines 1 and 2, delete "any one of claims 27 to 29" and replace by
--claim 27--.

Claim 34, line 4, delete "or claim 33"

[illegible]

The above amendments have been made to place the application in a more traditional format.

Respectfully submitted,

NIXON & VANDERHYE P.C.

By:

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In re Patent Application of

ROSS et al

Serial No. Unassigned

Filed: June 12, 2000

For: P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES

416 Rec'd PCT/PTO 12 JUN 2000

Atty. Ref.: 47-138

Group:

Examiner:

* * * * *

June 12, 2000

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

SUBMISSION OF SEQUENCE LISTING

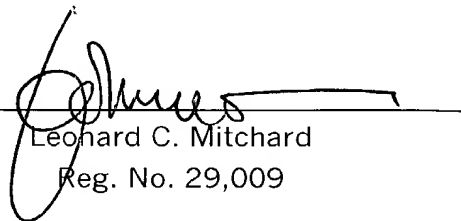
Attached is a printed sequence listing for this application and a copy of the computer readable CD-ROM disk in the attached envelope.

In accordance with 37 C.F.R. 1.821-1.825, I hereby state that the content of the paper and computer-readable copies of the sequence listing submitted in accordance with 37 C.F.R. 1.821(c) and (e), respectively, are the same. I hereby state that the submission, filed in accordance with 37 C.F.R. 1.821(g), does not introduce new matter.

Respectfully submitted,

NIXON & VANDERHYE P.C.

By: _____


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2 / PRTS

09/581286

416 Rec'd PCT/PTO 12 JUN 2000

WO 99/29870

PCT/AU98/01023

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***Porphyromonas gingivalis* polypeptides and nucleotides**

FIELD OF THE INVENTION

5 The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*. The *P. gingivalis* polypeptides and nucleotides can be used in compositions for use in raising an immune response in a subject against *P. gingivalis* and
10 treating or preventing or reducing the severity of the condition known as periodontitis.

BACKGROUND OF THE INVENTION

15 Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated with a subgingival infection of a consortium of specific Gram-negative
20 bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is *P. gingivalis* as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically cultivable flora, whereas *P. gingivalis* is rarely recovered, and then in low
25 numbers, from healthy sites. A proportional increase in the level of *P. gingivalis* in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of the disease. The progression of periodontitis lesions in non-human primates
30 has been demonstrated with the subgingival implantation of *P. gingivalis*. These findings in both animals and humans suggest a major role for *P. gingivalis* in the development of adult periodontitis.

35 *P. gingivalis* is a black-pigmented, anaerobic, asaccharolytic, proteolytic Gram-negative rod that obtains energy from the metabolism of specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III)

oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

5 In order to develop an efficacious and safe vaccine to prevent, eliminate or reduce *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens possibly through the generation of specific antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis*
10 this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates
15 potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in
20 low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of
25 response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

It is also well known that *P. gingivalis* produces a range of broadly
30 active proteases (University of Melbourne International Patent Application No PCT /AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

In a first aspect the present invention consists in an isolated antigenic
20 *Porphyromonas gingivalis* polypeptide, the polypeptide comprising;
an amino acid sequence selected from the group consisting of SEQ.
ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO.
532; or
an amino acid sequence at least 85%, preferably at least 95%,
25 identical to an amino acid sequence selected from the group
consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO.
531 and SEQ. ID. NO. 532; or
at least 40 amino acids having a contiguous sequence of at least 40
amino acids identical to a contiguous amino acid sequence selected
30 from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528,
SEQ. ID. NO. 531 and SEQ. ID. NO. 532.

In an embodiment of the present invention the polypeptide comprises;

an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or

an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or

- 5 at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.

- 10 As used herein % identity for polypeptides is to be calculated using the alignment algorithm of Needleman and Munsch (9) using a standard protein scoring matrix (Blosum 50).

In a preferred embodiment of the present invention the polypeptide comprises an amino acid sequence selected from the group consisting of
15 SEQ. ID. NO. 386, SEQ. ID. NO. 424, SEQ. ID. NO. 425, SEQ. ID. NO. 434, SEQ. ID. NO. 447, SEQ. ID. NO. 458, SEQ. ID. NO. 475, SEQ. ID. NO. 498, SEQ. ID. NO. 499, SEQ. ID. NO. 500, SEQ. ID. NO. 501, SEQ. ID. NO. 387, SEQ. ID. NO. 400, SEQ. ID. NO. 411, SEQ. ID. NO. 419, SEQ. ID. NO. 420, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 433, SEQ. ID. NO. 437, SEQ. ID. NO. 438, SEQ. ID. NO. 443, SEQ. ID. NO. 444, SEQ. ID. NO. 448,
20 SEQ. ID. NO. 449, SEQ. ID. NO. 452, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 462, SEQ. ID. NO. 463, SEQ. ID. NO. 467, SEQ. ID. NO. 468, SEQ. ID. NO. 469, SEQ. ID. NO. 482, SEQ. ID. NO. 484, SEQ. ID. NO. 485, SEQ. ID. NO. 494, SEQ. ID. NO. 508, SEQ. ID. NO. 509, SEQ. ID. NO. 510, SEQ. ID. NO. 520, SEQ. ID. NO. 521,
25 SEQ. ID. NO. 522, SEQ. ID. NO. 525, SEQ. ID. NO. 526, SEQ. ID. NO. 528, SEQ. ID. NO. 389, SEQ. ID. NO. 390 and SEQ. ID. NO. 391.

In another preferred embodiment of the present invention the polypeptide comprises an amino acid sequence selected from the group consisting of residue 422 to residue 531 of SEQ. ID. NO. 303, residue 534 to
30 residue 582 of SEQ. ID. NO. 303, residue 127 to residue 232 of SEQ. ID. NO. 301, residue 240 to residue 259 of SEQ. ID. NO. 301, residue 139 to residue 156 of SEQ. ID. NO. 295, residue 160 to residue 178 of SEQ. ID. NO. 295, residue 180 to residue 207 of SEQ. ID. NO. 295, residue 221 to residue 257 of SEQ. ID. NO. 295, residue 259 to residue 323 of SEQ. ID. NO. 295, residue
35 885 to residue 985 of SEQ. ID. NO. 299, residue 147 to residue 259 of SEQ. ID. NO. 363, residue 140 to residue 252 of SEQ. ID. NO. 344, residue 247 to

residue 356 of SEQ. ID. NO. 353, residue 359 to residue 391 of SEQ. ID. NO. 353, residue 120 to residue 254 of SEQ. ID. NO. 300, residue 287 to residue 311 of SEQ. ID. NO. 286, residue 313 to residue 352 of SEQ. ID. NO. 288, residue 354 to residue 401 of SEQ. ID. NO. 286, residue 208 to residue 252 of
5 SEQ. ID. NO. 287, residue 259 to residue 373 of SEQ. ID. NO. 287, residue 5 to residue 120 of SEQ. ID. NO. 293, residue 123 to residue 139 of SEQ. ID. NO. 293, residue 233 to residue 339 of SEQ. ID. NO. 265, residue 67 to residue 228 of SEQ. ID. NO. 278, residue 130 to residue 172 of SEQ. ID. NO. 274, residue 174 to residue 238 of SEQ. ID. NO. 274, residue 99 to residue
10 112 of SEQ. ID. NO. 274, residue 114 to residue 128 of SEQ. ID. NO. 274, residue 26 to residue 69 of SEQ. ID. NO. 285, residue 71 to residue 128 of SEQ. ID. NO. 285, residue 130 to residue 146 of SEQ. ID. NO. 285, residue 620 to residue 636 of SEQ. ID. NO. 327, residue 638 to residue 775 of SEQ. ID. NO. 327, residue 397 to residue 505 of SEQ. ID. NO. 301, residue 528 to
15 residue 545 of SEQ. ID. NO. 301, residue 556 to residue 612 of SEQ. ID. NO. 301, residue 614 to residue 631 of SEQ. ID. NO. 301, residue 633 to residue 650 of SEQ. ID. NO. 301, residue 553 to residue 687 of SEQ. ID. NO. 299, residue 305 to residue 447 of SEQ. ID. NO. 289, residue 1 to residue 52 of SEQ. ID. NO. 364, residue 65 to residue 74 of SEQ. ID. NO. 364, residue 486
20 to residue 604 of SEQ. ID. NO. 275, residue 158 to residue 267 of SEQ. ID. NO. 272, residue 270 to residue 282 of SEQ. ID. NO. 272, residue 163 to residue 237 of SEQ. ID. NO. 273, residue 240 to residue 251 of SEQ. ID. NO. 273, residue 213 to residue 344 of SEQ. ID. NO. 282, residue 183 to residue 324 of SEQ. ID. NO. 292, residue 327 to residue 341 of SEQ. ID. NO. 292,
25 residue 352 to residue 372 of SEQ. ID. NO. 292, residue 141 to residue 166 of SEQ. ID. NO. 271, residue 168 to residue 232 of SEQ. ID. NO. 271, residue 1 to residue 13 of SEQ. ID. NO. 302, residue 15 to residue 28 of SEQ. ID. NO. 302, residue 30 to residue 72 of SEQ. ID. NO. 302, residue 476 to residue 529 of SEQ. ID. NO. 277, residue 41 to residue 146 of SEQ. ID. NO. 299, residue
30 149 to residue 162 of SEQ. ID. NO. 299, residue 166 to residue 177 of SEQ. ID. NO. 299, residue 192 to residue 203 of SEQ. ID. NO. 299, residue 71 to residue 343 of SEQ. ID. NO. 290, residue 346 to residue 363 of SEQ. ID. NO. 290, residue 36 to residue 240 of SEQ. ID. NO. 331, residue 242 to residue 270 of SEQ. ID. NO. 331, residue 1 to residue 192 of SEQ. ID. NO. 375,
35 residue 286 to residue 290 of SEQ. ID. NO. 375, residue 23 to residue 216 of SEQ. ID. NO. 279, residue 220 to residue 270 of SEQ. ID. NO. 279, residue

285 to residue 386 of SEQ. ID. NO. 279, residue 84 to residue 234 of SEQ. ID. NO. 297, residue 248 to residue 259 of SEQ. ID. NO. 297, residue 261 to residue 269 of SEQ. ID. NO. 297, residue 275 to residue 402 of SEQ. ID. NO. 294, residue 1 to residue 171 of SEQ. ID. NO. 298, residue 403 to residue 417
5 of SEQ. ID. NO. 307, residue 420 to residue 453 of SEQ. ID. NO. 307, residue 456 to residue 464 of SEQ. ID. NO. 307, residue 468 to residue 690 of SEQ. ID. NO. 307, residue 1 to residue 285 of SEQ. ID. NO. 304, residue 287 to residue 315 of SEQ. ID. NO. 304, residue 318 to residue 336 of SEQ. ID. NO. 304, residue 255 to residue 269 of SEQ. ID. NO. 342, residue 271 to residue
10 337 of SEQ. ID. NO. 342, residue 347 to residue 467 of SEQ. ID. NO. 281, residue 116 to residue 136 of SEQ. ID. NO. 375, residue 138 to residue 357 of SEQ. ID. NO. 375, residue 133 to residue 423 of SEQ. ID. NO. 364, residue 141 to residue 299 of SEQ. ID. NO. 305, residue 202 to residue 365 of SEQ. ID. NO. 296, residue 134 to residue 426 of SEQ. ID. NO. 288, residue 1 to
15 residue 218 of SEQ. ID. NO. 276, residue 1 to residue 246 of SEQ. ID. NO. 280, residue 444 to residue 608 of SEQ. ID. NO. 364, residue 10 to residue 686 of SEQ. ID. NO. 283, residue 1 to residue 148 of SEQ. ID. NO. 296, residue 1 to residue 191 of SEQ. ID. NO. 287, residue 193 to residue 204 of SEQ. ID. NO. 287, residue 209 to residue 373 of SEQ. ID. NO. 287, residue
20 211 to residue 470 of SEQ. ID. NO. 284, residue 472 to residue 482 of SEQ. ID. NO. 284, residue 133 to residue 144 of SEQ. ID. NO. 281, residue 146 to residue 336 of SEQ. ID. NO. 281, residue 1 to residue 264 of SEQ. ID. NO. 303, residue 265 to residue 295 of SEQ. ID. NO. 303, residue 297 to residue 326 of SEQ. ID. NO. 303, residue 328 to residue 338 of SEQ. ID. NO. 303,
25 residue 247 to residue 356 of SEQ. ID. NO. 353, residue 358 to residue 391 of SEQ. ID. NO. 353, residue 257 to residue 288 of SEQ. ID. NO. 298, residue 290 to residue 385 of SEQ. ID. NO. 298, residue 245 to residue 256 of SEQ. ID. NO. 298, residue 422 to residue 802 of SEQ. ID. NO. 303, residue 803 to residue 814 of SEQ. ID. NO. 303, residue 139 to residue 156 of SEQ. ID. NO.
30 295, residue 160 to residue 340 of SEQ. ID. NO. 295, residue 145 to residue 361 of SEQ. ID. NO. 282, residue 363 to residue 387 of SEQ. ID. NO. 282, residue 398 to residue 471 of SEQ. ID. NO. 282, residue 573 to residue 679 of SEQ. ID. NO. 320, residue 27 to residue 168 of SEQ. ID. NO. 291, residue 170 to residue 183 of SEQ. ID. NO. 291, residue 185 to residue 415 of SEQ. ID.
35 NO. 291, residue 1 to residue 301 of SEQ. ID. NO. 364, residue 114 to residue 702 of SEQ. ID. NO. 337, residue 377 to residue 412 of SEQ. ID. NO. 321,

residue 413 to residue 772 of SEQ. ID. NO. 321, residue 14 to residue 454 of SEQ. ID. NO. 265, residue 129 to residue 614 of SEQ. ID. NO. 268, residue 1 to residue 930 of SEQ. ID. NO. 300, residue 932 to residue 1046 of SEQ. ID. NO. 300, residue 1 to residue 301 of SEQ. ID. NO. 364, residue 1 to residue 42 of SEQ. ID. NO. 381, residue 44 to residue 973 of SEQ. ID. NO. 381, residue 1 to residue 93 of SEQ. ID. NO. 358, residue 95 to residue 179 of SEQ. ID. NO. 358, residue 181 to residue 227 of SEQ. ID. NO. 358, residue 114 to residue 702 of SEQ. ID. NO. 337, residue 1 to residue 659 of SEQ. ID. NO. 355, residue 661 to residue 907 of SEQ. ID. NO. 355, residue 1 to residue 131 of SEQ. ID. NO. 370, residue 133 to residue 601 of SEQ. ID. NO. 370, residue 1 to residue 813 of SEQ. ID. NO. 344, residue 377 to residue 412 of SEQ. ID. NO. 321, residue 413 to residue 772 of SEQ. ID. NO. 321, and residue 189 to residue 614 of SEQ. ID. NO. 364.

In a second aspect the present invention consists in a n isolated antigenic *Porphorymonas gingivalis* polypeptide, the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532 less the leader sequence set out in Table 3.

In a third aspect the present invention consists in an isolated DNA molecule, the DNA molecule comprising a nucleotide sequence which encodes the polypeptide of the first aspect the present invention or a sequence which hybridises thereto under stringent conditions.

It is preferred that the isolated DNA molecule comprises a nucleotide sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 264, SEQ. ID. NO. 529 and SEQ. ID. NO. 530.

In a fourth aspect the present invention consists in a recombinant expression vector comprising the DNA molecule of the second aspect of the present invention operably linked to a transcription regulatory element.

The present invention also provides a cell comprising this recombinant expression vector.

In a further aspect the present invention consists in a method for producing a *P. gingivalis* polypeptide comprising culturing the cell under conditions that permit expression of the polypeptide.

In yet a further aspect the present invention provides a composition for use in raising an immune response directed against *P. gingivalis* in a subject, the composition comprising an effective amount of at least one

polypeptide of the first aspect of the present invention, or at least one DNA molecule of the second aspect of the present invention, or both, and a pharmaceutically acceptable carrier. It is preferred that the pharmaceutically acceptable carrier is an adjuvant. In other aspects the present invention

5 provides methods of treating *P. gingivalis* infection in subject comprising the administration of the composition to the subject such that treatment of *P. gingivalis* infection occurs. The treatment may be prophylactic or therapeutic.

In yet another aspect the present invention provides an antibody

10 raised against a polypeptide of the first aspect the invention. The antibody may be polyclonal or monoclonal. The present invention also provides compositions including these antibodies. It is preferred that these compositions are adapted for oral use and may be, for example, dentrifices, mouthwashes, etc.

15 In a still further aspect the present invention provides a nucleotide probe comprising at least 18 nucleotides and having a contiguous sequence of at least 18 nucleotides identical to a contiguous nucleotide sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 121, SEQ. ID. NO. 529, and sequences complementary thereto. It is preferred that

20 the probe further comprises a detectable label.

The present invention also provides a method for detecting the presence of *P. gingivalis* nucleic acid in a sample comprising:

- (a) contacting a sample with the nucleotide probe under conditions in which a hybrid can form between the probe and a *P. gingivalis*
- 25 nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *P. gingivalis* nucleic acid in the sample.

30 DETAILED DESCRIPTION

Definitions

A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a

35 polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also

separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains: sufficient polypeptide to
5 allow protein sequencing; at least 1, 10, or 100 mg of the polypeptide.

A purified preparation of cells refers to, in the case of plant or animal cells, an in vitro preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least 10% and more preferably 50% of the subject cells.

10 A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally occurring genome of
15 the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a
20 prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *P. gingivalis* DNA sequence.

25 A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from
30 a stop to stop codon or from a start to stop codon.

As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five
35 prime terminus and a translation stop code at the three prime terminus. A

coding sequence can include but is not limited to messenger RNA synthetic DNA, and recombinant nucleic acid sequences.

A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernible to one of ordinary skill in the art using routine experimentation.

Homologous refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100.

The terms peptides, proteins, and polypeptides are used interchangeably herein.

An "immunogenic component" as used herein is a moiety, such as an *P. gingivalis* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as *P. gingivalis* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with sufficiently high affinity to form a detectable antigen-antibody complex.

5 As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected
10 DNA primarily in one tissue, but cause expression in other tissues as well.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in
15 prokaryotes, such control sequences generally include a promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and
20 may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way
25 that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue
30 sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology well known to those
35 skilled in the art. Such techniques are described and explained throughout the literature in sources such as, J. Perbal, A Practical Guide to Molecular

Cloning, John Wiley and Sons (1984), J. Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbour Laboratory Press (1989), T.A. Brown (editor), Essential Molecular Biology: A Practical Approach, Volumes 1 and 2, IRL Press (1991), D.M. Glover and B.D. Hames (editors), DNA
5 Cloning: A Practical Approach, Volumes 1-4, IRL Press (1995 and 1996), and F.M. Ausubel et al. (Editors), Current Protocols in Molecular Biology, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present). The disclosure of these texts are incorporated herein by reference.

10 Pharmaceutically Acceptable Carriers

The antibodies, polypeptides and DNA of the present invention can be included in compositions which include a carrier or diluent. These compositions include pharmaceutical compositions where the carrier or
15 diluent will be pharmaceutically acceptable. Pharmaceutically acceptable carriers or diluents include those used in compositions suitable for oral, rectal, nasal, topical (including buccal and sublingual), vaginal, parenteral (including subcutaneous, intramuscular, intravenous, intradermal, intrathecal and epidural) administration. They are non-toxic to recipients at
20 the dosages and concentrations employed. Representative examples of pharmaceutically acceptable carriers or diluents include, but are not limited to; water, isotonic solutions which are preferably buffered at a physiological pH (such as phosphate-buffered saline or Tris-buffered saline) and can also contain one or more of, mannitol, lactose, trehalose, dextrose, glycerol,
25 ethanol or polypeptides (such as human serum albumin). The compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well known in the art of pharmacy.

As will be well understood by those skilled in the art alterations may
30 be made to the amino acid sequences set out in the Sequence Listings. These alterations may be deletions, insertions, or substitutions of amino acid residues. The altered polypeptides can be either naturally occurring (that is to say, purified or isolated from a natural source) or synthetic (for example, by performing site-directed metagenesis on the encoding DNA). It is
35 intended that such altered polypeptides which have at least 85%, preferably at least 95% identity with the sequences set out in the Sequence Listing are

within the scope of the present invention. Antibodies raised against these altered polypeptides will also bind to the polypeptides having one of the sequences set out in the Sequence Listings. The level of % identity is to be calculated as set out above.

- 5 Protein sequences are homologous if they are related by divergence from a common ancestor. Consequently, a species homologue of the protein will be the equivalent protein which occurs naturally in another species. Within any one species a homologue may exist as numerous allelic variants, and these will be considered homologues of the protein. Allelic variants and
10 species homologues can be obtained by following standard techniques known to those skilled in the art.

An allelic variant will be a variant that is naturally occurring within an individual organism.

15 Mutants, Variants and Homology - Nucleic Acids

- Mutant polynucleotides will possess one or more mutations which are deletions, insertions, or substitutions of nucleotide residues. Mutants can be either naturally occurring (that is to say, isolated from a natural source) or synthetic (for example, by performing site-directed metagenesis on
20 the DNA). It is thus apparent that polynucleotides of the invention can be either naturally occurring or recombinant (that is to say prepared using recombinant DNA techniques).

An allelic variant will be a variant that is naturally occurring within an individual organism.

- 25 Nucleotide sequences are homologous if they are related by divergence from a common ancestor. Consequently, a species homologue of the polynucleotide will be the equivalent polynucleotide which occurs naturally in another species. Within any one species a homologue may exist as numerous allelic variants, and these will be considered homologues of the
30 polynucleotide. Allelic variants and species homologues can be obtained by following standard techniques known to those skilled in the art.

Antibody Production

- 35 Antibodies, either polyclonal or monoclonal, which are specific for a polypeptide of the present invention can be produced by a person skilled in the art using standard techniques such as, but not limited to, those described

by Harlow *et al.* Antibodies: A Laboratory Manual, Cold Springs Harbor Laboratory Press (1988), and D. Catty (editor), Antibodies: A Practical Approach, IRL Press (1988).

Various procedures known in the art may be used for the production of polyclonal antibodies to epitopes of a protein. For the production of polyclonal antibodies, a number of host animals are acceptable for the generation of antibodies by immunization with one or more injections of a polypeptide preparation, including but not limited to rabbits, mice, rats, etc. Various adjuvants may be used to increase the immunological response in the host animal, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminium hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*.

A monoclonal antibody to an epitope of a protein may be prepared by using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include but are not limited to the hybridoma technique originally described by Kohler and Milstein (1975, *Nature* 256, 493-497), and the more recent human B-cell hybridoma technique (Kesber *et al.* 1983, *Immunology Today* 4:72) and EBV-hybridoma technique (Cole *et al.* 1985, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. pp. 77-96). In addition, techniques developed for the production of "chimeric antibodies" by splicing the genes from antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity may be used (Morrison *et al.* 1984, *Proc. Natl. Acad. Sci.*, 81:6851-6855; Neuberger *et al.* 1984 *Nature* 312:604-608; Takeda *et al.* 1985 *Nature* 31:452-454). Alternatively, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce 4-specific single chain antibodies.

Recombinant human or humanized versions of monoclonal antibodies are a preferred embodiment for human therapeutic applications. Humanized antibodies may be prepared according to procedures in the literature (e.g. Jones *et al.* 1986, *Nature* 321:522-25; Reichman *et al.* 1988 *Nature* 332:323-27; Verhoeven *et al.* 1988, *Science* 239:1534-36). The

recently described "gene conversion metagenesis" strategy for the production of humanized monoclonal antibody may also be employed in the production of humanized antibodies (Carter et al. 1992 Proc. Natl. Acad. Sci. U.S.A. 89:4285-89). Alternatively, techniques for generating the recombinant phase library of random combinations of heavy and light regions may be used to prepare recombinant antibodies (e.g. Huse et al. 1989 Science 246:1275-81).

Antibody fragments which contain the idiotype of the molecule such as $F(ab1)$ and $F(ab2)$ may be generated by known techniques. For example, such fragments include but are not limited to: the $F(ab) E2$ fragment which can be produced by pepsin digestion of the intact antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragment, and the two Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent. Alternatively, Fab expression libraries may be constructed (Huse et al. 1989, Science 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragment with the desired specificity to a protein.

Adjuvants

"Adjuvant" means a composition comprised of one or more substances that enhances the immunogenicity and efficacy of a vaccine composition. Non-limiting examples of suitable adjuvants include squalane and squalene (or other oils of animal origin); block copolymers; detergents such as Tween®-80; Quil® A, mineral oils such as Drakeol or Marcol, vegetable oils such as peanut oil; *Corynebacterium*-derived adjuvants such as *Corynebacterium parvum*; *Propionibacterium*-derived adjuvants such as *Propionibacterium acne*; *Mycobacterium bovis* (Bacillus Calmetic and Guerin or BCG); interleukins such as interleukin 2 and interleukin-12; monokines such as interleukin 1; tumour necrosis factor; interferons such as gamma interferon; combinations such as saponin-aluminium hydroxide or Quil-A aluminium hydroxide; liposomes; ISCOM adjuvant; mycobacterial cell wall extract; synthetic glycopeptides such as muramyl dipeptides or other derivatives; Avridine; Lipid A; dextran sulfate; DEAE-Dextran or DHAE-Dextran with aluminium phosphate; carboxypolymethylene such as Carbopol® EMA; acrylic copolymer emulsions such as Neocryl A640 (e.g. U.S.

Pat. No. 5,047,238); vaccinia or animal poxvirus proteins; sub-viral particle adjuvants such as cholera toxin, or mixtures thereof.

As used herein, stringent conditions are those that (1) employ low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate/0.1% NaDodSO₄ at 50°C; (2) employ during hybridisation a denaturing agent such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS and 10% dextran sulfate at 42°C in 0.2 x SSC and 0.1% SDS

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As will be understood the present invention includes within its scope DNA vaccination. Further information regarding DNA vaccination may be found in Donnelly et al, Journal of Immunological Methods 176(1994) 145-152, the disclosure of which is incorporated herein by reference.

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Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer, or group of elements or integers.

25 Preparation of the *P. gingivalis* library for sequencing.

To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method described by Mamur J. (J. Mol. Biol. 3, 208-218, 1961). Cloning of DNA fragments was performed essentially as described by Fleischmann *et al.*, (Science; 269, 496-512, 1995)(2). Briefly, purified genomic DNA from *P. gingivalis* was nebulized to fragment the DNA and was treated with Bal31 nuclease to create blunt ends then run twice through preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from the gel and the DNA recovered. This DNA was then ligated to the vector pUC18 (*Sma*I digested and dephosphorylated; Pharmacia) and electrophoresed through a 1%

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preparative agarose gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the ligated DNA and plated out on SOB agar antibiotic diffusion plates containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 96 well gridded array and stored at -20C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Applied Biosystems).

The sequences obtained are set out below. The relationship between these sequences is set out in Table 1. The initiation codon was calculated using a combination of sequence homology alignment (FASTA), signal sequence prediction (PSORT, SignalP) or ORF prediction (GeneMark).

Table 1: Reference table indicating the relationships of each sequence ID to the selected proteins.

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG1	1	265	122	386
PG10	2	266	123	387
PG100	3	267	124	388
PG101	4	268		
PG102	5	269	125, 126	389, 390
PG104	6	270	127	391
PG105	7	271	128	392
PG106	8	272	129	393
PG107	9	273	130, 131, 132	394, 395, 396
PG108	10	274	133	397
PG109	11	275	134, 135	398, 399
PG11	12	276	136	400
PG110	13	277	137	401
PG111	14	278		
PG112	15	279	138, 139	402, 403
PG113	16	280	140	404
PG114	17	281	141	405
PG115	18	282	142	406
PG116	19	283	143	407
PG117	20	284	144	408
PG118	21	285	145	409
PG119	22	286	146	410
PG12	23	287	147	411
PG120	24	288	148	412

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG121	25	289	149	413
PG122	26	290	150	414
PG123	27	291	151	415
PG124	28	292	152	416
PG125	29	293	153	417
PG126	30	294	154	418
PG13	31	295	155	419
PG14	32	296	156	420
PG15	33	297	157	421
PG16	34	298	158	422
PG18	35	299	159	423
PG2	36	300	160, 161	424, 425
PG21	37	301	162	426
PG22	38	302	163	427
PG23	39	303	164	428
PG24	40	304	165	429
PG25	41	305	166	430
PG27	42	306	167	431
PG28	43	307	168	432
PG29	44	308	169	433
PG3	45	309	170	434
PG30	46	310	171	435
PG31	47	311	172	436
PG32	48	312	173	437
PG33	49	313	174	438
PG34	50	314	175, 176	439, 440
PG35	51	315	177	441
PG36	52	316	178	442
PG37	53	317	179, 180	443, 444
PG38	54	318	181	445

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG39	55	319	182	446
PG4	56	320	183	447
PG40	57	321	184	448
PG41	58	322	185	449
PG42	59	323	186	450
PG43	60	324	187	451
PG44	61	325	188	452
PG45	62	326	189	453
PG46	63	327	190	454
PG47	64	328	191	455
PG48	65	329	192	456
PG49	66	330	193	457
PG5	67	331	194	458
PG50	68	332	195	459
PG51	69	333	196	460
PG52	70	334	197	461
PG53	71	335	198	462
PG54	72	336	199	463
PG55	73	337	200	464
PG56	74	338	201, 202	465, 466
PG57	75	339	203, 204, 205	467, 468, 469
PG58	76	340	206, 207	470, 471
PG59	77	341	208, 209, 210	472, 473, 474
PG6	78	342	211	475
PG60	79	343	212	476
PG61	80	344	213	477
PG62	81	345	214	478
PG63	82	346	215	479
PG64	83	347	216	480
PG65	84	348	217	481

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG66	85	349	218	482
PG67	86	350	219	483
PG68	87	351	220, 221	484, 485
PG69	88	352	222	486
PG7	89	353	223	487
PG70	90	354	224	488
PG71	91	355	225	489
PG72	92	356	226	490
PG73	93	357	227	491
PG74	94	358	228	492
PG75	95	359	229	493
PG76	96	360	230	494
PG77	97	361	231	495
PG78	98	362	232	496
PG79	99	363	233	497
PG8	100	364	234, 235, 236, 237	498, 499, 500, 501
PG80	101	365	238	502
PG81	102	366	102	366
PG82	103	367	239	503
PG83	104	368	240	504
PG84	105	369	241, 242	505, 506
PG85	106	370	243	507
PG86	107	371	244, 245	508, 509
PG87	108	372	246	510
PG88	109	373	247, 248, 249	511, 512, 513
PG89	110	374	250	514
PG9	111	375	251, 252, 253	515, 516, 517
PG90	112	376	254, 255	518, 519
PG91	113	377	256	520

Protein name	DNA sequence of complete ORF	Amino acid sequence of complete ORF	DNA sequence of protein	Amino acid sequence of protein
PG92	114	378	257	521
PG93	115	379	258	522
PG94	116	380	259	523
PG95	117	381	260	524
PG96	118	382	261	525
PG97	119	383	262	526
PG98	120	384	263	527
PG99	121	385	264	528
PG127	529	531	530	532

DNA sequence analysis

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DNA files in FASTA format were converted to GCG format files and imported into a database. The DNA files were translated into amino acid files using the program Flip obtained from ANGIS(Australian Genomic Information Service, University of Sydney, Australia). A series of

10 bioinformatic analyses were performed on the proteins in order to select potential vaccine candidates. The programs used were FASTA homology searching (1), PSORT (2,3), SignalP (4), TopPred (5), and GeneMark (6). The proteins and their bioinformatic results were stored in the custom written database for search and retrieval of proteins with the desired characteristics

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The FASTA homology results for these proteins were then examined for any alignment with a protein suggesting surface location or vaccine efficacy. All proteins were searched for homology against a non-redundant bacterial protein database compiled by ANGIS using the FASTA algorithm. The settings used for the FASTA searches were Ktup = 2, gap creation

20 penalty = -12, gap extension penalty = -2, width for deriving alignment in opt = 16 and the Blosum 50 scoring matrix. Individual FASTA search results were examined for significant homology by statistical probability and amino acid alignments. The results are set out in Table 2.

Protein files were then trimmed to the first, second, third, fourth and fifth methionine residues using a protein trimming program (ANGIS). The trimmed proteins were then subjected to PSORT analysis for the detection of signal sequences and the prediction of cell location. Proteins exhibiting a PSORT probability of outer membrane >0.8 were considered to indicate surface localisation. A second signal sequence detection program SignalP was also performed and, in certain instances, this program detected signals not identified with PSORT. All proteins identified by other methods were also analysed by PSORT and SignalP. Previously, the C-terminal amino acid of bacterial outer membrane proteins has been shown to be important for the assembly of the protein on the outer membrane (7). A typical structure definition for outer membrane proteins has been determined as the presence of a signal sequence at the N-terminus and a tyrosine or phenylalanine at the C-terminus. A number of the selected proteins exhibit this characteristic structure. The program TopPred was used to determine the presence and number of membrane spanning domains (MSDs) and the presence of such sequences indicates a preference to be attached to membranes such as the outer membrane. The results of PSORT, SignalP and TopPred analyses with the C-terminal amino acids of the selected proteins are set out in Table 3.

The 70 amino acids from the C-terminus of a number of *P. gingivalis* outer membrane proteins share 50-100% protein sequence identity. These proteins included RGP1, RGP2, KGP, HagA, HagC, HagD, prtH and prtT. This conserved motif may be involved in the attachment or sorting of proteins to the outer membrane. The protein data set was searched using FASTA homology as described above and a number of novel proteins were identified which demonstrate similar motifs at their C-termini. The results are listed in Table 4

The TonBIII box is a 30 amino acid motif present within TonB outer membrane receptors in a wide variety of bacteria. The TonBIII box of *P. gingivalis* (8) was used to search the protein data set for homology by FASTA as described above. Those proteins demonstrating significant homology are listed in Table 5.

Table 2: FASTA protein homology results of complete ORFs against a non-redundant protein database.

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG1	46kD outer membrane protein, <i>Actinobacillus pleuropneumoniae</i>	U24492	449aa	451aa	32	454aa	1.40E-42
PG2	Outer membrane protein (susC), <i>Bacteroides thetaiotaomicron</i>	U49338	1038aa	1017aa, 1014aa	28	1099aa	4.60E-32
PG3	Outer membrane porin F adhesin, <i>Pseudomonas fluorescens</i>	U19743	317aa	223aa	35	187aa	1.10E-10
PG4	Outer membrane protein A, <i>Escherichia fergusonii</i>	M63352	243aa	672aa	48	88aa	4.10E-10
PG5	Adhesin protein (AdcA), <i>Streptococcus pneumoniae</i>	Z71552	423aa	315aa	25	279aa	9.40E-15
PG6	Hemolysin A (phvA), <i>Prevotella melaninogenica</i>	U27587	332aa	324aa	60	306aa	3.00E-74
PG7	Hemolysin (tlvC), <i>Serpulina hyodysenteriae</i>	X73141	268aa	404aa	33	268aa	1.40E-24
PG8	Heme uptake protein A, <i>Bacteroides fragilis</i>	X97122	431aa	598aa, 550aa, 458aa, 426aa	79	417aa	6.70E-121
PG9	Internalin A (inlA), <i>Lysteria monocytogenes</i>	M67471	744aa	1266aa, 1232aa, 1174aa	38	340aa	7.30E-23

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG10	Macrophage infectivity potentiator (MIP), <i>Legionella oakridgensis</i> .	U92214	234aa	195aa	50	201aa	4.70E-31
PG11	Haemagglutinin (phg), <i>Prevotella intermedia</i>	AF017417	309aa	313aa	44	309aa	3.80E-44
PG12	Outer membrane lipoprotein, <i>Haemophilus influenzae</i>	M88502	274aa	271aa	36	254aa	9.80E-27
PG13	Ferric receptor (cfrA), <i>Campylobacter coli</i>	U80812	696aa	757aa	24	625aa	1.20E-18
PG14	38kD antigen, <i>Helicobacter pylori</i>	U88610	329aa	331aa	37	326aa	1.10E-35
PG15	Outer membrane protein, <i>Erwinia amylovora</i>	X77921	377aa	287aa	30	253aa	5.40E-08
PG16	C terminal protease, <i>Bartonella bacilliformis</i>	L37094	434aa	589aa	36	357aa	3.00E-35
PG18	Protein-export membrane protein (secD), <i>Helicobacter pylori</i>	AEO06652	503aa	981aa	32	611aa	1.10E-36
PG21	Surface antigen gene, <i>Methanosarcina mazei</i>	X84710	783aa	821aa	37	331aa	6.20E-33
PG22	Alpha-hemolysin gene, <i>Aeromonas hydrophila</i>	L36482	85aa	106aa	57	87aa	2.60E-14
PG23	clpA/clpB protease, <i>Bacillus subtilis</i>	D26185	810aa	859aa	45	855aa	7.10E-122
PG24	Putative hemolysin, <i>Streptococcus mutans</i>	AF051356	445aa	417aa	29	432aa	1.80E-29

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG25	Cysteine protease, <i>Porphyromonas gingivalis</i>	U54691	1723aa	293aa	42	142aa	1.10E-12
PG27	TonB linked adhesin, <i>Porphyromonas gingivalis</i>	Y07818	1097aa	312aa	45	360aa	3.20E-41
PG28	Cysteine protease / hemagglutinin, <i>Porphyromonas gingivalis</i>	S75942	886aa	843aa	35	838aa	7.00E-90
PG30	Putative NlpD lipoprotein, <i>Aquifex aeolicus</i>	AE000754	187aa	337aa	42	142aa	1.80E-12
PG31	Hemolysin (HlyC), <i>Serpulina hyodysenteriae</i>	X73141	141aa	151aa	31	123aa	1.80E-07
PG32	Major outer membrane protein (oprF), <i>Pseudomonas aeruginosa</i>	M94078	350aa	391aa	26	382aa	3.40E-07
PG33	Major outer membrane protein (oprF), <i>Pseudomonas fluorescens</i>	L21200	317aa	385aa	32	163aa	2.30E-06
PG34	Putative membrane protein, <i>Rhodobacter capsulatus</i>	Q07396	193aa	190aa	46	190aa	2.20E-38
PG35	Colicin 1 receptor, <i>Escherichia coli</i>	J04229	863aa	833aa	25	590aa	2.40E-10
PG36	Outer membrane antigen (oma87), <i>Pasteurella multocida</i>	U60439	789aa	891aa	21	894aa	3.70E-10
PG37	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	M34854	164aa	174aa, 170aa	27	168aa	4.30E-07

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG38	Cationic outer membrane protein (ompH), <i>Yersinia enterocolitica</i>	M34854	164aa	163aa	23	180aa	5.90E-05
PG39	Outer membrane protein (susC) <i>Bacteroides thetaiotaomicron</i>	L49338	1038aa	827aa	24	347aa	1.50E-06
PG40	Heme receptor (Hut A), <i>Vibrio cholera</i>	Q56644	693aa	772aa	23	722aa	4.90E-09
PG41	Outer membrane protein (tolC), <i>Escherichia coli</i>	X54049	495aa	482aa	22	436aa	4.60E-09
PG42	Neuraminidase, <i>Micromonospora viridifaciens</i>	D01045	847aa	492aa	32	375aa	2.10E-22
PG43	Immunoreactive outer membrane protein (omp28), <i>Brucella melitensis</i>	U30815	250aa	245aa	24	178aa	0.0015
PG44	Macrophage infectivity potentiator, <i>Legionella israelensis</i>	U92208	242aa	275aa	35	218aa	9.10E-18
PG45	Outer membrane protein, <i>Neisseria meningitidis</i>	AF021245	787aa	775aa	21	899aa	0.0034
PG46	Outer membrane protein 85, <i>Neisseria gonorrhoeae</i>	U031959	792aa	774aa	31	117aa	0.00098
PG47	Outer membrane protein (susC) <i>Bacteroides thetaiotaomicron</i>	L49338	1038aa	867aa	20	982aa	1.00E-03

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG48	Immunoglobulin binding surface protein (sir22), <i>Streptococcus pyogenes</i>	X75750	365aa	431aa	25	269aa	5.20E-05
PG49	Fimbriin (orf2), <i>Porphyromonas gingivalis</i>	D42067	453aa	333aa	23	298aa	0.062
PG50	Outer membrane protein (susC) <i>Bacteroides thetaiotaomicron</i>	L49338	1038aa	948aa	26	579aa	1.80E-11
PG51	PGaA antigen, <i>Porphyromonas gingivalis</i>	X85938	202aa	202aa	54	126aa	1.20E-25
PG52	Alkaline protease secretion apparatus (aprF) <i>Pseudomonas aeruginosa</i>	X84558	481aa	455aa	21	427aa	3.50E-08
PG53	Protein export protein (tolC), <i>Salmonella enteritidis</i>	U25178	491aa	444aa	23	436aa	6.20E-11
PG54	Protease I, <i>Achromobacter lyticus</i>	J5128	853aa	940aa	24	695aa	1.50E-22
PG55	Fimbriin (orf3), <i>Porphyromonas gingivalis</i>	D42067	670aa	670aa	43	888aa	4.90E-108
PG56	Cysteine protease <i>Porphyromonas gingivalis</i>	U88488	384aa	1282aa, 1274aa	25	212aa	0.00012
PG57	Cysteine protease, <i>Porphyromonas gingivalis</i>	U68468	1358aa	924aa, 922aa, 921aa	31	742aa	1.40E-23
PG60	Outer membrane protein 11, <i>Helicobacter pylori</i>	AED00562	188aa	547aa	25	183aa	2.20E+00
PG61	Ferric pseudobactin M114 receptor protein (pbuA), <i>Pseudomonas</i> sp.	X73412	826aa	749aa	22	585aa	1.00E-05

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG66	Attachment and invasion protein (ail), <i>Salmonella typhimurium</i>	AF007380	185aa	208aa	21	140aa	1.90E+00
PG68	Serum opacity factor, <i>Streptococcus pyogenes</i>	U02290	1025aa	1225aa, 1224aa	24	178aa	2.10E-01
PG69	Vacuolating cytotoxin (vacA), <i>Helicobacter pylori</i>	U83281	180aa	425aa	32	111aa	1.20E+00
PG70	Outer membrane protein, <i>Neisseria gonorrhoea</i>	U52069	174aa	268aa	22	153aa	6.90E+00
PG71	Gliding motility protein (gldA), <i>Flavobacterium johnsoniae</i>	AF007381	578aa	834aa	23	572aa	3.90E-25
PG75	Class 3 outer membrane porin (porB), <i>Neisseria meningitidis</i>	U07191	332aa	391aa	23	239aa	4.60E-01
PG81	Outer membrane protein (ompA), <i>Shigella dysenteriae</i>	V01344	351aa	>235aa	28	188aa	3.10E-01
PG82	Outer membrane protein (alkL), <i>Pseudomonas cleovorans</i>	X85936	230aa	434aa	26	138aa	2.80E+00
PG83	Gliding motility protein (gldA), <i>Flavobacterium johnsoniae</i>	AF007381	578aa	928aa	21	638aa	6.50E-09
PG87	Hypothetical protein, <i>Mycobacterium tuberculosis</i>	AL021942	877aa	781aa	29	794aa	2.20E-34

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG89	NADH-ubiquinone oxidoreductase, <i>Helicobacter pylori</i>	AE000631	512aa	259aa	24	186aa	3.90E-01
PG91	Neuraminidase (nanH), <i>Bacteroides fragilis</i>	D28493	544aa	540aa	24	251aa	1.60E-00
PG92	Hypothetical protein, <i>Mycobacterium tuberculosis</i>	AL021942	877aa	771aa	29	770aa	8.00E-30
PG93	Cytoadherence protein P1, <i>Mycoplasma pneumoniae</i>	X07191	219aa	778aa	41	63aa	6.90E-01
PG94	Arginyl endopeptidase, <i>Porphyromonas gingivalis</i>	D28470	991aa	1157aa	24	328aa	7.80E-08
PG95	Sensor protein (EVGS), <i>Escherichia coli</i>	D14008	1197aa	961aa	28	511aa	2.60E-17
PG105	Plasma cell membrane glycoprotein, Human	P22413	873aa	449aa	34	404aa	5.80E-33
PG106	Hypothetical secreted protein, <i>Helicobacter pylori</i>	O24951	242aa	248aa	30	252aa	7.80E-22
PG107	Cell division ATP binding protein, <i>Mycobacterium leprae</i>	O32883	228aa	246aa, 241aa, 232aa	46	193aa	1.20E-26
PG108	ABC transporter, <i>Archaeoglobus fulgidis</i>	O29244	228aa	218aa	51	218aa	3.80E-41
PG109	Proteinase IV, <i>Escherichia coli</i>	F64936	618aa	595aa, 589aa	38	597aa	1.10E-57
PG110	Preprotein translocase, <i>Staphylococcus aureus</i>	O06446	843aa	523aa	43	521aa	8.00E-71
PG111	ABC transporter, <i>Synechocystis</i> sp.	P73758	574aa	> 720aa	40	579aa	1.70E-73
PG112	Glycosyl transferase, <i>Erwinia amylovora</i>	Q46834	351aa	375aa, 362aa	31	363aa	1.60E-32

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results
					Identity % Overlap E value
PG113	Heat shock protein (dnaK), <i>Treponema pallidum</i>	AE001203	835aa	640aa	62 644aa 9.10E-138
PG114	Dihydrolipamide dehydrogenase, <i>Clostridium magnum</i>	Q59299	578aa	449aa	37 450aa 3.80E-54
PG115	Zinc protease, <i>Escherichia coli</i>	P31828	931aa	941aa	27 890aa 8.60E-57
PG116	Heat shock protein (HSPG), <i>Escherichia coli</i>	P10413	624aa	684aa	32 627aa 4.60E-48
PG117	Transcriptional regulator, <i>Aquifex aeolicus</i>	O66591	506aa	464aa	39 389aa 2.40E-49
PG118	ABC transporter, <i>Bacillus subtilis</i>	H70019	281aa	250aa	59 251aa 1.50E-60
PG119	ATP-dependent protease, <i>Aquifex aeolicus</i>	O66827	444aa	461aa	46 458aa 1.80E-77
PG120	Nitrogen assimilation regulatory protein, <i>Bradyrhizobium</i> sp.	P10576	480aa	457aa	49 242aa 3.80E-45
PG121	Cobalamin synthesis protein, <i>Bacillus megaterium</i>	E1331323	367aa	602aa	36 324aa 9.20E-37
PG122	Outer membrane integrity (tolA), <i>Haemophilus influenzae</i>	P71397	819aa	443aa	37 441aa 1.90E-54
PG123	Fimbriin, <i>Porphyromonas gingivalis</i>	D1034032	490aa	479aa	32 480aa 7.30E-48
PG124	Heat shock protein (dnaJ), <i>Leptospira interrogans</i>	AF007813	369aa	383aa	46 358aa 2.30E-57

Protein name	Homology description	Genbank accession number	Length of homolog	Length of <i>P. gingivalis</i> protein	FASTA homology results		
					Identity %	Overlap	E value
PG125	Cobalamin biosynthesis protein(CBIK), <i>Salmonella typhimurium</i>	Q06592	264aa	293aa	37	259aa	3.70E-26
PG126	ABC-type permease, <i>Pseudomonas aeruginosa</i>	O88878	328aa	356aa	33	333aa	1.30E-30
PG127	Endonuclease excision repair protein (uvrB), <i>Pseudomonas aeruginosa</i>	X83486	670aa	678aa	56	675aa	1.10E-134

32

Table 3: Results of PSORT, SignalP and TopPred analysis of the proteins. The signal present column indicates the presence of a signal sequence detected with either PSORT or SignalP. The terms in parentheses indicates the type of signal sequence as determined by PSORT. The cell location & probability values are generated by PSORT and represent the probability of the protein being in the cell compartments outer membrane (OM), inner membrane (IM), periplasmic space (PC) or cytoplasm (C). The number of transmembrane domains (TMDs) was determined by TopPred and does not include uncleavable signal sequences.

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PC1	386	451aa	Y	1	24	34	0	0	0	0.22	N	0
PG2	424	1017aa	Y	1	20	20	0.94	0	0.33	0	F	3
PG2	425	1014aa	Y	2	17	17	0.94	0	0.29	0	F	3
PG3	434	223aa	Y (lipoprotein)	1	-	18	0.79	0.78	0	0	K	3
PG4	447	672aa	Y (lipoprotein)	1	22	22	0.79	0.7	0	0	R	0
PG5	458	315aa	Y	1	40	35	0	0.25	0	0	R	0
PG6	475	324aa	N	1	-	-	0	0	0	0.2	S	1
PG7	487	404aa	N	1	7	-	0	0.42	0	0	E	3
PG8	498	598aa	N	1	-	-	0	0	0	0.22	N	0
PC8	499	550aa	N	2	-	-	0	0	0	0.25	N	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG8	500	458aa	N	3	-	-	0	0	0	0.34	N	0
PG8	501	426aa	N	4	-	-	0	0	0	0.24	N	0
PG9	515	1260aa	N	1	7	-	0	0	0	0.22	E	1
PG9	516	1222aa	N	2	-	-	0	0	0	0.39	E	1
PG9	517	1174aa	N	3	-	-	0	0	0	0.47	E	1
PG10	387	185aa	N	1	-	-	0	0	0	0.11	K	0
PG11	400	313aa	Y	1	22	26	0.24	0	0.93	0	R	1
PG12	411	271aa	Y (lipoprotein)	3	27	29	0.79	0.7	0	0	R	0
PG13	419	757aa	Y	1	23	25	0.94	0	0.29	0	N	0
PG14	420	331aa	Y (uncleavable)	1	35	26	0	0.58	0	0	K	1
PG15	421	267aa	Y	2	24	18	0	0.11	0	0	K	1
PG16	422	569aa	Y (lipoprotein)	1	24	18	0.79	0.7	0	0	G	0
PG18	423	361aa	Y	1	30	-	0	0.58	0	0	K	11
PG21	426	821aa	Y	2	24	27	0.34	0	0.37	0	G	1
PG22	427	108aa	Y (uncleavable)	1	41	41	0	0.29	0	0	P	0
PG23	428	359aa	N	1	-	-	0	0.12	0	0	A	1

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG24	429	417aa	Y	1	19	19	0	0.44	0	0	N	3
PG25	430	293aa	Y	1	27	28	0.2	0	0.82	0	R	0
PG27	431	312aa	N	1	-	-	0	0	0	0.28	Q	1
PG28	432	843aa	Y	1	21	21	0.93	0	0.24	0	H	1
PG29	433	290aa	Y	1	18	18	0.28	0	0.94	0	K	1
PG30	435	337aa	Y	1	21	21	0.24	0	0.4	0	K	0
PG31	438	151aa	N	1	-	-	0	0	0	0.3	T	0
PG32	437	391aa	Y	1	20	20	0.62	0	0.13	0	K	0
PG33	438	365aa	Y	1	26	26	0.81	0	0.31	0	E	1
PG34	439	190aa	Y	1	-	13	0	0.5	0	0	A	5
PG34	440	186aa	Y (uncleavable)	2	-	47	0	0.5	0	0	A	4
PG35	441	833aa	Y	1	22	22	0.94	0	0.37	0	F	1
PG36	442	891aa	Y (uncleavable)	1	-	40	0	0.31	0	0	F	2
PG37	443	174aa	Y (uncleavable)	1	28	24	0	0.35	0	0	K	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG37	444	170aa	Y (uncleavable)	2	24	20	0	0.35	0	0	K	0
PG38	445	183aa	Y	1	18	18	0.21	0	0.93	0	K	1
PG39	446	827aa	Y	1	36	38	0.93	0	0.25	0	P	3
PG40	448	772aa	Y	2	19	19	0.94	0	0.32	0	F	4
PG41	449	482aa	Y	2	27	27	0.25	0	0.54	0	Q	2
PG42	450	482aa	Y	5	30	-	0	0	0.00	0.13	Q	2
PG43	451	245aa	Y (uncleavable)	2	28	22	0	0.38	0	0	K	1
PG44	452	276aa	Y	1	19	24	0.15	0	0.89	0	K	0
PG45	453	775aa	Y (lipoprotein)	1	19	23	0.79	0.7	0	0	P	4
PG46	454	774aa	Y	1	27	27	0.73	0	0.22	0	P	2
PG47	455	887aa	Y	1	24	24	0.94	0	0.38	0	P	2
PG48	456	431aa	Y	1	24	24	0	0.1	0	0	R	1
PG49	457	333aa	Y (uncleavable)	1	24	18	0	0.12	0	0	I	0
PG50	459	948aa	Y	1	21	21	0.94	0	0.34	0	F	3
PG51	460	202aa	Y	1	28	25	0.2	0	0.61	0	S	0
PG52	461	455aa	Y (uncleavable)	1	23	21	0	0.18	0	0	P	1

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG53	462	444aa	Y	1	14	17	0.36	0	0.22	0	D	2
PG54	463	940aa	Y	1	27	20	0.86	0	0.25	0	Q	5
PG55	464	670aa	Y (lipoprotein)	1	23	23	0.79	0.7	0	0	K	2
PG56	465	1282aa	Y (uncleavable)	1	-	21	0	0.04	0	0	K	4
PG56	466	1274aa	N	2	-	-	0	0	0	0.27	K	5
PG57	467	925aa	Y	1	28	24	0.53	0	0.2	0	P	3
PG57	468	922aa	Y	2	25	21	0.53	0	0.2	0	P	3
PG57	469	921aa	Y	3	24	20	0.53	0	0.2	0	P	3
PG58	470	593aa	Y	1	24	24	0.82	0	0.19	0	P	1
PG58	471	589aa	Y	2	20	20	0.82	0	0.19	0	P	1
PG59	472	348aa	Y	1	37	-	0	0.18	0	0	P	1
PG59	473	345aa	Y	2	36	56	0.92	0	0.15	0	P	1
PG59	474	330aa	Y	3	21	41	0.92	0	0.25	0	P	1
PG80	476	547aa	Y	1	28	28	0.93	0	0.25	0	P	0
PG81	477	749aa	Y	2	21	21	0.94	0	0.29	0	P	3
PG82	478	494aa	Y	1	21	21	0.93	0	0.24	0	P	2

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG63	479	294aa	Y	1	20	20	0.93	0	0.24	0	P	1
PG64	480	204aa	Y	1	20	20	0.83	0	0.19	0	P	1
PG65	481	243aa	Y	1	18	18	0.93	0	0.25	0	F	1
PG66	482	206aa	Y	1	21	21	0.94	0	0.3	0	F	1
PG67	483	950aa	Y	1	28	36	0.93	0	0.27	0	Y	4
PG68	484	1226aa	Y	1	25	25	0.91	0	0.31	0	Y	0
PG68	485	1225aa	Y	2	24	24	0.91	0	0.31	0	Y	0
PG68	486	425aa	Y	1	29	29	0.93	0	0.21	0	P	1
PG70	488	260aa	Y	1	18	24	0.93	0	0.24	0	P	0
PG71	489	334aa	Y	2	20	20	0.94	0	0.31	0	N	2
PG72	490	399aa	Y	1	27	27	0.94	0	0.32	0	H	2
PG73	491	382aa	Y	2	20	20	0.94	0	0.3	0	L	1
PG74	492	222aa	Y	1	24	24	0.94	0	0.32	0	L	0
PG75	493	391aa	Y	1	26	26	0.94	0	0.3	0	H	1
PG76	494	446aa	Y	1	21	22	0.94	0	0.32	0	V	3
PG77	495	308aa	Y	2	28	28	0.94	0	0.38	0	K	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG78	496	314aa	Y	1	23	23	0.94	0	0.29	0	D	0
PG79	497	285aa	Y	1	-	32	0.93	0	0.26	0	G	2
PG80	502	240aa	Y	1	19	19	0.93	0	0.22	0	N	2
PG81	366	>235aa	Y	1	28	20	0.93	0	0.21	0	Q	1
PG82	503	434aa	Y	1	30	24	0.93	0	0.2	0	N	3
PG83	504	828aa	Y	1	23	57	0.93	0	0.21	0	S	1
PG84	505	400aa	Y	1	25	25	0.93	0	0.25	0	N	1
PG84	506	398aa	Y	2	23	23	0.93	0	0.25	0	N	1
PG85	507	581aa	Y	1	20	20	0.93	0	0.46	0	L	2
PG86	508	239aa	Y	1	44	-	0	0	0	0.12	H	0
PG88	509	211aa	Y	2	16	46	0.91	0	0.03	0	H	0
PG87	510	781aa	Y	1	26	47	0.89	0	0.21	0	N	2
PG88	511	271aa	Y	2	28	19	0.89	0	0.25	0	P	0
PG88	512	270aa	Y	3	27	18	0.89	0	0.25	0	P	0
PG88	513	267aa	Y	4	24	15	0.89	0	0.23	0	P	0
PG89	514	259aa	Y	2	23	25	0.88	0	0.35	0	N	1

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG90	518	229aa	Y	1	22	21	0.85	0	0.44	0	K	0
PG90	518	228aa	Y	2	21	20	0.85	0	0.44	0	K	0
PG91	520	540aa	Y	1	25	25	0.85	0	0.30	0	E	0
PG92	521	771aa	Y	2	19	19	0.85	0	0.3	0	R	3
PG93	522	776aa	Y	1	25	25	0.85	0	0.37	0	R	4
PG94	523	1157aa	Y	1	23	28	0.8	0	0.25	0	Q	5
PG95	524	981aa	Y (lipoprotein)	1	-	19	0.79	0.87	0	0	V	1
PG96	525	563aa	Y	1	23	23	0.40	0	0.33	0	K	0
PG97	526	437aa	Y	1	23	23	0.32	0	0.65	0	Q	0
PG98	527	318aa	Y (lipoprotein)	1	19	19	0.79	0.7	0	0	L	1
PG99	528	461aa	Y (uncleavable)	1	22	20	0	0	0.3	0	R	0
PG100	388	279aa	Y	1	20	18	0.26	0	0.54	0	I	0
PG101	268	>157aa	N (ORF incomplete)								R	1
PG102	389	562aa	Y	1	29	29	0.19	0	0.4	0	S	3
PG102	390	558aa	Y	2	25	25	0.26	0	0.46	0	S	3
PG104	391	381aa	Y	1	17	17	0.62	0	0.22		R	0

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG105	392	449aa	Y	1	22	19	0.31	0	0.91	0	P	3
PG106	393	246aa	Y	2	41	48	0	0	0	0.02	L	0
PG107	394	246aa	N	1	-	-	0	0	0	0.32	D	1
PG107	395	241aa	N	2	-	-	0	0	0	0.3	D	1
PG107	396	232aa	N	3	-	-	0	0	0	0.21	D	1
PG108	397	219aa	N	1	-	-	0	0	0	0.19	R	1
PG109	398	595aa	Y	1	35	37	0.26	0	0.93	0	Y	3
PG109	399	589aa	Y	2	29	31	0.27	0	0.93	0	Y	3
PG110	401	>523aa	N	1	-	-	0	0	0	0.38	Incomplete	0
PG111	278	>720aa	N (ORF incomplete)	-	-	-	-	-	-	-	G	1
PG112	402	375aa	Y	1	-	43	0	0.12	0	0	N	1
PG112	403	362aa	Y	2	-	30	0	0	0.12	0	N	1
PG113	404	640aa	N	1	-	-	0	0	0	0.25	K	1
PG114	405	449aa	N	1	-	-	0	0.12	0	0	G	4
PG115	406	941aa	Y	1	23	22	0.13	0	0.92	0	Q	2
PG116	407	984aa	N	1	-	-	0	0.12	0	0	L	2

Protein name	Protein seqID number	Protein Length	Signal Present	Methionine in ORF	SignalP cleavage site	PSORT cleavage site	Cell Location & probability				C-terminal Amino Acid	Number of TMD's
							OM	IM	PS	C		
PG117	408	464aa	N	1	-	-	0	0.19	0	0	L	1
PG118	409	250aa	N	1	-	-	0	0	0	0.27	E	1
PG119	410	481aa	N	1	-	-	0	0.28	0	0	E	2
PG120	412	457aa	N	1	-	-	0	0	0	0.21	E	0
PG121	413	602aa	N	1	-	-	0	0	0	0.31	E	3
PG122	414	443aa	N	1	-	-	0	0	0	0.14	Q	4
PG123	415	478aa	Y	2	22	22	0.28	0	0.94	0	K	0
PG124	416	383aa	N	1	-	-	0	0	0	0.29	D	2
PG125	417	293aa	Y	1	23	15	0.18	0	0.93	0	R	1
PG126	418	356aa	N	1	-	-	0	0.52	0	0	D	9
PG127	532	678aa	N	1	-	-	0	0	0	0.28	A	2

Table 4: Percentage identity and percentage similarity of various proteins with the 70 amino acids from the C-terminal of the *P. gingivalis* arginine protease 1 (RGP1), arginine protease 2 (RGP2), and the cysteine protease/hemagglutinin (prtT).

5

Protein name	Percent identity			Percent similarity		
	RGP1	RGP2	prtT	RGP1	RGP2	prtT
PG21	17	29	21	40	57	49
PG25	43	41	9	64	73	14
PG27	41	33	7	73	74	11
PG28	21	26	34	49	57	74
PG54	19	13	16	40	43	33
PG57	11	14	19	20	24	34
PG91	31	21	39	57	53	74
PG96	0	13	20	0	24	43
PG97	10	26	33	14	47	61
PG98	16	20	0	47	54	0
PG99	19	0	26	41	0	54
PG100	20	21	24	39	57	41
PG101	11	16	27	17	39	60
PG102	27	20	31	50	61	61
PG104	16	23	26	46	44	49

Table 5: Percentage identity and percentage similarity of various proteins with the TonBIII box of *P. gingivalis*.

Protein name	Percent identity	Percent similarity
PG2	46	71
PG13	57	93
PG35	50	96
PG47	39	71
PG50	54	93

Cloning, expression and purification of recombinant *P. gingivalis* genes.

PG1

- 5 Oligonucleotides to the 5' and 3' regions of the deduced protein were used to amplify the gene of interest from a preparation of *P. gingivalis* W50 genomic DNA using the TaqPlus Precision PCR System (Stratagene) and a PTC-100 (MJ Research) thermal cycler or similar device. The 5' oligonucleotide primer sequence was GCGCCATATGCTGGCCGAACCGGCC, the 3' oligonucleotide primer sequence was GCGCCTCGAGTCAATTCATTTCCTTATAGAG. The PCR fragment was purified, digested with Nde I, Xho I restriction enzymes (Promega) and ligated into the corresponding sites of the plasmid pProEx-1 (Gibco-BRL) and transformed into *E. coli* ER1793 cells (a gift from Elizabeth Raleigh, New England Biolabs). A resulting clone expressing the correct insert was selected and induced with or without 0.1mM IPTG (Promega) for expression of the recombinant protein. Expression of the recombinant protein was determined by SDS-PAGE analysis and Western Blot using the one of the rabbit antisera described above or an anti-hexahistidine antibody (Clontech) that detects the hexahistidine tag that was fused to the *P. gingivalis* recombinant protein. PG1 was purified by disruption of the *E. coli* cells by sonication in binding buffer (Novagen) and solubilisation by the addition of sarkosyl (N-Lauroyl sarcosine) to a 1% final concentration. There after the preparation was diluted to 0.1% sarkosyl in binding buffer, bound to a Nickel-nitrilotriacetic acid column (Ni-NTA; Qiagen), after washing bound proteins were eluted with 1M imidazole in elution buffer (Novagen) according to the Qiagen recommendations with 0.1% sarkosyl added to all buffers. Following purification samples were dialysed against 500mM NaCl, 20mM Tris, 0.1% sarkosyl at pH7.4 to remove the imidazole, concentrated as required and stored at 4°C until used. Purity and antigenicity were assessed by SDS-PAGE and Western blot using selected antisera (from those described above) and the protein concentration was determined by the BCA assay (Pierce).
- 10
15
20
25
30

PG2

The methods used for PG2 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGAAAAGAATGACGC, the 3' oligonucleotide primer
 5 sequence was CGCGAGATCTGAAAGACAACCTGAATACC and the PCR product was cloned into pGex-stop RBS(IV) (Patent application WO9619496, JC Cox, SE Edwards, I Frazer and EA Webb. Variants of human papilloma virus antigens) using the BstZ 171 and Bgl II restriction sites. 2% sarkosyl was used to solubilise PG2 and 8M urea was added to the solubilisation buffer
 10 and to all other buffers. Urea was removed from the purified protein by sequential dialysis (4M then 2M then 1M then 0.5M then 0M urea all in 50mM Tris, 500mM NaCl, 0.1% sarkosyl, pH7.4). Purified protein was stored at 4°C until required.

15 PG3

The methods used for PG3 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGTATACATGAAGAAATCAAGTGTAG, the 3' oligonucleotide primer
 20 sequence was GCGCAGATCTCTTCAGCGTACCTTGCTGTG and DNA was amplified with Pfu DNA polymerase (Stratagene). The PCR product was cloned directly into pCR-Blunt and transformed into *E. coli* Top10F'(InVitrogen) before subcloning into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* BL21DE3 (Pharmacia Biotech). The following modifications were
 25 made to the purification of PG3 from the PG1 method. Cells expressing the recombinant protein were disrupted by sonication in binding buffer and the insoluble inclusion bodies concentrated by centrifugation. Inclusion bodies were then solubilised in 6M urea (Sigma) in binding buffer and eluted with 6M urea added to the elution buffer. In some instances 6M guanidine
 30 hydrochloride (Sigma) was used instead of urea for these steps. Urea (or guanidine hydrochloride when it was substituted) was removed from the purified protein by sequential dialysis against reducing levels of urea (3M then 1.5M then 0.5M then 0M urea all in 50mM Tris, 500mM NaCl, 8% glycerol, pH7.4). Purified protein was stored frozen at -80°C until required.
 35 Protein concentration was determined by the Coomassie Plus protein assay (Pierce).

PG4

The methods used for PG4 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CTTCTGTATACTTACAGCGGACATCATAAAATC, the 3' oligonucleotide
5 primer sequence was TTCCAGGAGGGTACCACGCAACTCTTCTTCGAT and DNA was amplified with the Tth XL PCR kit (Perkin Elmer). The PCR product was cloned into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Kpn I restriction sites and transformed into *E. coli* ER1793.

10 PG5

The methods used for PG5 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was TTGCAACATATGATCAGAACGATACTTTCA, the 3' oligonucleotide primer
15 sequence was AGCAATCTCGAGCGGTTTCATGAGCCAAAGC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24 (Novagen) using the Nde I and Xho I restriction sites and transformed into *E. coli* BL21 (Pharmacia Biotech). Removal of urea was not proceeded past 1M urea as the protein was insoluble at lower
20 concentrations of urea. Purified protein was stored at 4°C until required.

PG6

The methods used for PG6 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was TAAACATATGTGCCTCGAACCCATAATTGCTCCG, the 3' oligonucleotide
25 primer sequence was CGTCCGCGGAAGCTTTGATCGGCCATTGCTACT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Nde I and Hind III restriction sites and transformed into *E. coli* BL21.

30 PG8

The methods used for PG8 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGGAGTTCAAGATTGTG, the 3' oligonucleotide primer
35 sequence was CGCGAGATCTGTTTTCTGAAAGCTTTTC and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was

The methods used for PG11 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGTATACATGAGAGCAAACATTTGGCAGATACTTTCCG, the 3' oligonucleotide primer sequence was GCGCAGATCTGCGCAAGCGCAGTATATCGCC and DNA was amplified with Tli DNA polymerase (Promega). The PCR product was cloned into *pCR-Blunt* and transformed into *E. coli* Top10F' before subcloning into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* ER1793. PG11 was purified by solubilisation of *E. coli* cells with 2% sarkosyl in binding buffer (Qiagen) which was diluted to

0.1% sarkosyl in binding buffer, bound to a Nickel-nitrilotriacetic acid column (Ni-NTA; Qiagen), after washing bound proteins were eluted with 1M imidazole (0.7% CHAPS (Sigma) in elution buffer; Qiagen) according to the Qiagen recommendations. Following purification samples were dialysed
5 against 500mM NaCl, 20mM Tris, 0.7% CHAPS, 20% glycerol (Sigma) at pH7.4 to remove the imidazole, concentrated as required and stored at 4°C until used.

PG12

10 The methods used for PG12 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGTATACATGAATAGCAGACATCTGACAATCACAATCATTGCCGG, the 3' oligonucleotide primer sequence was
15 GCGCAGATCTGCTGTTCTGTGAGTGCAGTTGTTTAAGTG and DNA was amplified with Tli DNA polymerase. The PCR product was cloned into pCR-Blunt and transformed into *E. coli* Top10F' cells before subcloning into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* BL21. Purification of the
20 recombinant protein was essentially the same as PG11 except 0.5% DHPC (1,2-Diheptanoyl-*sn*-glycero-3-phosphocholine; Avanti) in 50mM Tris, 50mM NaCl, pH8.0 was used to solubilise the inclusion bodies instead of sarkosyl and the DHPC was diluted to 0.1% before addition to the Ni-NTA and 0.1% DHPC was added to all buffers.

25 PG13

The methods used for PG13 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCCATATGCGGACAAAACTATCTTTTTTGCG, the 3' oligonucleotide
30 primer sequence was GCGCCTCGAGGTTGTTGAATCGAATCGCTATTTGAGC and DNA was amplified with Tli DNA polymerase. The PCR product was cloned the expression plasmid pET24b using the Nde I and Xho I restriction sites and transformed into *E. coli* BL21. Purification of the recombinant protein was essentially the same as PG3 using 6M urea and 1% NOG (n-octyl glucoside;
35 Sigma) was added to the dialysis buffer. Removal of urea was not proceeded

past 2M urea as the protein was insoluble at lower concentrations of urea. Purified protein was stored at 4°C until required.

PG14

- 5 The methods used for PG12 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGGCGCCATGACGGACAACAAACAACGTAATATCG, the 3' oligonucleotide primer sequence was GCGCCTCGAGTTACTTGGCTATGATCACGGACATACCC and DNA was
10 amplified with Tli DNA polymerase. The PCR product was cloned the expression plasmid pProEx-1 using the Ehe I and Xho I restriction sites and transformed into *E. coli* BL21. Purification of the recombinant protein was essentially the same as PG12.

15 PG15

- The methods used for PG15 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CAAAAGTATACTAATAAATATCATTTCTCAA, the 3' oligonucleotide primer sequence was GCTTATGGTACCTTTGGTCTTATCTATTAT and DNA was
20 amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Kpn I restriction sites and transformed into *E. coli* ER1793.

PG22

- 25 The methods used for PG22 were essentially the same as for PG1 with the following exceptions. The 5' oligonucleotide primer sequence was CCCCGGATCCGATGCGACTGATCAAGGC, the 3' oligonucleotide primer sequence was CCCCTCGAGCGGAACGGGGTCATAGCC and DNA was
30 amplified with the TaqPlus Precision PCR System. The PCR product was cloned into the expression plasmid pET24b using the Bam HI and Xho I restriction sites and transformed into *E. coli* BL21DE3. Once PG22 was purified dialysis was performed in the same manner as for PG1 but in the presence of 1M imidazole.

PG24

The methods used for PG24 were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGGTATACATGAATTACCTGTACATAC, the 3' oligonucleotide primer
5 sequence was CGCGGGATCCGTTTCGATTGGTCGTCGATGG and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was digested with Bst Z171 and Bam HI and ligated into the expression plasmid pGex-stop RBS(IV) using the Bst Z171 and Bgl II restriction sites and transformed into *E. coli* ER1793. Due to the low level of expression of PG24
10 purification was not proceeded with except on small scale.

PG24A

A modified version of PG24 was also cloned and expressed. PG24A is the same as PG24 with the predicted N-terminal sequence removed. The
15 methods used for PG24A were essentially the same as for PG3 with the following exceptions. The 5' oligonucleotide primer sequence was CGCGCATATGGAGATTGCTTTCCTTCTTCG, the 3' oligonucleotide primer sequence was CGCGCTCGAGTTAGTTCGATTGGTCGTCG and DNA was amplified with the TaqPlus Precision PCR System. The PCR product was
20 cloned into the expression plasmid pProEx-1 using the Nde I and Xho I restriction sites and transformed into *E. coli* ER1793. Purification of the recombinant protein was essentially the same as PG3 except 8M urea was used to solubilise the inclusion bodies and in the buffers used for the Ni-NTA column purification. Urea was removed by sequential dialysis (4M then 2M,
25 then 1M then 0.5M then 0M urea all in 50mM Tris, 500mM NaCl, 8% glycerol, pH7.4). Purified protein was stored frozen at -80°C until required.

PG29

The methods used for PG29 were essentially the same as for PG3 with
30 the following exceptions. The 5' oligonucleotide primer sequence was GCGCGATATCGCTAGCATGAAAAAGCTATTTCTC, the 3' oligonucleotide primer sequence was GCGCAGATCTCTCGAGTTTGCCATCGGATTGCGGATTG and DNA was amplified with Pfu DNA polymerase being used. The PCR product was
35 cloned into pCR-Blunt (InVitrogen) and transformed into *E. coli* Top10F' before subcloning into the expression plasmid pGex-stop RBS(IV)

using the EcoR V and Bgl II restriction sites and transformed into *E. coli* BL21. 6M urea was used throughout the purification process.

PG30

- 5 The methods used for PG30 were essentially the same as for PG3 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TACGGAATTCGTGACCCCGTCAGAAATGTGCGC, the 3' oligonucleotide primer sequence was
- 10 CTATGCGGCCGCTTTGATCCTCAAGGCTTTGCCCGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates of PG30. 10ml cultures of
- 15 recombinant *E. coli* were grown to an OD of 2.0 (A_{600nm}) in terrific broth and the cells were induced with 0.5mM IPTG and samples taken for analysis at 4 hours post induction. Purification was not done for these studies.

PG31

- 20 The methods used for PG31 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was CGGGGAATTCGCAAAAATCAATTTCTATGCTGAA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTGTATGCAATAGGGAAAGCTCCGA and DNA was amplified with the Tth XL PCR kit. The PCR product was
- 25 cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG32

- 30 The methods used for PG32 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGCAGAATTCCAGGAGAATACTGTACCGGCAACG, the 3'
- 35 oligonucleotide primer sequence was CTATGCGGCCGCTTGGAGCGAACGATTACAACAC and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
5 for these studies.

PG33

The methods used for PG33 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein.
10

The 5' oligonucleotide primer sequence was TGCAGAATTCCAAGAAGCTACTACACAGAACAAA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTCCGCTGCAGTCATTACTACAA and DNA was amplified with the Tth XL PCR kit. The PCR product was
15 cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

20 PG35

The methods used for PG35 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGAATTCATGAAACAATAACATTATCAGC, the 3' oligonucleotide primer sequence was GCGTGCGGCCGCGAAATTGATCTTTGTACCGACGA
25 and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

30

PG36

The methods used for PG36 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was AAAGGAATTCTACAAAAAGATTATTGCCGTAGCA, the 3' oligonucleotide
35 primer sequence was CTATGCGGCCGCGAACTCCTGTCCGAGCACAAAGT and DNA was amplified with the Tth XL PCR kit. The PCR product was

cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

5

PG37

The methods used for PG37 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was TGGCGAATTCAAACGGTTTTTGGATTTTGATCGGC, the 3' oligonucleotide
10 primer sequence was CTATGCGGCCCGCCTTGCTAAAGCCCATCTTGCTCAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates.
15 Purification was not done for these studies.

PG38

The methods used for PG38 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was
20 removed from the recombinant protein. The 5' oligonucleotide primer sequence was CCTCGAATTCCAAAAGGTGGCAGTGGTAAACACT, the 3' oligonucleotide primer sequence was CTATGCGGCCCGCCTTGATTCCGAGTTTCGCTTTTAC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the
25 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG39

The methods used for PG39 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
30 sequence was AGCTGGATCCCAAGGCGTCAGGGTATCGGGCTAT, the 3' oligonucleotide primer sequence was CTATGCGGCCCGCAATTTCGACGAGGAGACGCAGGT and DNA was

The methods used for PG42 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was GTTTGAATTCGCAAATAATACTCTTTTGGCGAAG, the 3' oligonucleotide

primer sequence was

GAGTGCGGCCGCTTTGCCGGACATCGAAGAGATCGTC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG43

The methods used for PG43 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was GCGCGAATTCAAAAAAGAAAAACTTTGGATTGCG, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTCAAAGCGAAAGAAGCCTTAAC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG44

The methods used for PG44 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was AGCCGAATTCTGTAAGAAAAATGCTGACACTACC, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTTTCCCGGGCTTGATCCCGAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG45

The methods used for PG45 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer

sequence was GACAGGATCCTGCTCCACCACAAAGAATCTGCCG, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGGGATAGCCGACAGCCAAAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

10 PG46

The methods used for PG46 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CTCGGAATTCCGTTATGTGCCGGACGGTAGCAGA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGGATAGCCTACTGCAATGT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG47

The methods used for PG47 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGCCGAATTCCAAACAGTGGTGACCGGTAAGGTGATCGATTTCAGAA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGTTTACACGAATACCGGTAGACCAAGTGCGGCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

The methods used for PG50 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GCTGGGATCCGCGACAGACACTGAGTTCAAGTAC, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAACTTCACTACCAAGCCCATGT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG51

5 The methods used for PG51 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TCTTGAATTTCGCGCAAAGTCTTTTCAGCACCGAA, the 3' oligonucleotide primer sequence was
10 CTATGCGGCCGCACTTTTTCGTGGGATCACTCTCTT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
15 for these studies.

PG52

 The methods used for PG52 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was
20 AGAAGAATTCAAACGGACAATCCTCCTGACGGCA, the 3' oligonucleotide primer sequence was CTATGCGGCCGCGAAGTCTTTGCCCTGATAGAAATC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies
25 and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG53

 The methods used for PG53 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCTGAATTTCGCGAATCCCCTTACGGGCCAATCG, the 3' oligonucleotide primer sequence was
30 CTATGCGGCCGCGCTCCGAAAGGCAGCCGTAATAGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
35 expression plasmid pET24a using the Eco RI and Not I restriction sites and

transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

5 PG54

The methods used for PG54 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGCTGAATTCCAGATTTTCGTTCCGAGGGGAACCC, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTGCTTCACGATCTTTTGGCTCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG55

The methods used for PG55 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was CGAGGGATCCGAGCTCTCTATTTGCGATGGCGAG, the 3' oligonucleotide primer sequence was GAGTGC GGCCGCTCTTACCTGACTTCTTGTCACGAAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

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PG56

The methods used for PG56 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was AAATGGATCCCGAAAAATTTTGAGCTTTTGGATG, the 3' oligonucleotide primer sequence was CTATGCGGCCGCTTTGATTCGTAATTTTCCGTATC and DNA was amplified with the Tth XL PCR kit. The PCR product was

35

cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

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PG57

The methods used for PG57 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
10 sequence was TGCTGGATCCCAAGAGATCTCAGGCATGAATGCA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTCGGCCTCTTTATCTCTACCTTTTC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and
15 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG58

The methods used for PG58 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
20 sequence was CCGTGAATTCCAAACCCACGAAATACAGAAACC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTGAAAGTCCAGCTAAAACCGGCGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
25 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.
30

PG59

The methods used for PG59 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
35 sequence was TGCTGAATTCCAACAAGAGAAGCAGGTGTTTCAT, the 3'

oligonucleotide primer sequence was
GAGTGCGGCCGCTGAAGATGCTCTTATCGTCCAAACG and DNA was
amplified with the Tth XL PCR kit. The PCR product was cloned into the
expression plasmid pET24a using the Eco RI and Not I restriction sites and
5 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
studies were carried out on whole *E. coli* lysates. Purification was not done
for these studies.

PG60

10 The methods used for PG60 were essentially the same as for PG30
with the following exceptions. The predicted N-terminal signal sequence was
removed from the recombinant protein. The 5' oligonucleotide primer
sequence was GCGGGAATTCCAGATGCTCAATACTCCTTTTCGAG, the 3'
oligonucleotide primer sequence was
15 GAGTGCGGCCGCTGAAGAGGTAGGAGATATTGCAGAT and DNA was
amplified with the Tth XL PCR kit. The PCR product was cloned into the
expression plasmid pET24a using the Eco RI and Not I restriction sites and
transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
studies were carried out on whole *E. coli* lysates. Purification was not done
20 for these studies.

PG61

The methods used for PG61 were essentially the same as for PG30
with the following exceptions. The predicted N-terminal signal sequence was
25 removed from the recombinant protein. The 5' oligonucleotide primer
sequence was AGCAGAATTCCTCCCAACAGCGAGATAGAT, the 3'
oligonucleotide primer sequence was
GAGTGCGGCCGCTGAAATCGATTGTCAGACTACCCAG and DNA was
amplified with the Tth XL PCR kit. The PCR product was cloned into the
expression plasmid pET24a using the Eco RI and Not I restriction sites and
30 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
studies were carried out on whole *E. coli* lysates. Purification was not done
for these studies.

PG62

The methods used for PG62 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
5 sequence was TGCTGAATTCCAGCGGTTTCCGATGGTGCAGGGA, the 3' oligonucleotide primer sequence was
GAGTGCGGCCGCTGAAAGTGAAATCCGACACGCAGCTG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG63

15 The methods used for PG63 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAAGAAGCAAACACTGCATCTGAC, the 3' oligonucleotide primer sequence was
20 GAGTGCGGCCGCTGAAAGTGACGCAACACCCACGCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
25 for these studies.

PG64

The methods used for PG64 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
30 sequence was TGCTGAATTCCAGAGTCGTCCTGCTCTTAGACTG, the 3' oligonucleotide primer sequence was
GAGTGCGGCCGCTGAAGCGAACACCGAGACCCACAAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
35 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG65

- 5 The methods used for PG65 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGGATCCATCGGACAAAGCCGCCCGGCACTT, the 3' oligonucleotide primer sequence was
- 10 GAGTGCGGCCGCTAAAGCGGTAACCTATGCCCACGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 15 for these studies.

PG66

- The methods used for PG66 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was
- 20 removed from the recombinant protein. The 5' oligonucleotide primer sequence was GTTTGAATTCCAAGACGTTATCAGACCATGGTCA, the 3' oligonucleotide primer sequence was
- GAGTGCGGCCGCTAAAATGAGTGGAGAGCGTGGCCAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the
- 25 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

30 PG67

- The methods used for PG67 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GAACGAGCTCGCGGAACGTCCTATGGCCGGAGCA, the 3'
- 35 oligonucleotide primer sequence was
- GAGTGCGGCCGCTATACCAAGTATTTCGTGATGGGACG and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG68

The methods used for PG68 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GCTTGCGGCCGCCCTTATGAAAGATTTGCAGAT, the 3' oligonucleotide primer sequence was GGTGCTCGAGTATACTCAACAAGCACCTTATGCAC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Not I and Xho I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG69

The methods used for PG69 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGGAAGGGGAGGGGAGTGCCCGA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTGAAGCTGTAGCGGGCTTTGAACCA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG70

The methods used for PG70 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer

sequence was CGGTGGATCCTCGCAAATGCTCTTCTCAGAGAAT, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTAAACGAAATATCGATACCAACATC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

10 PG71

The methods used for PG71 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGAACAATACCCTCGATGTACAC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTATTGCCGGTAGGATTTCTTGTCC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG72

The methods used for PG72 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCGAGAGCGACTGGAGACGGACAGC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTATGATTGCCTTTCAGAAAAGCTAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed TGCTGAATTCCGAGAGCGACTGGAGACGGACAGC into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG73

The methods used for PG73 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
 5 sequence was CCGTGAATTCCAACAGACAGGACCGGCCGAACGC, the 3' oligonucleotide primer sequence was
 GAGTGCGGCCGCTTAAGAAAGGTATCTGATAGATCAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
 10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG74

15 The methods used for PG74 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAAGAAAATAATACAGAAAAGTCA, the 3' oligonucleotide primer sequence was
 20 GAGTGCGGCCGCTGAGGTTTAATCCTATGCCAATACT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
 25 for these studies.

PG75

The methods used for PG75 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
 30 sequence was GGCGGGATCCGCTCAGGAGCAACTGAATGTGGTA, the 3' oligonucleotide primer sequence was
 GAGTGCGGCCGCTGTGGAACAAATTGGGCAATCCATC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and
 35 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

- The methods used for PG78 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAGGATTCTTCCCACGGTAGCAAT, the 3' oligonucleotide primer sequence was GAGTGC GGCCGCTATCATGATAGTAAAGACTGGTTCT and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG79

The methods used for PG79 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was TGCTGAATTTCGTAGTGACGCTGCTCGTAATTGTC, the 3' oligonucleotide primer sequence was GAGTGC GGCCGCTGCCGTCCTGCCTTTCTGCCTGACG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG80

The methods used for PG80 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGAATTCCAAAACGTGCAGTTGCACTACGAT, the 3' oligonucleotide primer sequence was GAGTGC GGCCGCTGTTGAAAGTCCATTTGACCGCAAG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG81

The methods used for PG81 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GTTGAATTCCAGGATTTTCTCTATGAAATAGGA, the 3'

oligonucleotide primer sequence was
GAGTGC GGCCGCTTTGTTTATTACAAAAAGTCTTACG and DNA was
amplified with the Tth XL PCR kit. The PCR product was cloned into the
expression plasmid pET24a using the Eco RI and Not I restriction sites and
5 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
studies were carried out on whole *E. coli* lysates. Purification was not done
for these studies.

PG82

10 The methods used for PG82 were essentially the same as for PG30
with the following exceptions. The predicted N-terminal signal sequence was
removed from the recombinant protein. The 5' oligonucleotide primer
sequence was GAACGAATTCCAGAACAACAACCTTACCGAGTCG, the 3'
oligonucleotide primer sequence was
15 GAGTGC GGCCGCTGTTTCAGTTTCAGCTTTTTTAAACCA and DNA was
amplified with the Tth XL PCR kit. The PCR product was cloned into the
expression plasmid pET24a using the Eco RI and Not I restriction sites and
transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
studies were carried out on whole *E. coli* lysates. Purification was not done
20 for these studies.

PG84

The methods used for PG84 were essentially the same as for PG30
with the following exceptions. The predicted N-terminal signal sequence was
25 removed from the recombinant protein. The 5' oligonucleotide primer
sequence was TGCTGGATCCCAGAATGATGACATCTTCGAAGAT, the 3'
oligonucleotide primer sequence was
GAGTGC GGCCGCTATTGCGTCCCCGGCCACTACGTCC and DNA was
amplified with the Tth XL PCR kit. The PCR product was cloned into the
30 expression plasmid pET24a using the Bam HI and Not I restriction sites and
transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
studies were carried out on whole *E. coli* lysates. Purification was not done
for these studies.

PG85

The methods used for PG85 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
5 sequence was CCGTGAATTTCGTACCAACGGACAGCACGGAATCG, the 3' oligonucleotide primer sequence was
GAGTGCGGCCGCTCAGATTGGTGCTATAAGAAAGGTA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG86

15 The methods used for PG86 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGGATCCCAAACGCATGATCATCTCATCGAA, the 3' oligonucleotide primer sequence was
20 GAGTGCGGCCGCTGTGGTTCAGGCCGTGGCAAATCT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
25 for these studies.

PG87

The methods used for PG87 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
30 sequence was GGCGGAATTCCAGAGCTATGTGGACTACGTTCGAT, the 3' oligonucleotide primer sequence was
GAGTGCGGCCGCTATTACTGTGATTAGCGCGACGCTG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and
35 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity

The methods used for PG90 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAAACAACGACGAACAGTAGCCGG, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTTTTTGTGTGATACTGTTTGGGC and DNA was

amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
5 for these studies.

PG91

The methods used for PG91 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was
10 removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCCAGACGATGGGAGGAGATGATGTC, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTCCACGATGAGCTTCTCTACGAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the
15 expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

20 PG92

The methods used for PG92 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGAATTGCGCGATGCACAAAGCTCTGTCTCT, the 3'
25 oligonucleotide primer sequence was GAGTGCGGCCGCTTCGAGGACGATTGCTTAGTTCGTA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity
30 studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG93

The methods used for PG93 were essentially the same as for PG30
35 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer

GAGTGGCGCCGCTAACTGTCTCCTTGTGCGCTCCCCGG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG96

The methods used for PG96 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
 5 sequence was TGCTGAGCTCCAAACGCAAATGCAAGCAGACCGA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTTTGAGAATTTTCATTGTCTCACG and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Sac I and Not I restriction sites and
 10 transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG97

15 The methods used for PG97 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GCGGGATCCAGTTTGTTCGGCTCCCACCACA, the 3' oligonucleotide primer sequence was
 20 GAGTGCGGCCGCTCTGTTTGATGAGCTTAGTGGTATA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Bam HI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
 25 for these studies.

PG98

The methods used for PG98 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer
 30 sequence was AGCAGAATTCCAAGAAAGAGTCGATGAAAAAGTA, the 3' oligonucleotide primer sequence was GAGTGCGGCCGCTTAGCTGTGTAACATTAAGTTTTTTATTGAT and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into
 35 the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and

immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done for these studies.

PG99

- 5 The methods used for PG99 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was TGCTGAATTCAAGGACAATTCTTCTTACAAACCT, the 3' oligonucleotide primer sequence was
- 10 GAGTGCGGCCGCTTCGAATCACGACTTTTCTCACAAA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 15 for these studies.

PG100

- The methods used for PG100 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCAGAATTCCAGTCTTTGAGCACAATCAAAGTA, the 3' oligonucleotide primer sequence was
- 20 GAGTGCGGCCGCTGATAGCCAGCTTGATGCTCTTAGC and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the expression plasmid pET24a using the Eco RI and Not I restriction sites and transformed into *E. coli* BL21DE3. Expression studies and immunoreactivity studies were carried out on whole *E. coli* lysates. Purification was not done
- 25 for these studies.

30 PG101

- The methods used for PG101 were essentially the same as for PG30 with the following exceptions. The 5' oligonucleotide primer sequence was TGCTGAATTCAAAGGCAAGGGCGATCTGGTCCGG, the 3' oligonucleotide primer sequence was
- 35 GAGTGCGGCCGCTTCTTCTCTCGAACTTGCCCGAGTA and DNA was amplified with the Tth XL PCR kit. The PCR product was cloned into the

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The methods used for PG102 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GGCCGAATTCCAGATGGATATTGGTGGAGACGAT, the 3' oligonucleotide primer sequence was

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The methods used for PG104 were essentially the same as for PG30 with the following exceptions. The predicted N-terminal signal sequence was removed from the recombinant protein. The 5' oligonucleotide primer sequence was GAACGGATCCAACGTGTCTGCTCAGTCACCCGA, the 3' oligonucleotide primer sequence was

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Various antisera were raised for detecting the expression and refolding of the recombinant *P. gingivalis* proteins. A whole cell antisera was raised by injecting New Zealand White rabbits with 3 doses of sonicated

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P. gingivalis (strain W50) containing approximately 2mg of protein. The first dose was given in Freund's complete adjuvant (FCA) and the second and third doses were given in Freund's incomplete adjuvant (IFA) at 3 week intervals. Doses (1ml) were given intramuscularly into the hind legs and rabbits bled 7 days after the last dose, the blood clotted and serum removed and stored at -20°C until required. A second rabbit antiserum was produced in a similar manner but using a sarkosyl insoluble fraction (each dose was 0.69mg of protein) derived from *P. gingivalis* W50 according to the method of Doidg and Trust T. *et al* 1994 as the immunogen. A third rabbit antiserum was produced in a similar manner to the first only the sarkosyl soluble fraction (1mg of protein per dose) derived from *P. gingivalis* W50 cells according to the method of Doidg P. and Trust TJ. (1994 Infect Immun 62:4526-33) was used as the immunogen.

A "protected rat serum" pool was also used in these studies and was obtained from rats immunised with formalin killed whole *P. gingivalis* cells in FIA (strain ATCC 33277; 2 doses of 2×10^9 cells, 3 weeks apart). Rats were then challenged 2 weeks after their last dose with live *P. gingivalis* cells (strain 33277) given orally as previously described (Klaussen B. *et al.* 1991, Oral Microbiol Immunol 6:193-201) and the serum obtained from these rats 6 weeks after the final challenge inoculation at the time of sacrifice.

Human sera were obtained from adult patients undergoing treatment or assessment for periodontitis at an outpatient clinic. These patients had at least 6 teeth with 6mm attachment loss and had *P. gingivalis* present in their sub-gingival plaque as detected using a *P. gingivalis* specific DNA probe. Sera was pooled from these patients and compared to a pool of sera from periodontally healthy patients.

Immunization and Murine Lesion Model Protocols

The mouse abscess model was used to assess the efficacy of immunising mice with recombinant *P. gingivalis* proteins in protecting mice from formation of a subcutaneous abscess. This model has been used by others as a predictor of potential vaccines against periodontal disease (Bird PS, *et al.* 1995 J. Periodontol. 66:351-362. BALB/c mice 6-8 weeks old were immunised by subcutaneously injecting them with 0.1 ml containing either 10 or 20µg of recombinant *P. gingivalis* protein, 20µg of *E. coli* lysate protein,

2 x 10⁹ formalin killed cells of *P. gingivalis* strain 33277 emulsified in incomplete Freund's adjuvant (IFA; Sigma) on day 0. At day 21 mice were re-injected with the same dose and then bled 1 week later and evaluated for antibody levels. At day 35 mice all mice were challenged with approximately 2 x 10⁹ cells of live *P. gingivalis* (ATCC 33277) by subcutaneous injection in the abdomen. Following challenge mice were monitored daily for weight loss and the size of the lesion measured for the next 10 days. Lesion sizes were measured by length and width and expressed as mm². Groups were statistically analysed using a Kruskal-Wallis one-way ANOVA and were also individually examined using the unpaired t test or Mann-Whitney rank sum test using the Instat statistical package.

Figure 1 shows the results of one experiment at day 4 after challenge (lesions were at maximum size at this time point). Control mice immunised with *E. coli* lysate showed large lesions while mice immunised with killed cells of *P. gingivalis* strain 33277 were fully protected. This indicates that whole cells provide protection against *P. gingivalis* while *E. coli* protein immunised mice were not protected. Mice given the various PG recombinant proteins showed significant levels of protection for PG2, PG22, PG24 and PG29 (p<0.05 unpaired t test) while PG8A was not quite significantly different (p=0.07) compared to the *E. coli* control group.

Figure 2 shows the results of a separate experiment using combinations of recombinant proteins. Mice given PG1 + PG2 showed a significant level of protection compared to control mice give *E. coli* lysate (p<0.026 unpaired t test).

Immunoscreening

Cloned candidates were cultured in 15ml of Terrific broth, induced with IPTG and sampled at 4h post-induction. One ml of culture was removed, pelleted and the cells resuspended in a volume of PBS determined by dividing the OD A_{600nm} of the culture by 8. An aliquot of lysate (100µl) was added to 100µl of 2x sample reducing buffer (125mM Tris pH 6.8, 20% glycerol, 4% SDS, 80mM DTT, 0.03% bromophenol blue) and boiled for 10min. SDS-PAGE was performed according to the method of Laemmli UK. 1970 (Nature 227:680-685) using 4-20% 1.0mm Tris-Glycine gels (Novex) according to the manufacturers recommendations. Proteins were transferred

onto Hybond-C Extra nitrocellulose membranes (Amersham) by transblotting and the membranes were then blocked for 2h at room temperature (RT) in 5% skim milk in 20mM Tris, 0.5M NaCl, 0.05% Tween-20, pH 7.5 (TTBS).

Immunoscreening was performed separately with the rabbit anti-*P. gingivalis* whole cell serum, the rat protective serum, a pool of human periodontal patients serum, and in many cases an anti-T7-Tag antibody HRP conjugate (Novagen). Prior to use, the rabbit, rat and human sera were diluted 1/5000, 1/1000 and 1/500 respectively in 5% skim milk in TTBS and absorbed with 100µl (for the rabbit serum) or 250µl (for the rat and human sera) *E. coli* extract (20mg/ml; Promega) for 6h at RT.

Membranes were incubated overnight at RT with the absorbed antisera, or for 1 hr at RT with 1/5000 diluted anti-T7-Tag conjugate. Following 3x10min washes with TTBS, HRP-conjugated anti-rabbit (Silenus), anti-mouse (Silenus) or anti-human (KPL) antibody, diluted 1/5000 in 5% skim milk in TTBS, was added for 1h at RT. Membranes were washed as before, prior to addition of TMB membrane peroxidase substrate (KPL) for detection of immunoreactive proteins. Results of reactivity for the recombinant *P. gingivalis* proteins is shown in Table 7.

In addition some of the sera (pooled sera diluted 1/1000) from the mice immunised with *P. gingivalis* recombinant proteins (prior to challenge) were analysed for their reactivity against Western blots of whole native W50 *P. gingivalis* proteins using similar techniques as those outlined above. PG2, PG8A, PG29 and PG3 all showed bands at a similar molecular weight to that of the recombinant PG protein in the native W50 blot. This indicates that PG proteins are expressed in the W50 strain and that the recombinant proteins have at least some identical immunogenicity to the native proteins.

m-RNA analysis

Hot Phenol RNA Extraction

P. gingivalis W50 cells (150ml culture) were grown anaerobically to mid log phase (OD A_{600} =0.18) mixed with 50% glycerol and stored at -70°C until RNA extraction. Cells were pelleted by centrifugation at 6000g, and resuspended in 8ml ASE (20mM NaOAc, 0.5% SDS, 1mM EDTA). An equal volume of 20mM NaOAc(pH 4.5)-saturated phenol was added and mixed by

shaking for 30 seconds, incubated at 65°C for 5 minutes, followed by a further 5 second shaking and repeated incubation. After cooling, 2ml chloroform was added and mixed by shaking for 5 seconds, and the mixture spun at 10000g for 10 minutes at 4°C. The top aqueous phase was transferred and re-extracted by repeating the phenol and chloroform steps. The aqueous phase was transferred again and 100U RNase inhibitor (RNasin; Promega) were added. RNA was precipitated with 3 volumes 100% ethanol at -20°C overnight. The RNA precipitate was recovered by centrifugation at 10000g at 4°C for 15 minutes, then washed with 100% ethanol, dried and resuspended in 600µl sterile, deionised, dH₂O with 1µl of fresh RNase inhibitor. RNA was aliquoted and stored at -70°C. The RNA concentration was determined spectrophotometrically. A formaldehyde RNA gel confirmed RNA integrity (Sambrook J. et al. 1989, Molecular Cloning. A laboratory manual. Cold Spring Laboratory Press, New York. 2nd Edition).

15

RT-PCR

The isolated RNA was used as a template for Reverse Transcription (RT) to produce cDNA. Varying RNA concentrations were used for the RT as each RNA transcript was potentially present at different levels. Subsequent amplification of the cDNA was performed using Polymerase Chain Reaction (PCR). RT-PCR was performed using GeneAmp® RNA PCR Kit (Perkin Elmer) according to the manufacturer's protocol with the following exception to the PCR; 35 cycles were performed as follows: Melt phase 95°C for 30 seconds, Anneal phase varied between 50-60°C for 30 seconds, Extension phase 72°C for 1 minute. Amplification was performed in a PTC-100 Programable Thermal Controller (MJ Research Inc.). As a control to demonstrate that the amplified product did not arise from contaminating DNA, Reverse Transcriptase (RTase) was omitted from a parallel tube. The PCR products were examined against DNA markers (GIBCO 1kB ladder) on a 1% agarose gel stained with ethidium bromide.

RT-PCR results are shown in Table 6 using the oligonucleotide primers as used in "Cloning, expression and purification of recombinant *P. gingivalis* genes" section described above, except for the following changes. For PG1 the 3' reverse primer used was

- CGGCCTCGAGATTCATTTCTTATAGAG, for PG4 the 5' forward primer was CTTCTTGTCGACTACAGCGGACATCATAAAATC and the 3' reverse primer was TTCCACCTCGAGTTAACGCAACTCTTCTTCGAT, for PG6 the 5' forward primer was TAAAGAATTCTGCCTCGAACCCATAATTGCTCCG, for
- 5 PG10 the 5' forward primer was CGCGCATATGGATAAAGTGAGCTATGC and the 3' reverse primer was CGCGCTCGAGTTTGTTGATACTCAATAATTC, for PG13 the 5' forward primer was GCGCGGCGCCATGCGGACAAAACTATCTTTTTTGCG and the 3' reverse primer was
- 10 GCGCGGCGCCTTAGTTGTTGAATCGAATCGCTATTTGAGC. Amplification of *P. gingivalis* transcripts is a likely indication that RNA for a specific candidate is present and that the protein is produced. However, where there is no amplification achieved this does not indicate that this gene is never transcribed and may be the result of the culture conditions or the state of the
- 15 cells when harvested.

Table 6. Expression of PG m-RNA with *in vitro* grown *P. gingivalis* W50. The symbols are + band visible on agarose gel, - no band present on agarose gel, ND not detected.

20

PG #	RNA μg	Annealing temp. °C	RT-PCR	PCR (-RT)	Approx. fragment size bp	Expected fragment size bp
1	0.15	55	+	-	1300	1362
2	1.0	50	+	-	3200	3051
3	0.15	60	+	-	720	690
4	2.9	55	-	-	N.D.	2000
5	0.02	50	+	-	1000	947
6	1.0	55	+	-	1000	972
8A	0.15	50	+	-	1200	1278
10	0.15	55	+	-	590	585
11	0.10	60	+	-	960	942
12	0.02	60	+	-	880	831
13	1.0	50	+	-	2150	2274
14	0.15	60	+	-	1050	996

PG #	RNA µg	Annealing temp. °C	RT-PCR	PCR (-RT)	Approx. fragment size bp	Expected fragment size bp
22	1.0	60	-	-	N.D.	228
24	1.0	55	+	+	1150	1194
29	0.15	60	+	-	880	885

5 **Table 7:** Immunoblot results of proteins expressed in *E.coli* against rabbit, rat and human antisera. Deduced MW was calculated from amino acid sequence of the *P. gingivalis* proteins, some of which had their N-terminal signal sequences removed. Apparent MW was determined from SDS-PAGE gels. The N- and C-terminal tags add approximately 2.5 KDa to the deduced MW of the recombinant proteins. The symbols are + positive, - negative, +/- weak positive, ND not done.

10

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG1	47.5	63	ND	-	-	-
PG2	112.4	125.7	ND	+	-	-
PG3	22.6	18.3	ND	- ^a	-	-
PG4	75	90.6	ND	-	-	-
PG5	34.9	43.8	ND	-	-	-
PG6	36.7	47.1	ND	-	-	-
PG8	67.5	63.1	ND	- ^b	-	-
PG8A	47.7	90.6	ND	-	-	-
PG10	21.3	25.5	ND	+	-	+
PG11	36.2	42.4	ND	-	-	-
PG12	30.7	30.6	ND	-	-	-
PG13	84.5	101	ND	-	-	-
PG14	36	42.4	ND	-	+	+
PG22	8.6	11.1	ND	-	-	-
PG24A	47	63.1	ND	-	-	-
PG29	31.1	40.9	ND	+	+	+

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG30	35.1	46.9	+	-	-	-
PG31	16.7	-	-	-	-	-
PG32	41.2	59.5	+	+	+	-
PG33	39.9	52.7	+	+	+	-
PG35	92.6	116.6	+	-	-	-
PG36	98.9	120.2	-	-	-	-
PG37	18.8	23.1	+	+	-	-
PG38	16.1	22.9	+	-	-	-
PG39	87.9	116.6	+	-	-	-
PG40	76.6	103.1	+	-	-	-
PG41	48.3	81.1	+	-	+	+
PG42	59.3	73.9	+	-	-	-
PG43	27.1	50.3	+	-	-	-
PG44	28.6	32.3	+	-	+	-
PG45	84	100.6	+	-	-	-
PG46	83	97.7	+	-	-	-
PG47	93.7	42.5	+	+	-	+
PG48	45.2	37.9	+	-	-	-
PG49	33.3	64.1	+	-	+	-
PG50	91.9	113.2	+	+	-	-
PG51	19.6	27.2	+	-	-	-
PG52	50.4	64.4	+	+	-	+
PG53	47.4	45.4	+	-	-	+
PG54	101.4	46.7	+	+	-	-
PG55	70.4	68.4	+	-	-	-
PG56	142.3	-	-	-	-	-
PG57	100	134.5	+	+	+	+
PG58	63	82.9	+	-	-	-
PG59	33.3	43.6	+	-	-	-
PG60	55.6	77.8	+	-	-	-
PG61	81.5	107.3	+	-	-	-

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG62	51.9	58.4	+	-	-	-
PG63	29.6	43.6	+	-	-	-
PG64	18.5	26.9	+	-	-	-
PG65	25.9	28.8	+	-	-	-
PG66	22.2	25.1	+	+	-	-
PG67	103.7	105	+	-	-	-
PG68	133.3	30.7	+	-	+	+
PG69	44.4	50.8	+	-	-	-
PG70	25.9	30.8	+	-	-	-
PG71	88.9	105.5	+	-	-	-
PG72	40.7	49.8	+	-	-	-
PG73	40.7	29	+/-	-	-	-
PG74	22.2	32.5	+	-	-	-
PG75	40.7	46.7	+	-	-	-
PG76	48.1	55.6	+	-	-	+
PG77	29.6	36.9	+	-	-	-
PG78	33.3	35.4	+	-	-	-
PG79	33.3	-	-	-	-	-
PG80	25.9	20.5	+	-	-	-
PG81	23	25.8	+	-	-	-
PG82	44.8	48.5	+	-	-	-
PG84	41.7	52.4	+	-	-	+/-
PG85	62.7	72.4	+	-	-	-
PG86	21.7	27.4	+	-	-	+/-
PG87	83	91.3	+	-	-	+
PG88	27	40.1	+	-	-	-
PG89	26.2	29.4	+	-	-	-
PG90	23	28.4	+	-	-	-
PG91	57.2	85.7	+	+	+	+
PG92	83.6	110.4	+	-	-	+
PG93	83.4	110.4	+	-	-	+

Protein number	Deduced MW (KDa)	Apparent MW (KDa)	Antisera reactivity			
			T7	Rabbit	Rat	Human
PG96	59.3	70.3	+	+	+	+
PG97	44.4	57.5	+	-	+	+
PG98	33.3	36	+	-	-	-
PG99	40.7	55.6	+	-	+	+
PG100	29.6	10.8	+	-	-	-
PG101	14.8	19.7,14.1	+	-	-	-
PG102	59.3	70.3	+	-	-	+
PG104	40.7	57.5	+	-	-	+

- 5
 - a. Positive reaction detected with the rabbit antiserum to sarkosyl insoluble *P. gingivalis* antigen.
 - b. Purified protein demonstrated weak positive reaction with the rabbit antiserum to whole *P. gingivalis*.

- 10

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

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- 30

CLAIMS:-

1. An isolated antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising;
an amino acid sequence selected from the group consisting of SEQ.
5 ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532; or
an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532;
10 at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 15 2. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 20 3. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 25 4. A polypeptide as claimed in claim 1 in which the polypeptide comprises at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 265 to SEQ. ID. NO. 528, SEQ. ID. NO. 531 and SEQ. ID. NO. 532.
- 30 5. A polypeptide as claimed in claim 1 in which the polypeptide comprises;
an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or
an amino acid sequence at least 85%, preferably at least 95%, identical to an amino acid sequence selected from the group
35 consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532; or

at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.

- 5 6. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.
7. A polypeptide as claimed in claim 1 in which the polypeptide comprises an amino acid sequence at least 85%, preferably at least 95%,
10 identical to an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.
8. A polypeptide as claimed in claim 1 in which the polypeptide comprises at least 40 amino acids having a contiguous sequence of at least 40 amino acids identical to a contiguous amino acid sequence selected from the
15 group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532.
9. A polypeptide as claimed in claim 6 in which the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386, SEQ. ID. NO. 424, SEQ. ID. NO. 425, SEQ. ID. NO. 434,
20 SEQ. ID. NO. 447, SEQ. ID. NO. 458, SEQ. ID. NO. 475, SEQ. ID. NO. 498, SEQ. ID. NO. 499, SEQ. ID. NO. 500, SEQ. ID. NO. 501, SEQ. ID. NO. 387, SEQ. ID. NO. 400, SEQ. ID. NO. 411, SEQ. ID. NO. 419, SEQ. ID. NO. 420, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 433, SEQ. ID. NO. 437, SEQ. ID. NO. 438, SEQ. ID. NO. 443, SEQ. ID. NO. 444, SEQ. ID. NO. 448,
25 SEQ. ID. NO. 449, SEQ. ID. NO. 452, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 462, SEQ. ID. NO. 463, SEQ. ID. NO. 467, SEQ. ID. NO. 468, SEQ. ID. NO. 469, SEQ. ID. NO. 482, SEQ. ID. NO. 484, SEQ. ID. NO. 485, SEQ. ID. NO. 494, SEQ. ID. NO. 508, SEQ. ID. NO. 509, SEQ. ID. NO. 510, SEQ. ID. NO. 520, SEQ. ID. NO. 521,
30 SEQ. ID. NO. 522, SEQ. ID. NO. 525, SEQ. ID. NO. 526, SEQ. ID. NO. 528, SEQ. ID. NO. 389, SEQ. ID. NO. 390 and SEQ. ID. NO. 391.
10. An isolated antigenic *Porphyromonas gingivalis* polypeptide, the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ. ID. NO. 386 to SEQ. ID. NO. 528 and SEQ. ID. NO. 532
35 less the leader sequence set out in Table 3.

- SUBSTITUTE SHEET (Rule 26) (RO/AU)

23. A composition as claimed in claim 22 in which the pharmaceutically acceptable carrier is an adjuvant.
24. A method of treating a subject for *P. gingivalis* infection comprising administering to the subject a composition as claimed in claim 22 or claim 23
5 such that treatment of *P. gingivalis* infection occurs.
25. A method as claimed in claim 24, wherein the treatment is a prophylactic treatment.
26. A method as claimed in claim 24, wherein the treatment is a therapeutic treatment.
- 10 27. An antibody raised against a polypeptide as claimed in any one of claims 1 to 10.
28. An antibody as claimed in claim 27 in which the antibody is polyclonal.
29. An antibody as claimed in claim 27 in which the antibody is
15 monoclonal.
30. A composition comprising at least one antibody as claimed in any one of claims 27 to 29.
31. A composition as claimed in claim 30 in which the composition adapted for oral use.
- 20 32. A nucleotide probe comprising at least 18 nucleotides and having a contiguous sequence of at least 18 nucleotides identical to a contiguous nucleotide sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 121, SEQ. ID. NO. 529 and sequences complementary thereto.
33. A nucleotide probe as claimed in claim 32 in which the probe further
25 comprises a detectable label.
34. A method for detecting the presence of *P. gingivalis* nucleic acid in a sample comprising:
 - (a) contacting a sample with the nucleotide probe as claimed in claim 32 or claim 33 under conditions in which a hybrid can form between
30 the probe and a *P. gingivalis* nucleic acid in the sample; and
 - (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *P. gingivalis* nucleic acid in the sample.

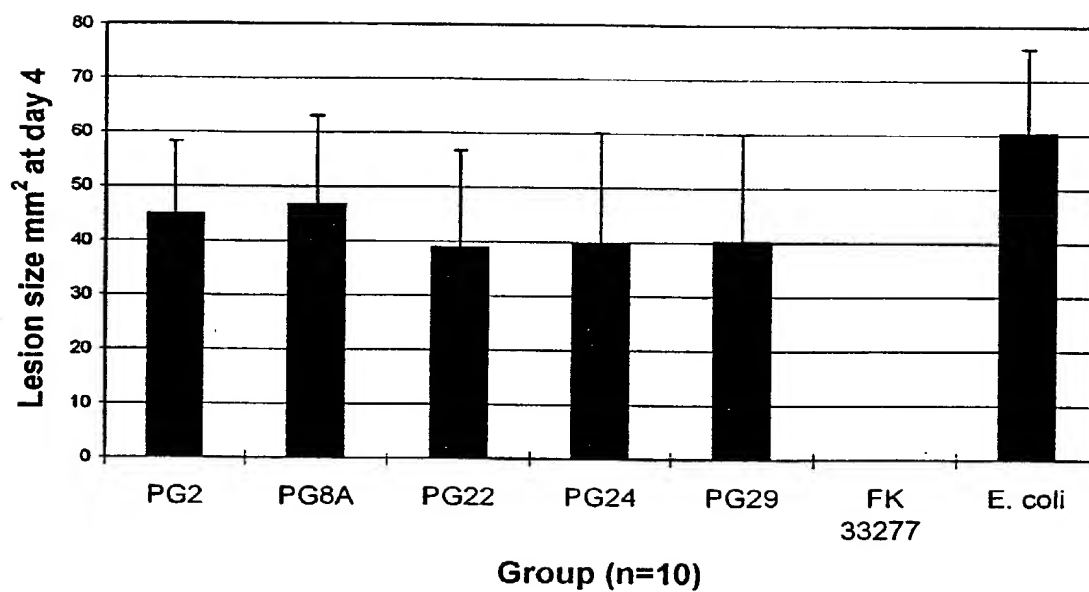


Figure 1

WO 99/29870

PCT/AU98/01023

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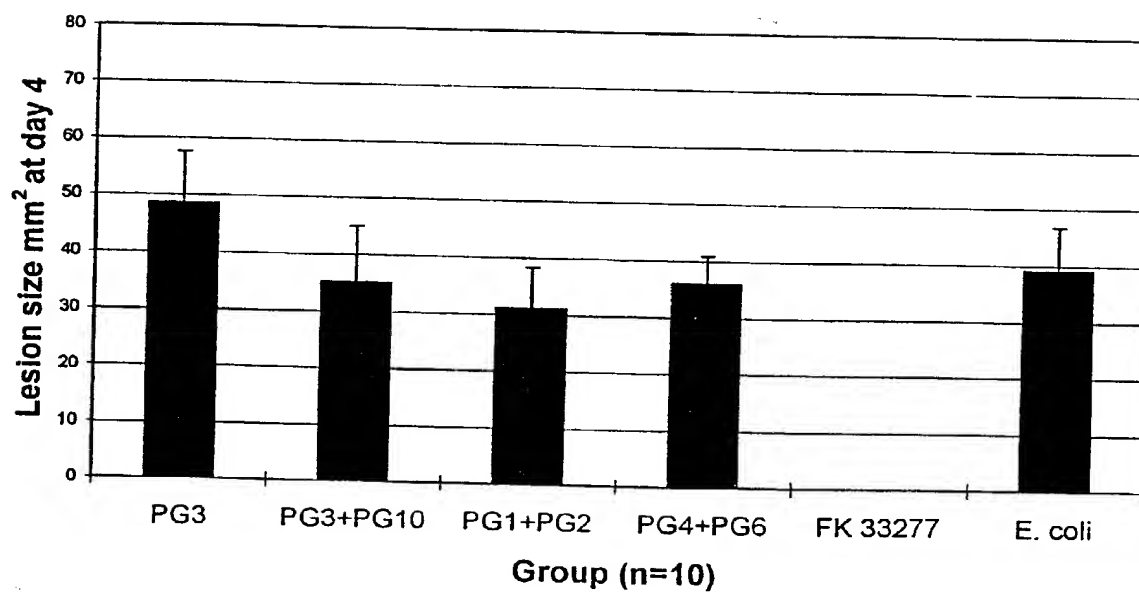


Figure 2

47-138
92432

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(Domestic Non-Assigned/Foreign) Page 1 of 3

RULE 63 (37 C.F.R. 1.63)
INVENTORS DECLARATION FOR PATENT APPLICATION
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name, and I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES

the specification of which (check applicable box(es)):

☐ is attached hereto
☒ was filed on _____ as U.S. Application Serial No. Unassigned (Atty Dkt. No. 47-138)
☒ was filed as PCT international application No. PCT/AU98/01023 on 10 December 1998
and (if applicable to U.S. or PCT application) was amended on _____

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with 37 C.F.R. 1.56. I hereby claim foreign priority benefits under 35 U.S.C. 119/365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed or, if no priority is claimed, before the filing date of this application:

Priority Foreign Application(s):

Application Number	Country	Day/Month/Year Filed
PP0839	Australia	10 December 1997

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

Application Number	Date/Month/Year Filed
--------------------	-----------------------

I hereby claim the benefit under 35 U.S.C. 120/365 of all prior United States and PCT international applications listed above or below and, insofar as the subject matter of each of the claims of this application is not disclosed in such prior applications in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose material information as defined in 37 C.F.R. 1.56 which occurred between the filing date of the prior applications and the national or PCT international filing date of this application:

Prior U.S./PCT Application(s):

Application Serial No.	Day/Month/Year Filed
PCT/AU98/01023	10 December 1998

Status: patented
pending, abandoned

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon. And on behalf of the owner(s) hereof, I hereby appoint NIXON & VANDERHYE P.C., 1100 North Glebe Rd., 8th Floor, Arlington, VA 22201-4714, telephone number (703) 816-4000 (to whom all communications are to be directed), and the following attorneys thereof (of the same address) individually and collectively owner's/owners' attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith and with the resulting patent: I also authorize Nixon & Vanderhye to delete any attorney names/numbers no longer with the firm and to act and rely solely on instructions directly communicated from the person, assignee, attorney, firm, or other organization sending instructions to Nixon & Vanderhye on behalf of the owner(s).

1. cc	Inventor's Signature: <u>[Signature]</u>	Date: <u>6 JUN 2000</u>
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2. cc	Inventor's Signature: <u>[Signature]</u>	Date: <u>6 June 2000</u>
	Inventor: <u>Ian</u> <u>G.</u> <u>Barr</u>	<u>Australia</u>
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	(Zip Code) <u>3108</u>	

FOR ADDITIONAL INVENTORS, check box ☒ and attach sheet with same information and signature and date for each.

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(2)

47-138
Serial No. Unassigned

Nixon & Vanderhye P.C. (10/99
(Domestic Non-Assigned/Foreign)
Page 2 of 3

RULE 63 (37 C.F.R. 1.63)
INVENTORS DECLARATION FOR PATENT APPLICATION
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name, and I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES

the specification of which (check applicable box(es)):

☐ is attached hereto
☒ was filed on _____ as U.S. Application Serial No. Unassigned (Atty Dkt. No. 47-138)
☒ was filed as PCT International application No. PCT/AU98/01023 on 10 December 1998
and (if applicable to U.S. or PCT application) was amended on _____

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with 37 C.F.R. 1.56. I hereby claim foreign priority benefits under 35 U.S.C. 119/365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed or, if no priority is claimed, before the filing date of this application:

Priority Foreign Application(s):	Country	Day/Month/Year Filed
Application Number <u>PP0839</u>	<u>Australia</u>	<u>10 December 1997</u>

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

Application Number	Date/Month/Year Filed
--------------------	-----------------------

I hereby claim the benefit under 35 U.S.C. 120/365 of all prior United States and PCT international applications listed above or below and, insofar as the subject matter of each of the claims of this application is not disclosed in such prior applications in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose material information as defined in 37 C.F.R. 1.56 which occurred between the filing date of the prior applications and the national or PCT international filing date of this application:

Prior U.S./PCT Application(s):	Day/Month/Year Filed	Status: patented pending, abandoned
Application Serial No. <u>PCT/AU98/01023</u>	<u>10 December 1998</u>	

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon. And on behalf of the owner(s) hereof, I hereby appoint **NIXON & VANDERHYE P.C., 1100 North Glebe Rd., 8th Floor, Arlington, VA 22201-4714, telephone number (703) 816-4000 (to whom all communications are to be directed)**, and the following attorneys thereof (of the same address) individually and collectively owner's/owners' attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith and with the resulting patent: I also authorize Nixon & Vanderhye to delete any attorney names/numbers no longer with the firm and to act and rely solely on instructions directly communicated from the person, assignee, attorney, firm, or other organization sending instructions to Nixon & Vanderhye on behalf of the owner(s)

3. ∞	Inventor's Signature: <u>[Signature]</u>	Date: <u>8/6/00</u>
	Inventor: <u>Michelle</u> <u>A.</u> <u>Patterson</u> (first) (last) (citizenship) <u>MI</u> <u>(last)</u> Residence: (city) <u>Victoria</u> <u>AUX</u> (state/country) <u>Australia</u> Post Office Address: <u>14 Cotterell Way, Laverton, Victoria, Australia</u> (Zip Code) <u>3021</u>	
4. ∞	Inventor's Signature: <u>[Signature]</u>	Date: <u>20.6.00</u>
	Inventor: <u>Catherine</u> <u>T.</u> <u>Agius</u> (first) (last) (citizenship) <u>MI</u> <u>(last)</u> Residence: (city) <u>Victoria</u> <u>AUX</u> (state/country) <u>Australia</u> Post Office Address: <u>250 Elgar Road, Box Hill South, Victoria, Australia</u> (Zip Code) <u>3128</u>	
5. ∞	Inventor's Signature: <u>[Signature]</u>	Date: <u>6.6.00</u>
	Inventor: <u>Linda</u> <u>J.</u> <u>Rothel</u> (first) (last) (citizenship) <u>MI</u> <u>(last)</u> Residence: (city) <u>Victoria</u> <u>AUX</u> (state/country) <u>Australia</u> Post Office Address: <u>10 Rothschild Street, Glenhuntly, Victoria, Australia</u> (Zip Code) <u>3128</u>	
6. ∞	Inventor's Signature: <u>[Signature]</u>	Date: <u>6.6.00</u>
	Inventor: <u>Mai</u> <u>B.</u> <u>Margetts</u> (first) (last) (citizenship) <u>MI</u> <u>(last)</u> Residence: (city) <u>Victoria</u> <u>AUX</u> (state/country) <u>Australia</u> Post Office Address: <u>92 Bent Street, Monce Ponds, Victoria, Australia</u> (Zip Code) <u>3039</u>	

FOR ADDITIONAL INVENTORS, check box ☒ and attach sheet with same information and signature and date for each.

430944

47-138
Serial No. Unassigned

Nixon & Vanderhye P.C. (10/99
(Domestic Non-Assigned/Foreign)
Page 3 of 3

RULE 63 (37 C.F.R. 1.63)
INVENTORS DECLARATION FOR PATENT APPLICATION
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name, and I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES

the specification of which (check applicable box(es)):

☐ is attached hereto
☒ was filed on _____ as U.S. Application Serial No. Unassigned (Atty Dkt. No. 47-138)
☒ was filed as PCT International application No. PCT/AU98/01023 on 10 December 1998
and (if applicable to U.S. or PCT application) was amended on _____

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with 37 C.F.R. 1.56. I hereby claim foreign priority benefits under 35 U.S.C. 119/365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed or, if no priority is claimed, before the filing date of this application:

Priority Foreign Application(s): Application Number	Country	Day/Month/Year Filed
PP0839	Australia	10 December 1997

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

Application Number	Date/Month/Year Filed
--------------------	-----------------------

I hereby claim the benefit under 35 U.S.C. 120/365 of all prior United States and PCT international applications listed above or below and, insofar as the subject matter of each of the claims of this application is not disclosed in such prior applications in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose material information as defined in 37 C.F.R. 1.56 which occurred between the filing date of the prior applications and the national or PCT international filing date of this application:

Prior U.S./PCT Application(s): Application Serial No.	Day/Month/Year Filed	Status: patented pending, abandoned
PCT/AU98/01023	10 December 1998	

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon. And on behalf of the owner(s) hereof, I hereby appoint **NIXON & VANDERHYE P.C., 1100 North Glebe Rd., 8th Floor, Arlington, VA 22201-4714, telephone number (703) 816-4000** (to whom all communications are to be directed), and the following attorneys thereof (of the same address) individually and collectively owner's/owners' attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith and with the resulting patent. I also authorize Nixon & Vanderhye to delete any attorney names/numbers no longer with the firm and to act and rely solely on instructions directly communicated from the person, assignee, attorney, firm, or other organization sending instructions to Nixon & Vanderhye on behalf of the owner(s).

7. cc Inventor's Signature: *D. Hocking* Date: 6 June 2000
Inventor: Dianna M Hocking Australian
(first) (last) (citizenship)
Residence: (city) Victoria (state/country) Australia
Post Office Address: 49 Illawarra Road, Victoria, Australia
(Zip Code) 3031

8. cc Inventor's Signature: *Elizabeth A. Webb* Date: 8 June 2000
Inventor: Elizabeth A. Webb Australian
(first) (last) (citizenship)
Residence: (city) Victoria (state/country) Australia
Post Office Address: 36 Zigzag Road, Victoria, Australia
(Zip Code) 3422

WO 99/29870

PCT/AU98/01023

1 / 490

(2) INFORMATION FOR SEQ ID NO:1

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

25	TTCTGTGTCA TGGCAAAAGT TATAAAAACA AAAAAAGGCC TTGCACTTAA TCTGAAAGGA	60
	AAACCGCTGC CCGAGATGCT GGCCGAACCG GCCCAAAGTC CTACTTACGC GGTCTGTGCC	120
	GACGATTTTG AAGGTGTTAT CCCCAAGGTG ACGGCTCGTC CGGGGATAA GGTGCGTGCC	180
	GGCTCAGCAC TGATGCACCA CAAGGCATAT CGGGAGATGA AGTTTACAAG TCCGGTTAGC	240
	GGCGAAGTGA TCGCGGTGAA TCGCGGTGCC AAGCGCAAGG TGTTGAGCAT CCAGGTGAAA	300
30	CCGACGGAC TGAACGAATA CGAGTCATTC CCTGTCCGGG ATCCGCTCTGC CCTCTCTGCC	360
	GAACAGATCA AGGAGCTTTT ACTGTGAGG GGTATGTGGG GTTTTATTAA GCAACGTCCT	420
	TACGACATAG TGGCTACACC GGTATAGCT CCACGCGACA TTTATATTAC TGCCAACTTT	480
	ACTGCACCAT TGGCTCCGGA CTTCGATTTC ATCGTTCGAG GAGAAGAAGC CGCCCTGCAG	540
	ACTGCCATCG ATGCCCTGGC CAAACTCAG ACAGGAAAGG TGTATGTGGG CCTGAAGCCG	600
35	GGTTCATCTC TGGGCTTGCA CAATGCAGAA ATCCTAGAAG TACACGGACC TCATCCGGCA	660
	ACGCTCAAGG CTACCGACCT GATCGTGATC GGACGTTTCC TGCTTACGGG CAAAGCCGAT	720
	TTTACCAGAA TGATTGCCAT GACCGGCTCA CACGCTGCAG CTCACGGATA CGTCCGTATT	780
	ATGCCGGGTT GCAATGTCTT TGCTTCCTTC CCGGCCGAC TGACAATAAA GGAATCTCAC	840
40	GAGCGTGTGA TCGATGGCAA TGTGCTGACC GGTAAAGAAG TCTGCGAGAA GGAGCCTTTC	900
	CTGTGAGCCC GGTGTGACCA GATCAGGTTG ATCCCGAAG GCGACGATGT GGACGAACTC	960
	TTCCGGTGGG CTGCACCCCG TCTCCGATCA TACAGCATGA GCAGAGCTTA TTTCTCTTGG	1020
	TTGCAGGGGA AAAACAAGA GTACGTACTC GATCCCGGGA TCAAGGGTGG CGAACGTGCT	1080
	ATCATCATGA GCAACGAGTA TGACCGCGTT TTCCCGATGG ACATCTATCC GGAGTATTTG	1140
	CTCAAGGCTA TTATAGCATT CGACATCGAC AAGATGGAGG ACTTAGGCAT ATATGAAGTG	1200
45	GCTCCGGAGG ACTTTGCCAC TTGCGAATT GTGGATACAT CCAAGATCGA GCTGCAGCGT	1260
	ATCGTTCGCG AGGGCTTGA TATGCTCTAT AAGGAATGA AT	1320
		1362

(2) INFORMATION FOR SEQ ID NO:2

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

50	GAACAAAGCA AGTGTACAT GGATAAAGTG AGCTATGCTC TGGGATTGAG CATCGGTAAT	60
	AATTTCAAGT CTTGGGCGAT CGACAGCGTC GTTATGGATG ATTTTCATGA AGGTCTGTCT	120
55	GATGTAATGG AAGAAAAAGC CCCTCAGCTC TCGTATGACG AGGCCAAGCG CGAAATAGAG	180
	GCGTATTTCA TGGATTGCA GCAGAAGGCT GTCAACTGA ACAAAGAGGC CGGAGAAGAA	240

WO 99/29870

PCT/AU98/01023

3 / 490

5
GATGTTCTCC AGCATAGGAT GAAAGTGTAT CCCAACCCCTG CCACGACGGA GCTGCATGTG 300
GAAGCCCTGT CGCATGGGT GGGCGAGCAG GCTGCGGTAT ATGATATGCG TGGTCGTGG 360
GTAATCGGCTC GGACGGTGA TAGCGAGAAG CTGTGCATCG ACATTGCCCTC ACTGCCCGTG 420
GGCGTCTATA TGCTGCGCAT CGGCAGCTAC TCGGCCAAGT TCGAGAAGAG A 471

(2) INFORMATION FOR SEQ ID NO:5

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1686 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
15 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
25 (A) NAME/KEY: misc_feature
(B) LOCATION 1...1686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

30 ACAAGAAATG TTCACTCAT AAAAATGCCA AGAATTATGA AATTAAAAAT TGCACTCAGA 60
CTGCTGCTGG CGACTTTTGC CATAGTTTTA TTTAGCCCTC TGGCCAAAGG CCAGATGGAT 120
ATTGTTGGAG ACGATGTATT GATCGAGACG ATGTCCACCC TATCAGGATA TTCAGAGGAT 180
TTTTATTACA AGATGGCTGT GGCAGACAAAT GGATGGATCT ATGTGATGTT GGATTTCTCT 240
CGTATTTATT TTGATGATGT CAGGCTGTAT CGTTCCAAAG ACGGTGGTGC TACTTACCAA 300
AAGTTAGGGT CTTTGGGGTC TTTGGTGCTT TATGACTTCG ATGTCTCGCA TTGCGATTTT 360
ATTGTAACGG GAAAGGATGA AGATGATATC AATGTTTGA CAGTCATGAC AGCATTCCGA 420
TATGTAGGTG GTACTATTGG CAATGGCGTT TTGCTGATGC ATGCCCATGA TGCAGATATC 480
AATAATACAG AGTGTGTGTA CAAGAAGGAT TTCCCTAATA ATAGACTGAT GGGGTAGGCC 540
ATCGCCTCCA ACTACCGTGC GCCCTCTCCT TACGGTTTGG GGGGCGATCC TTTTGCTCTC 600
GCTGTCCGGG TTAGTGGCTC GGGAAAGCGAT CACAGCTTCT TGGACTATAT TTTTCTGTTA 660
GATGTGGGAG TACACTTTGA GCAAAAGCGT ATTTACACAA GACCCCAAAA ACTGACTATC 720
AATAGAGTAG ACCTTTCATT AGGCAGTACA TCTCCTTCTC TTGGATTAA TACTTGGCCA 780
CTAATGGGAG TCGTATTGTA AATGAATAAG AACCTTGATG GCTTCGACAT TGGTTTCATT 840
TCCAACCTTG TGGACTATGA TCCCGCTAT CCGTGGTCTG AACCGATAAT AATAGAAGAA 900
GACTGTGGAT GGACTGATT TAATCCTTTG GGAGCACTAA GTATAGAGAT CCAATGATG 960
TTGGATGACA ATTCCGATAA TACCGTGGGT GGAGAAGCGT CCCATAACTT CCTGATCACT 1020
TACCGGGGCC ATTACGTATA TCCGAAGCAA TCTTTCAATT ATTCTCCCGG ACATACACCG 1080
ACAAAGAAAG ATCTGGTCTT TAAACACTGT ATAGGTATTC CGGCTTTGGC ATACGATAAG 1140
GAAGGCGATC GTTATCTGAC TACTTTTCAA GATCACAATC TAATGAGATA CAGATGGATC 1200
50 AAATACGATG ACATTAACTC TTTTATGGT TGGAGTTCCG CATATGTATA TGCAAAAGAA 1260
GCTAAAGATA AAAAGAGGCG CCGTCCGCAA GTAGCACTCA ATCCTACCAA TGGAAAGGCT 1320
TGTGGGTTAT GGCATACTCG CAAGAGCCCA TATGATGAAA CCAAAACCACA TCCTACTCCT 1380
GTAATTATTA AACATTTCTT ATGTTCCGAT ACGGAGTGGG TACATGCTCT GGACGTGGGG 1440
GACGTATTGC AGAAGGAGGG TAGCATGAAG CTCTACCCCA ATCCTGCCAA AGAATATGTT 1500
55 CTGATCAACC TACCCAAAGA AGGGGGGCAC GAGGCACTCG TATACGACAT GCAGGGCCGA 1560
ATCGTGGAGA AAGTTTCATT TTCAGGGAAA GAATATAAGC TGAATGTGCA GTATCTGTCC 1620
AAAGGTAGCT ACATGCTGAA AGTTGTAGCG GATACGGAGT ATTTCTGGGA AAAAATCATT 1680
GTAGAG 1686

(2) INFORMATION FOR SEQ ID NO:6

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
70 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: UNKNOWN
75 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

CAAATGAAC GATTACTCCC CTTTCTCCTT TTAGCAGGAC TCGTAGCCGT AGGAAACGTG 60
TCTGCTCAST CACCCCGAAT CCTCAAGTG GATGTACACA CTCGCATCGC AAGAAATGCC 120
CGTTATCGAC TGGACAAGAT CAGTGTCCTG GATTCTCGTC AGATATTCGA TTACTTCTAT 180
AAAGAAGAAA CGATACCCAC TAAATACAA ACGACCACAG GAGGTGCAAT TACAAGCATC 240
GATTCTGCTT TCTATGAAGA CGACAGGTTG GTTCAGGTGC GCTATTTTGA CAATAACCTT 300
GAATTAAAC AAGCGGAGAA GTATGTATAC GACGTTCTA AGCTGGTCTT TCGAGAAATT 360
CGCAAGTCGC CGACAGACGA AACGCCAATA AAGAAAGTTA GCTATCACTA TCTCTGTGGC 420
AGCGATATGC CTTTGTACAT TAGGACAGAG ATGAGCGATG GCTATTTTGA AAGCCATACG 480
CTTAACATATC TGAATGGAJA GATTGCCCGA ATAGATATCA TGACTCAACA GAACCCATCG 540
GCCGAATTGA TCGAAACGGG TAGMATGGTA TATGAGTTTG ATGCCAATAA TGATGCTGTA 600
CTGCTTCGTG ACAGTGTATT TCTTCTCTT CAAAACAAGT GGGTAGAAAT GTTACTCAC 660
CGTTATACAT ACGACAATAA GCATATTTGT ATTCGTTGGG AACAGACGA ATTCGGCACC 720
CTCACCCCTT CCAACAACCT CGAATACGAC ACCACTATCC CTCTGTCTG TGTATTGTTT 780
CCCACGCAAG AGGAGTTCTT CCGTCTCTT CTTCCTCAAT TTATGAAGCA TATGCGTACG 840
AAGCAAACTT ATTTCAATAA CTCCGGAGAA GGCTTGTGAG AGGTATGCGA TTACAACATC 900
TTCTATACCG ATATGCAAGG TAATGCACTG ACCGATGTTG CCGTGAACGA ATCGATCAAG 960
ATTATCTCTC GTCTGCGCAC GGATTTCTG CGTATAGAAC GTTCGCACT GCTTCGCTT 1020
TCGCTATTGG ACATGAACGG GAGGCTCATC AGAGTACCG AATTGACAGG CGATTGCGC 1080
ATTATCGGAG TTGCATCTCT TCGGAGAGGC ACTTACATCG CAGAAATAAC TGCTGCAAAAC 1140
AGCAAAACCA TACGTGCAAA AGTATCGCTC AGA 1173

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

AAGAGGAATC CCTTACCTTT GACGGCATCA AATCGAAAGA TTTTATAAAA AATGAGACAG 60
CATTTATCTC TATTTCTTTT TATCTTGTIT CTGCTTCTTG CCTTCTCTTA TGTGCGTTGC 120
AGAACAGTCC GACAAACACC TAAGCAGTCC GAACGGTACG TCGTAGTCTT GTCTTTGGAC 180
GGCTTCCGAC CGGACTATAC CGATCGGGCA CGTACACCGG CATTGGATCG GATGGCAGAG 240
GAGGGATTGA GCGGGTCTGT CCAACCATGC TTCCCTCTCG TTACATTTCC CAATCATTTAC 300
AGCATGGCTA CGGGGCTTTA CCCCATCAT CACGGTATCG TAGCCAATGA GTTTGTGGAT 360
TCGCTACTGG GCATCTTTCG TATATCCGAC CGAAAGCCG TGGAGACCCC CGGATTTTGG 420
GGCGGGGAGG CGGTTTGGAA TACGGCCGCA CGCCAAGGCA TCCGTACCGG TGTCTACTTT 480
TGGGTAGGAT CCGAAACGGC TGTGAACGGA AATCGGCGGT GCGGGTGGAA AAAATTCTCC 540
TCCACCGTTC CGTTTCGTGA CCGTGCAGAC TCCGTCTATG CGTGGCTUGG ACTGCCCGAA 600
AAGGAGCGAC CGCGCTTGGT CATGTGGTAC ATCGAGGAGC CGGATATGAT CGGACACAGC 660
CAAACGCCCG AAAGCCCGCT GACACTGGCA ATGGTAGAGC GATTGGACAG TGTGTCTGSC 720
TATTTCCGCA AGCGGTTGGA CTCTCTGCCC ATAGCCGAC AGACCGACTT CATCATAGTA 780
TCCGATCAGC GTATGGCCAC GTACGAAAT GAGAAATCTG TCAATCTGTG GCATATCTG 840
CCTGCGGACA GTTTCCTCTA CATGGCCACC GGGGCCCTCA CCCACTTGTG CCLGAAGCCC 900
TCCTATACCG AGCGAGCCTA TGAGATCCTG CGGGCCATTC CACATATATC GGTTTACCGC 960
AAGGGGGAGG TGCCCAAGCG TTTCGCGTGT GGCACCAATC CTGTTTGGG CGAAGTGGTC 1020
GTGATTCCGG ACATAGGCTC CACCGTCITT TTCGCAATAA ATGAAGACGT TCGTCCGGGA 1080
CGGGCAGATG GCTATGACAA CCAAGCACCG GAAATGCGGG CTTTACTCCG GGCTGTCCGA 1140
CCCGATTTCG GTCCGGGCGAG TAGGGTGGAA AACCTGCCGA ATATCCCAT CTATCCGCTC 1200
ATATGAGAGC TGTGGGTAT AGAGCCTGCA CCCAACGATG CGGACGAAAC GTTGTGAAC 1260
GGCCTGATCC GAGACAAACG ACCA 1284

(2) INFORMATION FOR SEQ ID NO:8

5 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

10 (11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

15 (1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...846

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

CTTCCCGTG	GAGTTTTC	CCTGATGTAT	GGCCGAAGAG	GAAGCATTCTG	TGCCTCTTCA	60
GGGCATAGGG	ACAAAATTTT	TAAGAATACA	ATTATCAGAT	TTATCACAAT	GAAAGTAGGT	120
TTGTTTCATCC	CCTGTTATGT	CAATGCAGTG	TATCCGGGAG	TGGGTATCGC	CACGTACAAA	180
CTGCTGAAGA	GTTTGGACAT	AGATGTCGAC	TACCCGATGG	ATCAGACATG	TTGCGGCCAG	240
CCTATGCECA	ATGCCGGATT	CGAACAGAAA	GCTCAAAAGC	TGGCTTTGCG	ATTCTGAAGAG	300
CTGTTGAGT	CGTATGATGT	AGTCGTAGGG	CCATCGGCCA	GTTGCGTTGC	TTTCGTGAAA	360
GAAACTATG	ATCATATCCT	CAGACCGACA	GGACATGTCT	GCAAGTCGGC	AGCCAAGGTT	420
CGGGATATAT	GCGAGTTCTT	GCACGATGAC	CTGAAGATCA	CCAGCCCTCC	CTCCCGATT	480
GCCCATAAGG	TGAGCCTGCA	CAACAGTTGC	CACGGTGTGC	GCGAAGTGA	TCGTCCACC	540
CCCAGTGAAG	TGCACCGACC	GTACCACAAC	AAGGTGCGCC	GGCTATTGGA	GATGGTGCA	600
GGCATAGAGG	TATTCGAGCC	GAAGCGAATA	GACGAATGCT	GCGTTTCGG	CGGTATGTAC	660
TGGGTGGAGG	AGCCGGAGGT	ATCCACCTGT	ATGGGGCATG	ACAAGGTGCT	GGATCACATA	720
TCCACAGGTG	CGGAGTACAT	CACAGGGCCG	GACAGCTCGT	GCCTCATGCA	TATGCAGGGA	780
GTGATAGACA	GAGAGAAATT	GCCGATCAAG	ACAATTCATG	CAGTAGAAAT	TTTAGCAGCA	840
AACTTA						846

(2) INFORMATION FOR SEQ ID NO:9

45 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

50 (11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

55 (1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

60 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...753

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

CCCTGAAAA	AACGAATGGA	TATTGTAAGT	ATGGCCGATA	AAGCTCTTGT	ACTGGAGATG	60
AGAGATCTGA	CGCTCTGTCA	GGAGGAAAAC	GTCAITTTTC	AAAATTTGAA	TCTGACCCTT	120
TCCGCCGGAG	ACTTCGTCTA	TCTGATAGGC	TCAGTGGGAT	CGGGGAAGAG	CACCTTGCTG	180
AAGGCTTTGT	ATGCTGAGGT	GCCTATCTCT	GCCGTTATG	CCCGCGTGAT	AGATTATGAT	240
CTGGCAAAAT	TGAAACGGAA	GCAGTTGCC	TATCTGCCCA	GGAATTTGGG	CATTGTGTTT	300
CAGGATTTCC	AGTTGCTGAA	CGGACGTACT	GTTGCGGAGA	ATTGGAATT	CGTTTTCGCA	360
GCTACGGACT	GGAAAAACCG	AGCCGATCGC	GAGCAGCGTA	TCCAGGAGGT	TTTGACCCGT	420
GTGGGAATGT	CTCGGAAGGC	TTATAAGAGA	CCGCACCAAC	TGTCCGGAGG	GGAGCAACAA	480
CGTGTGGGTA	TAGCCAGAGC	TTTGTGGCG	AAGCCTGCGT	TGATCCTGGC	CGACGAACCC	540
ACAGGCAACC	TCGATTCGGT	GACCGGATTG	CAGATCGCTT	CTCTGCTCTA	CGAAATCAGT	600

AAGCAGGGCA CTGCAGTACT TATGAGCAGC CACAACAGCA GCCTGCTGTC GCATCTGCCG 660
 GCACGGACAT TGGCCGTTTC TAAGAATGGC GATGCCTCCT CTTTGGTTCGA GCTGAGTGCA 720
 GATGCTGTTT CAAGAAAAA TACGGAAATA GAT 753

5

(2) INFORMATION FOR SEQ ID NO:10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 714 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...714

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

30 ACCAGGCAAT GTCCGGCTTG TCGCTCTTCC TTTCACCTCA TAAAAACAAG TAAACCAATG 60
 ATTGAATCA GCAACCTCAC CAAGGTTTTC AGAACAGAG AAATAGAGAC GGTAGCCCTC 120
 GATGGCGTAT CGCTCAAAGT GGACAAAGGC GAATTATCG CCATTAATGGG GCCTTCGGGA 180
 TGCCTTAAGT CCACTCTGCT CAATATCCTC GGCCCTTCTCG ACAATCCCAC TTCCGGTATC 240
 TACAAGCTCG ATGGGGCAGA AGTGGGCAAC CTCGGGGAAA AAGACAGGAC TGCCGTCCGT 300
 AAGGGCAATA TCGGCTTCGT ATTCCAGAGC TTCAACCTCA TCGAAGAGAT GACGGTAAGC 360
 35 GAGAACGTGG AGTTGCCGCT CGTCTATCTG GGTGTGAAG CCTCCGAGCG GAAAGAGCGA 420
 GTGGAGGAGG CACTGCGCAA GATGAGCATC AGCCACCGGG CCGGCCACTT CCCCATCAG 480
 CTCCTCCGAG GACAACAGCA GCGCGTGGCT ATCGCCCGTG CCGTGGTGGC CAATCCGAAG 540
 CTCATCCTCG CCGATGAACC CACGGGTAAC CTCGACTCCA AAAACGGAGC CGATGTCATG 600
 40 GAACTGCTCA GAGGTCTCAA TCGCGAAGGT GCAACCATCG TCATGGTGAC GCACTCCGAG 660
 CACGATGCAC GTAGTGCCGG CCGCATCATC AATCTGTTCG ACGGTAAGAT TCGC 714

(2) INFORMATION FOR SEQ ID NO:11

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1812 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 60 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...1812

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

AGCACAGAAA CAAATAGCAA ATCTGAAATG AAAGAATTTT TCAAAATGTT TTTCCGCTCG 60
 ATCCTCGGGG TTATAACGGC AGGAATCATC TTGTTCTGTA TCTTCTATT TATCTTTTTC 120
 GGCATCGTAG CCGGTATTGC CTCCTAAGGA ACGGGAGGAA CCATTCGGAA GATCGAAGCA 180
 AACTCCATCC TACATATANA CAATTCTTCT TTCCCTGAGA TCGTATCCGC CAATCCCTGG 240
 70 AGCATGCTCA CAGGCAAGA CGAGTCCGTA TCGCTCTCAC AGGCAGTCA AGCCATCGGC 300
 CAAGCCAAAA ATAATCCAA CATAACCGGT ATCTTCCTCG ATCTGGACAA CCTTCCGTC 360
 GGTATGGCAT CGGCAGAGGA ATTGCGTCGC GCGTTGCAGG ATTTCAAGAT GTCGGGCAAG 420
 TTCGTGCTAT CCTATGCCGA CAGATACACC CAAAAGGGTT ACTACCTCTC CAGTATTGCA 480
 GACAACTCT ACCTCAATCC GAAAGGAATG TTGGGGCTTA TCGGGATTGC GACCCAAACA 540
 75 ATGTTCTACA AAGATGCCCT CGACAAATTC GGCGTGAAGA TGGAGATCTT CAAGGTAGGC 600

WO 99/29870

PCT/AU98/01023

7 / 490

5 ACCTCAAGG CAGCCGTAGA GCCATTTCATG CTCAACAGGA TGAGCGATGC CAATCGCGAA 660
 CAAATCAGCA CATACATAAA CGGGCTTTGG GACAAGATCA CATCCGATAT TGCAGAGTCG 720
 CGCAAGACGG CAATGGATTC CGTGAAAATG TTTGCCGACA AAGGCGAAAT GTTCGGTCTT 780
 GCGGAGAAAG CGGTGGAGAT GAAGCTCGTG GATGAGCTGG CTTACCGTAC CGATGTGGAG 840
 AAAGAACTCA AAVAGATGTC CCAACGCGGA GAGAAAGATG AACTTCGGTT CGTATCGCTT 900
 TCTCAGGTTT TGGCCAATGG CCCGATGAAC AAAACGAAAG GCAGTCGGAT CGCGTTCTC 960
 TTTGCCGAAG GTGAAATAAC GGAAGAAATA ATAAAGAAAG CGTTCGACAC TGCAGGTAGC 1020
 TCCATCACAC AAGAACTCGC CAAAGAAATC AAGGCAGCAG CCGATGACGA TGATATCAAA 1080
 GCGGTAGTAC TTCGTGTCAA TTCTCCGGGA GGTAGTGCTT TCACTTCCGA ACAGATATGG 1140
 10 AAGCAGGTAG CCGATCTCAA GSCCAAAAG CCTATCGTGG TCTCCATGGG CGAGGTAGCA 1200
 GCCTCGGGCG GATACTACAT AGCCTGCGCA GCCAACAGTA TCGTGGCAGA GCATACGACT 1260
 CTGACCGGCT CCACTCGGCAT ATTCGGCATG TTCCCGAACT TCGCGGGCGT AGCCAAGAAG 1320
 ATAGGAGTGA ATATGGACGT CGTACAGACA TCCAGTATG CAGACTTGGG CAACACCTTC 1380
 GCTCCGATCA CGGTGGAAGA TCGTGCCCTC ATCCAACGCT ACATAGAGCA GGGCTACGAC 1440
 15 CTCTTCTCCA CTCGCGTATC GGAAGGCCGC AACCACACCA AGGCACAGAT CGACAGCATC 1500
 GCTCAAGGCC GTGTATGGCT CGGCGACAAA GCTCTTGCC TCGGTTTGGT GGATGAGCTT 1560
 GGAGTTTGG ACACAGCTAT CAAACGGGCC GCGAAGCTGG CTCAGCTCGG TGGCAACTAC 1620
 AGCATAGAGT ATGGCAAGAC CAAGCGCAAC TTCTTCGAG AGTTGCTCTC CTCATCAGCA 1680
 GCGGATATGA AGTCTGCCAT CCTGAGTACC ATTCTCTCCG ATCCGGAAAT AGAAGTTCTG 1740
 20 CGCGAATCC GCTCCATGCC GCGCCGTCCT TCGGGCATAC AGGCACGTCT CCCCTATTAC 1800
 TTCATGCCGT AC 1812

(2) INFORMATION FOR SEQ ID NO:12

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 972 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 35 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 40 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

CTAACGTTGT TTTGTTGCAA CTATTTCAAA CAGATGAGAG CAAACATTG GCAGATACTT 60
 TCCGTTTCGG TTCTCTTTT CTTCGGGACA GCGATCGGAC AGGCTCAGAG TCGAAACCGT 120
 50 ACATACGAGG CTTATGTGAA ACAGTACGCC GACGAAGCTA TCCGACAGAT GAGCCGCTAC 180
 AATATACCGG CAAGCATCAC CATAGCACAG GCTTTGGTGG AGACAGGAGC CGGAGCCAGT 240
 AACTGCCCCA GCGTACACAA CAATCACTTC GGGATCAAAAT GCCACAAATC GTGGACGGGC 300
 AAGCGCACCT ATCGTACCGA CGATGCGCGG AACGAATGCT TCCGCAGCTA TTCGGCCGCT 360
 CGCGAATCGT ATGAAGATCA TTCCCGATTT CTGCTCCAAC CACGCTATCG TCCCTGTTC 420
 AACTCGCA GAGAAGACTA TCGGGGCTGG GCTACGGGGT TGCAACGCTG TGGCTATGCC 480
 55 ACCAATCGGG GCTATGCCAA TCTGCTGATC AAGATGGTGG AGCTGTATGA GCTATATGCT 540
 TTGGATCGCG AGAAGTACCC CTCATGGTTC CACAAGTCTT ACCCGGGGTC CAACAAAAAA 600
 TCCCATCAAA CGACCAAGCA GAAGCAGAGC GGAATCAAGC ACGAAGCTTA CTTCACTAC 660
 GGACTGCTCT ACATCATAGC CAAGCAAGGC GATACCTTCG ATTCTTTGGC CGAAGAGTTC 720
 GACATGAGAG CCTCCAAACT GGCCAAATAC AACGATGCTC CCGTGGATTT CCCGATCGAA 780
 60 AAGGGCGATG TGATCTATCT GGAGAAAAAG CACGCATGCT CCATCTCCAA ACACACACAG 840
 CACGTAGTGC GTGTGGGCGA TTGCATGCAC AGTATCTCCC AACGTATGG CATCGGGATG 900
 AAGAACCTCT ACAAGCTCAA CGACAAGGAT GGCGAATATA TACCCCAAGA GGGCGATATA 960
 CTGCGCTTGC GC 972

(2) INFORMATION FOR SEQ ID NO:13

- 70 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1599 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 75 (ii) MOLECULE TYPE: DNA (genomic)

WO 99/29870

PCT/AU98/01023

9 / 490

5 AATATGAGCG AGACCCCTCTC TCTCATGCAG CAGGGCAACT ATCATGCTGC GATCGAACAG 660
 ACATTGATCG GTCTGGGCTT CGGCCGAGAG GACTTCCACC GCCCCACAGC CGATTTTCAGC 720
 GGAGGATGGC GTATGCGGAT AGAGCTGGCC AAACCTTCTGC TCCAAACGCC CGAAGTTTTC 780
 CTGCTCGAGC AGCCGACCAA TCACCTCGAC ATCGAATCCA TCGGCTGGCT GGAGCAGTTC 840
 ATCGCCACCA ATGCAGGAGC CGTTATCCTG GTGTCCGACG ACAGGGCATT CATCGACAAT 900
 ACCACGACAC GCACATATCGA AATAGAACTG GGACATATAI ACGACTACAA GACCAACTAC 960
 AGCCACTATG TGGAGCTGCG CGAAGAGCGG CTGCGACAGC AGATGCGTGC CTACGAGAAT 1020
 CAGCAGAAGA TGATCCGCGA TACGGAGGAC TTCATCGAAC GATTGAGATA CAAGGCCACG 1080
 AAGTCCGTAC AGGTACAGAG CCGGATCAAA CAGTTGGAGA AAGTAGAGCG CGTGGAGATA 1140
 GACGAGCGGG ATCGTTGCGC ATTTCACTTC CGCTTTATCC CGGCACAGCC TTCCGGCAGT 1200
 10 TATCCGCTAA TAGTGGATGA TTTGGCCAAAG GCTTATGGCG ATCACCAGGT GTTTTCCGGA 1260
 GCTACATACA CCATCGAAAG AGGGCAAAAG GTGGCTTTCG TAGGCAAAAA CGGTGCCGSC 1320
 AAAAGTACCA TGGTCAAGTG TATCATGGGA GAGCTGACAG ACTACACCGG CAGCTCGAA 1380
 CTGGGGCACA ACGTGCAGCT GGGCTACTTT GCCCAAAACG AAGCCCAAGA GCTAAGAGGG 1440
 15 GATCTCACGG TATTCGACAC GATAGACCGT GAGGCCGTGG GCGACATCCG TCTGCGCCTG 1500
 AAGGATTTCG TCGGGGCTTT TCTCTTCGGG GGGCAAGCAT CGGAAAGAA AGTAAGTGT 1560
 CTGAGTGGAG GAGAACGAGC ACGATTGGCT ATTATCAGGC TTTTGCTACA GCCGGCTAAC 1620
 TTCTTTATTC TCGATGAGCC GACCAATCAC CTCGATATGC GCTCGAAGGA TGTACTGAAA 1680
 20 GAGGCSATCA AGAAGTTCGA TGGGACTGTC ATCGTAGTAT CTCACGACCG TGAGTTCCTC 1740
 GATGGGCTTG TCAGCAAGGT GTATGAATTT GCAGATGGAC AGGTGAACGA ACACCTCGGA 1800
 GGTATATACG ACTATCTCCG GACCCGCGGT ATGCAGAGCG TGACAGAGCT GGAGCGAACC 1860
 ACTACGATCG AAACAAAAAC CACACGGGAG GCTATACCTG AAACGGAGC CAAAGCGGAC 1920
 TACCGTCCGG AAAGAGGAGT AGCCAAACAG CTGGCAGCGT TGGAGCGAAC CGTAGCAACC 1980
 25 TGCGAGGAGC GGATCGGAAA ATTGGAGTCG GAATTACAG CAATAGAGAT GCTACTGCAA 2040
 GATCCGAAC ATGCGACTGA CCGGAATCTG TTCGAGCGAT ACGCCGGCAT GAAACAAGAA 2100
 CTCGAAAAAG CCATGGAGGA CTGGGAACAG GCTTCCGAAG CTTTATCCGA AGCCCAAGCA 2160

30 (2) INFORMATION FOR SEQ ID NO:15
 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 40 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 45 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1158
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

55 TATTTGAAGC TATTAATACT ACAAATAGCC TTGATGAATT TCITAAAAAA AGAACCCTTT 60
 AAAATATTCT CTATGATTTA TCTGCTGTTA GATACAATAA CAAACCGTGC CGGTACAGAA 120
 CGGCCCGTGA TCAACTTGGC TAACAACCTG CATGCCAATG GTCATCGCGT ATCATTAGTC 180
 AGCGTTTGTA CAAAAGAAGG AGAGCCTTCC TTCCAAGTAG AAAAAGGAT AGAAGTACAC 240
 CATCTCGGAA TTAGGCTTTA TGGCAATGCA TTAGCCCGCA AAACAGTATA TTTCAAGGCT 300
 TATCGAAGGA TAAAAGCCCT ATACAAGAAG CGTGAACCGG TTTTATTGAT AGGGACTAAT 360
 ATTTTATCA ATACATTTT GTCTCAGATC AGTAACAGAG GCAGAATATT TACGATCGGA 420
 60 TGCGAACATA TCTCTTATGA TATTGCCCGC CCTATTACAA AACGCATAAG GGGGTTTCTG 480
 TATTCAGGGC TTGATGCCGT TGTAGCACTG ACAAAGAGAG ATCAGCAATC GTTCGAGGCA 540
 ATCTTACGTG GACGCTCTAA AGCATATGTC ATACCCAATC AAGTTTCATT TACTACAGTC 600
 CAAAGAGATG CTAATACTCA CAAACAAATG TTGGCGATTG GCAGGCTTAC CTACCAGAAG 660
 GGTTTTGAAT TCATGATAGA AGATGCATCA CGAGTGCTGC GAGAAAGGCC TGATTGGAAG 720
 65 CTTATCATAG TCGGAGATGG CGAAATGAA TCGATGCTAC GTAAAGAAAT TGCACTCGC 780
 AATATGGAGT CGCAATAGA AATACATCCA TCTACACCGG AAATTGCGAA ATACTACGAA 840
 TCATCTGCTA TTTATCTAAT GACGTCCCGT TTCGAAGGAC TAACCAATGGT ACTTCTCGAA 900
 GCAGAAAGCAT ATGCACTACC TATAATCTCA TACGATTGTC CGACCGGCCG GAGGGAAGT 960
 ATCGAAAAAG GTCCGAATGG TTTCTTGTG CCAATGGAAG CACATGAAGA CTTCGCGGAT 1020
 AAGTTACGCT TATTGATGGA TGATGAACT CTTCGTAAGA AAATGGGACA AGAATCAGAG 1080
 70 TTGATGGTCA AATCCTACTC TCCGGCAAT ATCTATGAAT GTTGGAGAA ACTATTGCTC 1140
 GAAATCGGCT ACATGAAT 1158

75 (2) INFORMATION FOR SEQ ID NO:16

WO 99/29870

PCT/AU98/01023

10 / 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1965 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ACAAACGAAAG	AAAACGAGAC	AACAACAAAA	AACGAATATA	GAATTATGGG	AAAAATCATT	60
GGAATTGACT	TAGGCACAAC	GAACCTCTGT	GTCTCTGTAT	TGGAAGGTAA	CGAACCTATC	120
GTTATTACAA	ACAGTGAGGG	CAAGCGCACA	ACGCCCTCGG	TAGTGGCTTT	TGTGGATGGT	180
GGCCGAGCGTA	AGGTGGCCGA	TCCGCGCAAG	CGTCAGGCCA	TCACCAATCC	GACCAAGACG	240
ATATACTCTA	TCAAACGCTT	CATGGGCGAA	ACTTACGATC	AGGTTCCAG	ACAAGTGGAG	300
AGAGTGGCAT	TCAAGGTAGT	ACGTGGGGAC	AATAATACTC	CGCGCGTAGA	TATAGACGGT	360
CGTCTCTATA	CGCCCGCAGGA	AATTTCCGCC	ATGATCCTTC	AGAAGATGAA	GAAGACGGCC	420
GAAGACTACC	TGGTTCAGGA	AGTAACGGAG	GCCGTGATCA	CTGTGCCCGC	ATACTTCAAC	480
GACGCTCAAC	GTCCAGGCAAC	GAAAGAAGCA	GGAGAGATCG	CGGGCTGAA	AGTTCCGCCGT	540
ATTGTGAACG	AGCCTACGGC	AGCTTCTCTG	GCCTACGGTC	TGGACAAGTC	CAATAAGGAT	600
ATGAAGATCG	CTGTCTTCGA	CTTGGGTGGC	GCTACCTTCG	ATATCTCTAT	CTTGAATTG	660
GGCGACGGCG	TTTTCGAAGT	GAAATCGACC	AACGGTGATA	CGCACCTCGG	AGGAGACGAC	720
TTCCGACCAG	TGATCATTGA	CTGGCTGGCA	GAAGAGTTCA	AGTCTCAGGA	AGGTGTGGAT	780
CTTCGCCCAG	ATCCTATGGC	TATGCAGCGT	CTGAAAGAA	CTGCCGAAAA	AGCCAAAGATA	840
GAGCTCTCCA	GCACTTCATC	TACGGAGATC	AACCTCCCCCT	ATATCATGCC	GGTGAACGGC	900
ATCCCAAGC	ACTTGGTGAT	GACGCTTACA	AGGGCTAAGT	TCCAGCAGTT	GGCCGATCGT	960
CTGATTCAAG	CATGTGTGGC	ACCCTGCGAA	ACGGCCTTGA	AAGATGCCGG	TATGTCACGT	1020
GGCGATATCG	ATGAAGTGAT	TCTCGTAGGT	GGTTCACAC	GATTTCTCTG	TATTCAGGAG	1080
ATTGTGGAGA	AGATCTTCGG	TAAGGCTCCG	TCCAAGGGTG	TGAATCCCGA	CGAAGTGGTA	1140
GCTGTGGGTG	CCGCTATTCA	AGGCGGTGTT	CTGACCGGTG	AGGTAAGGTA	TGTCTTGCTG	1200
TTGGACGTTA	CCCCCTTGTC	GCTCGGTATC	GAGACTATGG	GAGGCGTGAT	GACTCGCTTG	1260
ATCGATGCCA	ATACCACTAT	CCCGACGAA	AAGAGCGAAA	TCCTTACCAC	AGCAGTGGAC	1320
AATCAACCTT	CGGTAGAGAT	TCATGTACTT	CAGGCTGAGC	GTCTTTTGGC	TAAGGACAAT	1380
AAGAGCATCG	GCCGTTTCAA	CTTGGACGGT	ATTGCTCCGG	CGCCCCGTCA	GACACCGCAG	1440
ATCGAAGTAA	CGTTTGACAT	CGATGCCAAC	GGTATCTCTG	ATGTAACGGC	TCATGACAAA	1500
GCTACCGGCA	AGAAGCAGAA	TATCCGCATC	GAAGCCTCCA	GCGGTTTGTC	CGATGATGAG	1560
ATCAAGCGCA	TGAAGGAAGA	GGCGCAGGCC	AATGCCGAAG	CAGATAAGAA	AGAGAAAGAA	1620
CGTATCGACA	AGATCAATCA	GGCCGACAGC	ATGATCTTCC	AGACGGAAAA	GCAGTTGAAS	1680
GAGTTGGGAG	ACAAATTTCC	GGCCGACAAG	AAGGCTCCGA	TCCGATACGC	TCTCGACAAA	1740
CTGAAAGAA	CACACAAGC	ACAGGATGTA	GCTGCTATCG	ATACAGCCAT	GGCCGAAGT	1800
CAAAACCGCT	TTTCCGCAGC	GGGCGAAGAG	CTTTACAAGA	ATGCCGAGC	AGCCCAAGGT	1860
GGCGCACAC	CCGGTCCGGA	CTTCGGCGGT	GCTCAAGGTC	CCTCTGCCGG	TGATCAGCCC	1920
TCTGACGACA	AGAACGTCAC	AGACGTAGAC	TTCCAGGAAG	TGAAG		1965

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature

(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

5 AAGTGGGCGAC GTACAACTAC TTTAAGGATA TCGAACGCAA CAATCTATAA AACTATGCGC 60
TACGACTTAG CTATCATCGG TGGAGGGCCG GCGGTTATA CCGCTGCCGA ACGTGCTGCC 120
AAAGGTGGCC TGAACACCTT CCTAATTGAG AAGAATGCTC TCGGTGGTGT ATGCTCAAC 180
GAAGGATGTA TACCGACCAA GACGCTACTC TACTCGGCCA AAGTGCTACA TCAAAATGCT 240
ACGGCATCTA AATATGCAGT AAGTGGAAAG GCGATGGGAC TTGACCTCGG CAAGGTGATT 300
10 GCCAGAAAAG GTAAAATCAT TCGCAAGCTG ACTGCAGGCA TCCGTTCACG CCTGCAGAG 360
GCCGGAGTAG AGATGGTGAC GGCAGAAGCT ACGTAACGGG GATGCGATGC AGACGGCATC 420
ATCGGCATTA CTGCGGGCGA AGCAGATAC AAGCTGCCA ACCTGCTACT ATGTACCGGT 480
TCGGAGACGT TTATTCCACC CATCCCGGA GTGGAGCAGA CAGAGTATTG GACAAACCGT 540
GAAGCTCTAC AGAACAAGA GATTCCGACC TCTCTCTCA TCATCGGTGG TGGAGTGATC 600
15 GGAATGGAGT TCGTTCTTT CTTCAACGGT ATCGGTACGC AAGTGCAAGT GGTGGAGATG 660
CTGCCGAAA TACTCAACGG TATCGATCCC GAACATGCAG CTATGCTACG CGCTCACTAT 720
GAAAAAGAG GAATCAAAAT TACCTCGGG CACAAAGTAA CATCGGTTCC CAACGGAGCT 780
GTATCGGTAG AATACGAAGG AGAAGGCAA GAGATCGAAG GAGAAGCTAT CCTGATGAGT 840
GTGGGACGTC GCCCGTGCT GCAAGGATTC GAGTCGTCG GATTGGTGCT TGCCGGCAA 900
20 GGTGTAAAGA CTAATGAGAG GATGCAAACT TCCCTGCCCA ATGTCTATGC TGCAGGTGAT 960
ATTACAGGCT TCTCGCTTTT GGCACATACG GCTGTACGGG AAGCAGAGGT AGCAGTAGAT 1020
CAGATTTTGS GCAAAACAGA CGAAACGATG AGCTACCGTG CCGTACCAGG TGTGGTGTAC 1080
ACCAATCCCG AGGTCCGCGG TGTGGGAGAG ACGGAAGAAT CGCTTCGCAA AGCAGGACGT 1140
GCCTACACTG TTCGTCCCT TCCATGACC TTCTCCGGTC GATTGTAGC AGAAAACGAA 1200
25 CAAAGCAATG GAGAGTGCAA ACTACTACTT GATGAAGAGA ACCGCTTGAT CGGAGCACAC 1260
CTCATTCGCA ATCCGCGCGG CGAACTCATC GTAACGCTG CCAATGGCCAT CGAGACCGGC 1320
ATGACGGATC GACAAATCGA ACGAATCATA TTCCCTCATC CGACTGTAGG CGAAATCCTA 1380
AAAGAAACTC TCGCGGAGG T 1401

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(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(v) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

50

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

55 CCTAAGATAC TTATGGAAT GAAAAGATT TTATCACTTG GTCTTCTGCT TGTGGGATTC 60
ATTCCGATGA AGCTTTCTGC CCAACAGGCT CAGCCACTCC CTACAGATCC GGCTGTTCGT 120
GTGGGTAAAT TGGACAACGG ATTGACTTAT TTATCCGTC ACAACGAGAA CCGGAAAGAT 180
CGTGGGATT TCTTTATCGC ACAAAGGTA GGTCTATTTC TTGAAGAAGA TAGCCAGTCC 240
GGTTTGGCTC ACTTCTTGA ACACATGGCT TTCAACGTA CGAAGAACTT CCGCGTAAG 300
60 AACTTGATCA ACTATCTCGA AACGATCGGT GTACGTTTCG GTCAGAACCT GAACGCTTCT 360
ACCGGATTCG ACAAGACGGA ATATACGATA ATGGATGTGC CGACTACACG TCAGGGAATC 420
ATCGACTCCT GCTTGCTTAT CCTGCATGAT TGGAGTAACA ATATTACCCT CGACGGGCAT 480
GAGATCGACG AGGAGCGCGG TGTGATCCAG GAAGAGTGGC GTGCTCGTCG CGATGCCAAC 540
CTTCGTATGT TCGAGGCTAT ACTTGCCAA GCTATGCCGG GTAATAAATA TGCAGAACGC 600
ATGCCCATCG GTCTGATGGA CGTCGTGCTC AACTCAAGC ATGATGAGCT GCGCAACTAT 660
65 TATAAGAAAT GGTATCGTCC CGACCTGCAA GGTCTGTTGA TCGTGGGAGA TATCGATGTG 720
GACTATGTGG AGAACAAGAT CAAAGAATCT TTCAAGGACG TTCTCTCTCC CGTGAATCCA 780
GCAGAGCGTA TCTATACGCC GGTAGAGGAC AACGATGAGC CTATCGTAGC CATGTCTACC 840
GAGCTGAGG CTACTACCAC GCAGCTCTCC ATCAGCTTCA AGAGCGACCC CACTCCTCAA 900
GAAGTGGGAG GATCGATATT CGGACTTGTG GAAGACTATA TGAACAGGT GATCACTACA 960
70 GCCGTGAATG AGCSTCTGTC CGAGATTACT CACAAGCCTA ACAGTCTTCT CCTCAGTSCA 1020
GGAGCTTTCT TCTCTAATT CATGTACATC ACCCAGACTA AGGACGCATT CAATTTTGTT 1080
GCCACGGTTC GTGAGGTGA AGCGGAGAAA GCGATGAACG CATTGGTGGC AGAGATAGAA 1140
AGCCTCCGTC AGTTCGGTAT CACCAAGGC GAATACGATC GTGCAACGAC GAATGTGCTC 1200
AAGCGATACG AGAATCAATA CAACGAAAGA GACAGCGTA AGAACAATGC TTATGCCAAT 1260
75 GAATACTCCA CCTACTTCAC CGATGGCGGC TATATCCCG GTATTGAGGT GGAATATCAG 1320

WO 99/29870

PCT/AU98/01023

12 / 490

ACGGTGAATG CTTTGTCTC TCAGGTTCTT CTGGAAGCAT TCAATCAGGC TATTGCCCAA 1380
 ATGATCGATC CGGTGAAGAA TGCTGTGTT ACCCTCACCG GTCTTCAAA GGCTGAAGCC 1440
 AAGATCCGGA GCGAAGCAGA CTTCTCTGCT GCTTTCAAAG CTGCTCGTCA GCAGAAAGTA 1500
 5 GAAGCCCAAG AAGACGAAGT CTCCGACCAA AAATTGATGG AGAAAGCTCC TAAGGCCGGA 1560
 AAGATCGTTT CCGAGAAGAA AGATCAGAAG TTCGGTACCA CGGAACCTAC CCTTAGCAAT 1620
 GGCATCAAA TATACCTCAA GAAGACCGAT TTCAAATCAA ACCAAATCCT GATGAGTGCT 1680
 CTCAGCCCGG GTGGTATCCT CTCCGGAAG CATGCTCCCA ACCAATCTGT GATGAATTGG 1740
 TTATGAACG TGGGTGGCTT GGGCAACTTC GATGCTATCC AGCTGGATAA GGTGCTGACA 1800
 10 GGTGCTCTG CTTCCGTATC TCCTCTTTG TCTCTGCTCA GTGAAGTCT TTCGGGCAAA 1860
 ACJACTGTAG AAGATATGGA AACTTTCTTC CAGTTGATCT ATCTCCAAAT GACTGCTAAC 1920
 CGCAAGGATC CCGAAGCGTT CAAGGCCACA CAGGAAAGT TGTACAATAA CTTGAAAAAT 1980
 CAGGAAGCCA ACCCGATGGC TGCGCTTATG GACTCTATCC GTCATACCAT GTACGGCGAT 2040
 AATCCGATGA TGAACCCAT GAAAGCTGCT GACGTGGAGA AAGTAAATTA CGATCAGGTA 2100
 15 ATGCTTTCT ACAATGAGCG ATTCTGCTGAT GCCGGCGACT TTATGTTCTT CTTTATCGGT 2160
 AATCTGGATG AAGCCAGAT GAAGCCATTG ATCGAACTT ATCTTGCTTC ATTGCCCAAC 2220
 CTCAGCGTG GCGATAAGAT GAATAAGGCT CAGGTACCGG CTGCCGTTT GGGAAAGATC 2280
 GATTGCAAGT TCGNAGAGGA AATGGATACT CCTTCGACTA CTATATTCGA TGTGCTGTCC 2340
 GGAATGTGG AATATACGCT CAAGAACAGT CTCCTGCTGG AAGTCTTCTC AGCCGTAATG 2400
 20 GATCAGGTGT ACACGGTAC CGTTCGCGAG AAGGAAGCG GTGCATACAG TGTGGCTGCA 2460
 TTCGGCGGTC TCGAGCAATA TCCTCAGCCC AAGGCTCTGA TGCAGATCTA TTCCCCACG 2520
 GATCTGCTC GTGCCGAGGA AATGAATGCT ATCGTTTGTG CTGAGTTGGA GAAGCTTGCC 2580
 AAGGAGGGCC CCAATGTGGA ATACTTTAAG AAGACTATCG AAAACCTGAA TAAGCAGCAC 2640
 AAAGAAAGTC TGGGTGAGAA TCGTTTCTGG CTCGAAGCCA TGAAGGCGTC TTCTTCGAA 2700
 25 GGAATGACT TCATCAGAA CTACGAATCC GTACTGAACG GTCTTACTCC TGCTGAATTG 2760
 CAAAAGTTT CCGCAGACCT CTTGAAGCAG CAGAATCGGG TTGTTGTCAT GATGCTCCT 2820
 GTTGCAAGG CTCRA 2885

(2) INFORMATION FOR SEQ ID NO:19

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 40 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
 45 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2058
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

TACACTATGA GTAAGAAAGG AACAATCGGG GTAACGAGCG ACAATATATT CCCGTCATC 60
 AAAAAATTCC TGTACAGCGA CCATGAGATA TTCCTGCGTG AGATCGCTTC CAATGCCGTG 120
 55 GATGCTACGC AGAAGCTGAA AACGCTTACA TCGCTCGGCG AATTCAAAGG CGAGACGGGT 180
 GACCTCGCGG TAACGGTCAG CGTGGATGAA GTGGCAGCGA CGATCAGGTT CAGCGACCGC 240
 GCGGTAGGGA TGACCGAAGA GGAGGTGGAG AAGTACATCA ATCAGATTGC TTCTCCAGT 300
 CGCGAAGAGT TTCTTAAAA GTACAAAGAC GACAAGGCCG CCATTATCGG CCACCTCGGA 360
 CTCGGATTTT ACTCGGCTTT CATGGTGTCC GAGCGAGTGG ACGTGATCAC GCGCTCTTTC 420
 60 CGAGATGATG CTACGGCGGT GAAATGGAGC TGCGACGCGT CGCCCGAATA CACGCTCGAA 480
 CCTGCGGACA AGGCTGACCG TGCCACCGAC ATCGTGATGC ACATCGATGA GGAGAATAGC 540
 GAGTTCCTCA AAAAAGAAVA GATAGAGGGG CTCCTCGGCA AATACTGTAA GTTCTTACC 600
 GTGCCGATCA TTTTCGGCAA GAAGCAGGAA TGGAAAGACG GCAAGATGCA AGATACGGAC 660
 GAGGACATC AGATCAACGA CACACATCCT GCCTGGACCA AAAAGCCTGC CGACCTCAAG 720
 65 GACGAAGACT ATAAGGAATT TTACCGTTCC CTCTATCCCA TGTCCGAAGA GCCTCTCTTC 780
 TGGATCCACC TCAATGTGGA CTATCGTTTC AATCTGACAG GTATCTCTTA TTTCGGGAG 840
 ATCAAAAACA ACTTGGATCT GCAGCGCAAC AAGATTGAGC TCTACTGCAA TCAGGTTTAC 900
 GTCACCGATG AAGTACAGGG TATCGTGCCG GACTTCTCA CCTCTGCA CGGGGTCTATC 960
 70 GATTGCGCGG ATATTCCCTT CAACGTATCG CGCTCCTATC TGCAGAGCGA TGCCAAATGTG 1020
 AAGAAGATCT CGTCTCATAT CACCAAGAAG GTGGCAGACC GTCTGGAAGA AATTTTCAA 1080
 AACGACCGCC CCACATTCGA GGAGAATGG GATAGTCTGA AGCTCTTCTG CGAATACGGT 1140
 ATGCTGACGG ATGGAAGTT CTATGAGCGT GCAGCCAAAT TCCTCTTTT CACCGATATG 1200
 GACGGACAGA AGTACAGTT GCAGCAATAC CGAAGCTCG TCGAAGGTGT ACAGACGGAT 1260
 AAGGACGGAC AGGTAGTGT TCTTATGCT ACGGACAGC ATGGACAGTA CAGCCACGTG 1320
 75 AACGTGATC CCGACAAAGG CTACAGCGTG ATGCTGTTGG ATGGTCAGT GGATCCGCAT 1380
 ATCGTGAGCC TGCTGGAGCA AAGTTGGAG AAGACACACT TTGTCGTTG CGATAGCGAT 1440

WO 99/29870

PCT/AU98/01023

14 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...789

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

AGATCTCTGC	AATCATTTCA	AAATAAAAAA	CACTCAAGTA	TGCTTAAGAT	AAAGAACCTC	60
CACGCCACAG	TACAGGGGCA	AGAGATATTG	AAAGGAATCA	ATCTGGAGAT	CAATGCCCGA	120
GAGATTCAIG	CTATCATGGG	GCCGAACGGA	TGGGGGAAAI	GTACGCTCTC	TTCCGTTTTG	180
GTGGGACATC	CCTCCTTTGA	AGTCACGGAA	GGAGAGGTGA	CATTCAATGG	AATCGACCTG	240
CTCGAACTCG	AACCGGAAGA	ACGTGCACAC	CTCGGACTCT	TTCTCAGTTT	CCAATATCCG	300
GTGAGATCC	CGGGCGTCAG	CATGGTGAAT	TTCTGAGGG	CAGCTGTCAA	TGAACATAGG	360
AAAGCGATCG	GAGCAGAACC	CGTATCGGCA	AGCGACTTCC	TCAAGATGAT	GCGAGAGAAG	420
CGTGCCATTG	TGGAGCTGGA	CAACAAATTG	GCCAGCCGTT	CTGTGAACGA	AGGCTTCTCC	480
CGTGGAGAAA	AAAAGAGSAA	CGAAATCTTC	CAAATGGCTA	TGCTCGAACC	CAAGCTGGCT	540
ATTTTGGACG	AAACCGATAG	CGGGCTCGAT	ATCGACGCTC	TCCGCATCGT	AGCAGGCGGG	600
GTAAACCGAC	TCCGCTCTCC	GGAGAATGCT	GCTATTGTGA	TCACACACTA	TCAGCGTTTG	660
CTCGAGTACA	TCAAGCCGGA	CTTCGTACAC	GTCCCTTACA	AGGGGCGCAT	CGTCAAGTCG	720
GGAGGAGCCG	AGCTGGCTCT	CACGCTCGAA	GAATAAGGCT	ACGACTGGAT	CAAGGAAGAG	780
ATAGGAGAA						789

(2) INFORMATION FOR SEQ ID NO:22

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1386

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

AGCATGGCTA	AGGAGAAAC	GATCTACGTC	TGCCGTTTCT	GCGGAACCAA	ATACGCCAAA	60
TGGCAAGGCA	ACTGCAATGC	CTGTGGAGAG	TGGAAGTGA	TTGATGAGGA	GAAGGTGCCG	120
GCACCGGCAT	CGGGCAAGCA	TGCAGCCAAG	AGTTTATATG	CTCGGGAGCA	GGACAACCGG	180
CCAGACTCT	TACAGGATGT	GGAGTCCGGC	GATGAAGAGC	GTATTGCGCT	CGGCGATGAA	240
GAGTTGACAC	GCGTACTGGG	TGGAGGAATT	GTCAAAGGAG	CATTGTCTCT	GCTTGGGGGC	300
GAGCCGGGAA	TGGGTAAGTC	CACGCTTATC	CTCCAGACGG	TGCTGCGTCT	GCCGCACTTG	360
CGCACGCTCT	ATGTGTGCGG	CGAAGAAAGT	GCCCGACAAC	TGAAGATGCG	CGCCGAACGA	420
CTGGGGCAAG	CCATGAATGG	GTGCTACGTA	TACTGCGAAA	CGAATATAGA	GAGGATACTC	480
TCCCGTGCA	AAGAACTCAC	ACCCGATCTC	CTCGTGATAG	ACTCTATACA	GACGGTCTAT	540
ACCGAGGAAA	TGGAAAGCTC	GCGCGGCAGC	GTGGGGCAGA	TCCGCGAATG	TGCCGCTTAA	600
CTGCTCAAT	ACTGCAAGAC	TACGGGTATC	CCCGTCATCG	TCATCGGACA	CATCACCAAA	660
GAAGGTAGCA	TAGCCGGACC	GAAGGTGCTG	GAGCATATAG	TGGATACGGT	GCTTCTCTTC	720
GACGGGGATA	AGCATCATCT	CTACCGGATA	CTCCGAGGAC	AGAAGAACCG	CTATGGCAGT	780
ACTTCCGAGC	TGGGGATATA	CGAGATGCGG	CAGGACGGTC	TGCGTGGCGT	GGAGAATCCG	840
AGCGAACATC	TCATCACACG	CAATAGGGAA	GACCTCAGTG	GCATAGCAAT	AGCCGTAGCG	900
ATGGAGGGCA	TTCCGCCGAT	ACTCATCGAA	GCGCAGGCTT	TGGTCAGCTC	GGCCATTAT	960
GCCAACTCCG	AGCGTTCGGC	CACGGGCTTC	GATATTCCGG	GGATGAACAT	GCTCTTAGCC	1020
GTACTGGAGA	AACGTGCGGG	CTTCAAGCTC	ATACAGAAGG	ATGTGTTTCT	GAACATTGCT	1080
GGAGGTATCA	AAATAGCCGA	TCCGGCTACG	GATCTGGCCG	TTATCTCGGC	AGTGCTGGCG	1140
TGAGTCTCGG	ACATCGTTAT	CCCGCCGGCC	GTATGCATGA	CGGGCGAGGT	CGGACTCTCC	1200
GAGAGATAC	GTCCCGTGAG	CCGCATCGAG	CAGCGCATAA	CGGAAGCGCG	TCCGATAGGG	1260
TTCAVAGAGA	TATTGGTACC	GGCCGATAAT	TTCCGGCAGG	AGGATGCGGG	CCGCTTCGGT	1320
ATTCCGCTCG	TGCCGGTCAG	AAAGGTGGAG	GAAGCCTTCC	UCCATCTGTT	CTCGAAAGGA	1380
AGAGAA						1386

WO 99/29870

PCT/AU98/01023

15 / 490

(2) INFORMATION FOR SEQ ID NO:23

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

25 GGGTCTTGTG GAAGTAGCCC AGCAATGGGC CGATCAGGGT GTTCGGGTG TGATCSCCGG 60
 ATTGGACATG GACTTTCGAC GTCAGCCTTT CGGACCTATG CCGGGCTTGT GTGCCATAGC 120
 CGACTCCGTG ACCAAAGTTC ATGCCGTGTG TGTGGAATGC GGCCGATTGG CCAGCTATTC 180
 TTTCGGTCGT GTCCAAGGCG ATCAGCAAGT GATGCTGGCG GAACTGAACG AATACAGTCC 240
 CCTCTGCAGA ACCTGCTACA GGAATGCGAG TTCTCCCCCA CAAACAGAAG AAATCCATTC 300
 30 GACAATATGA ATAGCAGACA TCTGACAATC ACAATCATTC CCGGCTCTCT CCTCTTTGTA 360
 CTGACATTGG GCGGCTGCTC CGTAGCCCAA CAAGATACGC AGTGGACTCT CGGCGGAAG 420
 CTCTTTACTT CCGCGTGGAT ACAACGTTTC GCCGAATATC AAGCGCTTTG CATTGAGGCA 480
 TACAACATCG CTACGGAAAG AGTGGACGCT CTACCGGCAG AACGTAAACA AGGAGATAGG 540
 35 TATCAGGCTC TCAGGGGCAA GGATTATGAT GAAGAGACTT GGGGGAAATG GTGTGCACAG 600
 GCCGATGCCG ACACACTGGC AGSAGCTTTG TCTTTCTTCC TCCATGCAGC GAACAAGGGG 720
 ATCGAGGTCT TTACGTCAC CAACCGCAGA GACAATCTGC GCGAAGCAAC TCTTCAGAAC 780
 CTTGAGGCTT ACGGATTCCC CTTTGCCGAT GAAGAACATT TGCTTACGAC CCATGGGCCA 840
 40 TCCGACAAAG AACCCCGTCG GCTCAAAATA CAAGAACAGT ATGAAATAGT ATTGCTCATA 900
 GGAGACAACCT TGGGCGACTT CCACCACTTC TTCAATACGA AAGAAGAGTC CGGACGCAAA 960
 CAGGCTCTGG GCCTGACAGC CGGGGAGTTT GGGCCGCACT TCATCATGCT GCCCAATCCC 1020
 AACTACGGAT CTGGGAACC GGCATGGTAC GGGCGGAAGT ATCCGCCACT GCCCGAAAGA 1080
 GACAAAGCAC TTAACAACCT GCACTCACAG AACAGCAGA 1119

(2) INFORMATION FOR SEQ ID NO:24

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 60 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1278
- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

70 CGTTGGGGTT TTTCTAATTT TGTGGCCATG AGCACCATA TAGATGTACA ACAGATCAAA 60
 CAGCGTTTCG GCATCATCGG TAGCAGTCCG CTGATGGAAC ATGCCATACG AGTGGCAGCA 120
 CAGGTGGCTC CTACCGACAT GTCCGTCTCT GTGACGGGCG AGAGCGGTTT CCGGAAAGAG 180
 TTCTTCCCACT AGATAATCCA CTAATACAGC GCGCGGAAAC ATCATAGCTA CATTGCAGTC 240
 AATTGGGAG CCATCCCGCA AGGAACCATC GATTCGAGC TGTTCCGACA CCGCAAAAGT 300
 75 TCTTTACCG GAGCCGTATC GATCGCAAG GGGTACTTTC AAGAAGCATC CCGCGGCAGC 360
 ATCTTTCTGG ACGAAGTGGG CGAAGTGCCT TTGCCACGC AGGCGAGGCT GCTGAGGGTG 420

WO 99/29870

PCT/AU98/01023

18 / 490

5 GGTACCAGCC GGGTGGAAAT TCCTTCGGTA GTCATTACAG GCCGCAATAG AACAAAAGCT 300
CTCAAGCGTG AAATCGCATT TAGTTCGGCT TTGCCCAAG CAAAACATGC AGCTCAATAC 360
ATTCCCGCTC ATAATGGGAA GAGCGAGCAG TTTGCTTTTA CAGGAGAACA TGCTTATGCA 420
TCATGGATGA TGGATGCCAA GTTTGTGGTT CGTGAGGAGG TACGAGGTTG TGCTAAATGC 480
CCTGTAGGTC TCTCGAGTAA TATTGTTCTT TTTGATCCAC TCTTCAATCC GGCAGAGGCT 540
CCTTATTGTT TGGCACACAT TACTCCGGCA GAAGAAGTGG AAAACACGCG AGAGTCCAGC 600
TTCCGATGCT ATATCAACTT CAAAGTCAAT AAGGCAGATG TCCTTCCTGA GTATCGCAAC 660
AATAAGGCGG AGTTAGAGAA AATCAAAGAA TTTGTAAACA CCGTTAAGGC TAA'CCCAAC 720
TATTCCGGTCA ATAAATGAT CATCGAAGGG TTTGCTTCT CCGAGGCTTC AATAGCCAC 780
10 AATAAGGCTT TGTCGGAGCG CCGTGTCTAA AGACTCGCGG AAGAATTGGT GCGTAAGTAT 840
GGCAAAACAT TGCCGAATAT AACCACTGAA TTCGSCGGTG AAGATTGGAA GGGGCTGAAA 900
CTGGCTATCG AAAAGAGTGA TATAGCCGAT CGTGACCGCG TATTGGAGAT AATCAACTCC 960
GATAAATATG CCGATGATGA TGCACGTGAA CAGGCTCTGA AGCAACTTTC GTCTTATCGT 1020
TATATCTTGG ATCAGATCTA TCCGAATTG CGTCGCAATA CGATAACCAT GGGGTATATC 1080
15 GTTCGTGATT ATACCCTCGA AGAAGCTCGT GAAATCATTA AGACTGCTCC GAAAGAACTT 1140
AGTGAGGCGG AAATGTACCG TGTGGCAATG TCTTATCCTG AGGGGCACCA AGAGCGTTTG 1200
TTTGCTCTGA ATACGACCCT TAAGTATTTT CTTGAAAGTG TAAACGGGCG AATCAATTTG 1260
GCTGTAGCCG CTTTAAATGG TGGAGACGTT CAACAGGCAA TTGCTCTGTT GAGTCCGATT 1320
CAGACAGAAA AGGGTGTAA GAAATCCTT GGAGCTGCTT ATGCTCGTAC GGGAGATTTT 1380
20 GCTCGTCCG AAACCTTCTT CCGTAAGGCC GTTGCAGAAG GAGATGCAAA TGCGCAGCGC 1440
AACCTCGATA TGCTGCTTGG CAAAAAG 1467

(2) INFORMATION FOR SEQ ID NO:28

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

50 GACATGGCAG AAAAAAGAGA CTATTACGAA GTCCTCGGTG TATCGAAGAA TGCCACCGAC 60
GATGAACTGA AAAAAAGCATA TCGCAAGAAG GCTATCCCAT ACCATCCTGA TAAGAACCCC 120
GGTGACAAGG AGGCCGAAGA GCACCTCAAA GAGGTAGCTG AAGCCTACGA CGTATTGAGC 180
GATCCGCAGA AGCGCAGTCA ATATGACCAG TTGCGCCATG CCGGATTGGG CGGAGCTGCC 240
GGTGGAGGTT TCAGCGGAGG CGGTATGTCC ATGGAGGATA TTTTCAGTCG CTTGGGTGAT 300
CTATTCGGTG GGTTCGGCGG TTTCCGGCGA TTCTCCGATA TGGGCGGTGG CAGTCGCAGA 360
CGTGTTCGCA GAGGGTCTGA CCTGCGAGTA CGAGTGAAGC TTTCTTTGGC CGATATAAGT 420
55 AAGGTGTGG AGAAGAAAGT GAAGGTAAAA AAGCAGGTAG TGTGCAGCAA ATGTCGTGGC 480
GATGGCACGG AAGAAGCCAA TGGCAAGACT ACCTGCCAGA CTTGCCATGG AACCGGCGTG 540
GTTACACGTS TGAGCAACAC TTTCTTGGG GCCATGCAGA CCCAGAGCAC TTGTCCTACT 600
TGCCACGGAG AGGGTGAGAT CATCACGAAG CCATGCTCCA AGTGTAAAGG CGAAGGTGTG 660
GAGATCGGCG AAGAGGTGAT CTCATTCCAC ATCCCTGCCG GTGTAGCCGA AGGAATGCAA 720
ATGTCCTGTA ACGGCAAGGG AAATGCCGCG CCCCAGGAG GCGTGAATGG CCACTTGATA 780
60 GTCGTGATCG CCGAGGAACC GGATCCGAAT CTGATCCGCA ATGGCAACGA TCTGATATAC 840
AATCTGCTTA TATCCGTTCC GTTGGCTATA AAAGGAGGTA GTGTGGAAGT GCCGACGATA 900
GACGGACGAG CCAAGATCCG CATCGAGGCG GGGACACAA CCGGCAAGAT GCTGCGTTTG 960
CGCAATAAGG GATTGCCCG CGTAAACGGC TATGCCATGG GAGACCAACT GGTGAATGTC 1020
AATGTCTATA TCCCGGAATC GATCGATGCC AAAGATGAGC AGGCTATCGC AGCGATGGAA 1080
65 AACTCGGACA GCTTCAAACC TACCGATGCT GTCGTGAAGG ATATAGACAA GAAATACAGA 1140
GAGATGCTGG AT 1152

(2) INFORMATION FOR SEQ ID NO:29

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

WO 99/29870

PCT/AU98/01023

19 / 490

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

CGATTGCGATT	CAACAACATAA	TGCTCACA	ATTAAATTTAA	GAACAGAGAT	GAAAAAAGT	60
ATTTTAGCGA	CITTTGGGACT	TATGGCCATT	GCCATGCTCT	CATGTTCAAG	CAACAACAAG	120
GATTTTGAGA	ACAAAGGGGA	GGCTACTCTT	TTGGTAACGT	TTGGTAGCTC	CTATAAAGCT	180
CCACGGGAAA	CCTATGCGAA	GATTGAGAAG	ACTTTTGCCG	CAGCTIATCC	CGATCAAAGG	240
ATAGGTGGA	CATACACGTC	TTCTATTATC	CGAAAGAAAC	TGGCTCAGCA	GGGTATTAT	300
ATCGATGCTC	CGGATGAGGC	TTTGGAGAAA	TTGGCTCGTC	TGGGTATATA	GAAGATCAAT	360
GTACAGAGTC	TTATGTGTAT	TCCCGGCCGA	GAATATGATG	AGATGATCGA	CTTTGTCAAT	420
AAGTTTAAGG	CAGCACATAG	TGATATTACT	GTGAAGGTAG	GGGCTCCGCT	TTTGGATACC	480
GATGAAGATA	TGCGGAGGT	GCCAGAGATC	TTGCACAAGC	GTTTTCAGCA	AACGATAGAG	540
AAAGGTGAAG	CTATTGTATT	CATGGGACAC	GGCACCAGGC	ATGCTGCCAA	TGACAGGTAT	600
GCCCGTATCA	ATAAGATCAT	GAAGAATAT	AGCAAGTTCA	TGATCGTCGG	AACCGTCGAG	660
TCCGATCCCT	CTATCAATGA	TGTTATTGCC	GAAGTAAAG	AAACCGGTGC	CACGGCCGTA	720
ACAATGATGC	CGCTGATGAG	TGTGGCAGGC	GACCATGCTA	CGAATGATAT	GGCCGGAGAT	780
GAGGACGATA	GCTGGAAGAC	GTTGCTGACC	AATGCCGGCT	ACACAGTTTC	TATAGACAAG	840
CTGGACATG	GCAATTCTC	AGCTCTTGGG	GATATAGAAG	AGATCCGGAA	TATCTGGCTC	900
AAGCATATGA	AAGCCACCTC	TGCTCGC				927

(2) INFORMATION FOR SEQ ID NO:30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

CGGAGAGATG	CGCGGAGGCA	ACTGGTACGC	CGTAGGAGGA	AAGAGCTATC	TGGCACAGCA	60
AATACCGGAT	GCCGGAGGAG	AGTATTTTCT	GAAAGACGAT	CAGCGATCCG	GTGGTGTTTC	120
CCTCGACTTC	GAGACGGTCT	ACAGCCGATC	CGATTCCGGT	CGCTACTGGC	GAATCCTCAA	180
CAGCTATCCC	GGGGAGTTTC	GTTACGAAGC	TTTGAAAGCC	GAAGACAGCC	GATATGCCGA	240
TTTCAGGGCA	TTCAAGGAAA	AAGGCGTGAT	ATACTGCAAC	CTGAGGGAAA	CAGCCTTCTA	300
CGAATCATG	CCCATGCCATC	CCGATTGGGT	GCTGGCCGAT	CTTATCGCTA	TCITGACACC	360
CGGACTACTT	CCCGACCAAC	AACCGCATTT	CTATTATTTG	CTCCAATGAC	ATCCGTGAGC	420
CACTTACGTA	CAATTCTCTT	CGCAGGTATC	CTGGCTGCGC	TGGGAGGGGC	TGTAATCATT	480
CTCTTCGGGG	TTAATCTCTT	CCTCGGCTCG	GTGGCTATTC	CGATGAGCGA	GATCTTCCGA	540
CATCTTTTTT	CAGATCGTCC	CGAAGGAGGA	GAAGCACTCG	TGCACTACAA	TATCCTATGG	600
AAATCCCGCC	TGCCCGAAGC	CCTCACGGCT	GCTTTTGCCG	GCGCAGGTTT	ATCCGTTAGT	660
GGCTTCGAGA	TGCAGACCGT	CTTTCCGAAT	CCTTTGGCCG	GTCCGTCCGT	TCTCGGCATC	720
AGCTCCGGTG	CCAGTTTGGG	TGTTGCTTTG	GTGTTCTGTC	TGAGCGGGTC	GCTGGGAGGA	780
GTGGCATTTA	GTAGCTTGGG	TTATATGGGC	GAGGTGCCCA	TGAATATAGC	CGCTGCCGTA	840
GGCTCGCTGG	CAGTAATGGG	GCTGATCGTT	TTTGTGAGCA	CCAAGGTGCG	CAGCCACGTT	900
ACGCTGCTCA	TTATCGGCGT	TATGATCGGA	TATGTAGCCA	CTGCCGTGAT	CGGGGTATTC	960
AAGTTTTCAT	GTATCGAAGA	AGATATTCGG	GCATACGTAA	TTTGGGGGTT	GGGCAGCTTT	1020
TCCCGTGCCA	CGAATTCGCA	ACTGAGTTTC	TTTGGCATTC	TGATGTTGAT	CTTTATTCGG	1080

WO 99/29870

PCT/AU98/01023

20 / 490

5 GCGGCTATGC TCCTTGTCAA GCAGTTGAA CTCTTATTGC TGGGAGAAAG CTACGCACGT 1140
AATCTGGGAC TGAATACTCG TCAGGACACG CTGCTCGTGA TCTCTTCCGC CAGTTTGTCTC 1200
ATCGCTACCG TCAGGAGCTA TTGGGTCCTC ATCGGCTTT TGGGATGGC TGTGCCACAC 1260
TTGGCACGGG TTATCTTTCA CACATCGGAT CATCGGATCC TGATGCCTGC TACCTGTTTG 1320
ATTGGAAGTG CTCTGGCTCT TTTCTGCAAT ATCATTTGCTC GTATGCCGGG GTTTGAGGGG 1380
GCTTTGCCCG TCAATTCCGT AACGGCTTTG GTGGGAGCAC CTATTATCGT CACCGTTTTC 1440
TTCCGGCGCA GACGCTTCAA GGAAGAAACC GAC 1473

10 (2) INFORMATION FOR SEQ ID NO:31

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
(11v) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2289
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

35 CATTTTTTAG TAACGATTAT GCGGACAAA ACTATCTTTT TTGCGATTAT CTCTTTTATT 60
GCTCTATTGT CGTCTTCTCT GTGGGCTCAG AGCAAAGCCG TTTTAACCGG TAGTGTGTGG 120
GATGCGCGAA CCGGAGAGCC TCTTGCCGGT GCTCGAATCG AAGTCAAACA CACCAACATA 180
GTAGCCGGTG CCGATGCCGG CCGACATTTT GAGATCAAGA ACCTGCCGGC AGGGCAGCAT 240
ACTATTATAT GTTCGTTGGG GGGGTATGGA CAGAAAGAGG AGGTGGTTGC CATCGAAGCC 300
GGACAGACCA AACGATCTC TTTTGCAATG CGACTGCGAA CGAACAACTT GGAGGAAGTC 360
GTCCGTACCG GTACCGGTAC ACGTTACCGC TTGGTCCGAT CTCTGTGGC AACGGAAGTC 420
CTTACCGCTA AGGACATAGC CTCCTTCTCG GCTCTACTT CCGAGGCGCT ATTGCAGGGG 480
CTGAGTCCGT CTTTGTGACT CGGCCCCAAT CTGATGGGCT CTTTCATGCA GCTGAACGGC 540
CTTAGCAGTA AGTATATCCT CATCCTTATC GATGGTAAGC GTGTGTACCG CGATGTAGGC 600
GGTCAGGCGG ATTTGAGTCG TATTTCTCCT GATCAGATCG AACGGATCGA ACTGGTGAAA 660
GGTGCTTCGA GTTCGCTCTA CCGATCCGAT GCCATCGCCG GGGAATCAA TGTGATCACA 720
AAAAAAGATA CGAATCGACT GAGTGCAATC ACGTCACATC GCATATCGAA GTACAACGAT 780
CGGCAAAACA ATACTTCGCT CGATATAAAC ATCGGTAAGT TCAGTAGCAA TACCAACTAT 840
TTCTTCTACC ATACGGATGG CTGGCAGAA AGTCCGTTCC AAATAAAAAA GAAAAAAGGA 900
TCCGCGCAAC CGGTCTTGA GGAAGCTAT AAGAAACTT TCTGTGCACA GGAATATCAG 960
GGTGAAGGCC AATCGCTTTC CTATTATGCA ACTAACATC TTAGCTTCAG CGGAATGTG 1020
CAGTACAATA AACGTCAGAT CTTCACTCCG ACTTTTCCG AAAAGAAGGC CTATGACATG 1080
GATTATCGTG CPTTGACGGC TTCACTCGGT ACGAACTATC TTTTCCCAA TGGTCTGCAT 1140
ACGCTTTCTT TCGATGCCG CTACGATCGC TTCCGTTTCG GATATTGTGA TCATGACAA 1200
GACAGCAGTG AGAGCCTGAT CAACAACCAA GGTCAGACCG AGCAACCCAC ATTCTTTCCG 1260
GGTCAGCTAC GCAATAAAAA CGATCAGATC CGATACACGG CAGAGGCTCG CGGTGTATTT 1320
55 ACACTGCCTT ATGCGCAGAA ACTGACCGGC GGTTTGGAGT APTTCCGTGA GGAATTGATC 1380
TCTCCCTATA ATTTGATTAC CGACAAGGCA GATGCTTCCA CGCTCTCTGC TTATGTACAA 1440
GATGAATGGA AACCGCTCGA TTGGTTCAAT ATGACAGCCG GTTTCGCTCT GGTACACCAT 1500
CAGGAGTTTG GTACACGAAT GACGCCTAAG GTATCCATAC TCGCCAAATA TGGGCGCGTG 1560
AACTTCCGGC CTACGTATGC TAACGGCTAT AAGACTCCCA CGCTGAAAGA GCTTTTGTGA 1620
60 CGGAACGAAC TCACCACTAT GGGTTCGCAC AATCTCTATC TCGGCAATGC GGATCTTAAG 1680
CCACAGATGT CGGATTATTA TGCTTTGGGC TTGGAGTACA ATCAAGGCCC TATCTCGTTC 1740
AGTGCAACGG TTTATGACAA TGAATTCGCG AATCTGATCT CCTTTATGGA TATACCGACC 1800
TCACCGGAGC ACGAAGCTCA GGAATCAAG AAAACCAAGC AGTATGCCAA CATAGGAAA 1860
GCTCCGAGCC GCGCCCTTGA TGCTCTATGT GATGCTCTA TCGGTTGGGG TATCAAGTTA 1920
65 GGAGGCGGAT ACAGCCTCGT GGAAGCTAAG AATCTCCAGA CCGATGAGTG GCTGGAAGGA 1980
GCTCCACGTC ATCGTGCCAA TGTGCACGCT GATTGGGTTT ACTACTGGGG TCAGTATAGA 2040
CTTGGCGTGA GCTTTTTCGG CCGTATTTCG AGCGAGCGTT ACTACAAAGA CCGCAATGCT 2100
CCGCACTATA CCTGTGGCG ACTCGCCACA TCGCATCGTT TCGCTCATTT CCGCCACATC 2160
ATCCTGGATG GAACGCTCGG TATAGACAAC CTGTTTGAAT ACGTGGATGA TCGTCTATG 2220
70 GGTGTCAATT ATGCTACCGT AACGCCGGGA CGTACTTTCT TTGCTCAAAT AGCGATTCCA 2280
TTCAACAAC 2289

75 (2) INFORMATION FOR SEQ ID NO:32

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1095 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

25	TGCTGCGCAA	GGCTTCGGGA	CACCTCTCCU	CGGAAGAAGT	CGTTTCGGAA	TGATACCGTT	60
	TTTCCTTATT	TCGTTATTCA	TCTGATCAAA	CATATTATCA	TTATGACGGA	CAACAAACAA	120
	CGTAATATCG	TATTCCTGGC	GTTCCTCCTC	TTGCTGGGAG	TCATCGCAGT	GSTGACGATC	180
	GTTGGTTTTT	TCATGCTCAG	ACCGGCCGAG	GAGATTATCC	AAGGACAGAT	AGAAGTGACC	240
	GAATACCGAG	TGTCCAGCAA	AGTGCCCGGG	CSCATCAAGG	AACCTAGGST	ATCCGAGGGA	300
	CAGCAGSTGC	AGGCCGGCGA	TACCTCTGGT	GTCTCGAAG	CCCCCGACGT	AGCGGCTAAG	360
	ATGGAGCAGG	CAAAGGCTGC	CGAAGCAGCT	GCACAGGCTC	AGAACGCCAA	GGCTCTCAAA	420
	GGAGCAGGCA	GCGAACAGAT	ACAGGCAGCC	TATGAGATGT	GGCAGAAAGC	TCAGGCCGGC	480
	GTAGCCATAG	GCACCAAGAC	ACACCAAGCC	GTGCAGAAC	TCTATGACCA	CGGAGTGGA	540
	CCGGCTCAGA	AGTTGGAAGA	AGCCACTGCC	CAGCGCGATG	CGGCCATCGC	TACGCAAAAA	600
	CGGCCCGAAG	CCCACTACAA	TATGGCTCGC	AACGGTGCCG	AACGCGAAGA	CAAGCTGGCA	660
	GCTTCTGCCC	TGCTCGATAG	AGCGAGAGGA	GCCGTGCGCG	AGGTGGAGTC	GTACATCAAC	720
	GAACCTTACC	TCATCGCCCC	ACGGGCAGGC	GAAAGTGTCG	AGATATTCCC	CAAGCCCGGC	780
	GAACCTGTAG	GTACCGGCGC	ACCTATCATG	AATATCGCCG	AGATGGGCGA	TATGTGGGCC	840
	AGCTTTGCGG	TTCTGTAGGA	TTTCTCTCAG	AGCATGACCA	TGGGAGCCGT	TCTGGAGACT	900
	CTGGTCCCGG	CTCTGAATGA	AGAAAAAGTA	CGCTTCAAGA	TCACATTCAT	CAAGAACATG	960
	GGTACCTATG	CTGCCCTGGA	AGCGACCAAG	ACAACAGGGC	AGTACGACCT	GAAGACCTTC	1020
	GAGGTAAAGG	CCACCTTTCG	GGATAAAGAC	AAGGCACAAA	AGCTACGCCC	GGGTATGTCC	1080
	GTGATCATAC	GCAAG					1095

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 960 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

65	CCGCAATCCT	CTCCTGATCG	AAGAAGCTTC	CAAAACGTCA	TGAATAAATA	TCATTCTCAA	60
	AGCGTTTTAG	AGGTGCGGCA	AAITGGGATT	GTGATTATCT	TTGCGCCCAT	AGTACGGAAT	120
	GTACATCAAC	AACCCCTTTT	TTTAAAGCAT	AAATCAATTA	TGCGTATTGT	CAGTAATTTT	180
	TTGTTCTGCT	CTTTTTCGGT	TTTGCTTTTT	GCATCATGCC	GTTCGCCAGC	AGAAAAGGTC	240
	CTTTACCTGC	AAGATATCCA	AACCTTTAAT	CGGGAGATTA	TCGCTAAACC	ATATGACGTA	300
	AAAATTGAGA	AGGACGATGT	GCTGAACATC	CTTGTCAGCA	GTAGAGACCC	GGAGCTTTCA	360
	ACGCCCTACA	ACCAAGTGTT	GACCACTCGT	GCACTGGCCC	GCAACGGCTA	TGGAACGAAC	420
	TCGAACGAAG	GCTTCTTGST	CGATTTCGAA	GGGTACATCA	ATTATCCTAT	TTAGGCCAG	480
	ATCTATGTAG	AGGCCCTTAC	TCGTACCGAA	CTGGAGAAGG	AGATAAGAA	GAGGATTATT	540
	TCCAGTGGAT	TTATCAAGGA	TCCTACGGTA	ACGGTGCAGC	TTCAAAATTT	CAAGGTGTCG	600

WO 99/29870

PCT/AU98/01023

24 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS

5 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...3138

10 (x) SEQUENCE DESCRIPTION: SEQ ID NO:36

GACTTCCCTT	GGGTTAGGCT	AAAACCGGAG	AAGAAAGGAA	AACAACATAA	CAGTAATAAT	60
TTTAAAGTTA	ACGCAAAAGA	AAAGTCTATG	AAAAGAATGA	CGCTATTCTT	CCTTTGCTTG	120
CTGACGAGCA	TTGGGTGGGC	TATGGCCGAG	AATAGAACCG	TGAAGGGTAC	AGTTATCTCC	180
15 TCCGAGGATA	ATGAGCCCTT	GATCGGCGCG	AATGTCGTGG	TTGTCGGAAA	CACCACTATC	240
GGTGTGCAAA	CGGACTTGGG	TGGCAACTTC	ACGCTTAGCG	TGCTCGCCAA	TGCCAAAATG	300
TTGAGAGTGT	CCTATTCCGG	TATGACTACC	AAAGAGGTCC	CCATCGCTAA	TGTGATGAAG	360
ATCGTACTGG	ATCCGGACTC	TAAGGTTCTG	GAGCAGGTAG	TTGTATTGGG	TTACGGTACG	420
GGACGAGAAC	TCAGCACTGT	TTCCGGTTCT	GTGGCCAAAG	TGTCCAGCGA	AAAGCTCGCG	480
20 GAAAAGCCCG	TTGCCAATAT	CATGGATGCC	CTCCAAGTTC	AGGTAGCCGG	TATGCAGGTT	540
ATGACTACAT	CCGGTGACCC	TACTGCCGTC	GCCTCTGTGG	AGATCCATGG	TACAGGGTCG	600
TTGGGGGGCAA	GCTCTGCACC	ATTGTATATC	GTGGATGATA	TGCATACTTC	TTTGGATGTT	660
GTGGGCTACGA	TGAATCCGAA	TGATTTTGAA	TCTATGTCCG	TTTGAAGA	TGCTTCTGCA	720
ACATCTATTT	ATGGAGCTCG	TGCTGCAAAC	GGAGTCGTTT	TCATTCAAAC	GAAGAAAGGT	780
25 AAAATGAGCG	AGAGAGGTCC	TATTACCTTT	AATGCCAGTT	ACGGGATTTT	TCAATCCTTG	840
AATACTAAGC	CCCTTGATTA	TATGATGACT	GGAGATGAAT	TGCTGGATTT	TCAGGTGAAG	900
GCAGGTTTTT	GGGGGAACAA	TCAAACCGTT	CAGAAGGTTA	AAGATATGAT	CCTTGCCGGA	960
GCTGAAGATT	TGTATGGCAA	TTATGATTCT	TTGAAAGATG	AGTATGGTAA	GACATTGTTC	1020
CCAGTGGATT	TTAATCATGA	TGCAGACTGG	CTCAAGGCTT	TGTTTAAAC	AGCACCCACC	1080
30 AGTCAAGGTG	ATATTTCTTT	CTCCGGAGGG	TCTCAGGGAA	CTTCATATTA	TGCCCTCTATA	1140
GGCTACTTCG	ATCAGGAAGG	TATGGCTCGT	GAACCGGCAA	ATTTTAAGCG	CTATAGTGGC	1200
CGGCTCAACT	TCGAAAGTCG	TATCAATGAA	TGGCTGAAGG	TTGGTGCAAA	TTTGTCTGGT	1260
GCGATAGCGA	ATAGACGATC	TGCCGACTAT	TTTGGAAAGT	ATTATATGGG	GTACGGTACT	1320
35 TTCTGTGTGT	TAAAGATGCC	TCGTTATTAT	AACCTTTTGG	ATGTGAATGG	GGATTAGACA	1380
GATGTCTATT	ACATGTATGG	AGCTACACGA	CCTTCATGTA	CAGAACCCTA	CTTCGCAAAA	1440
ATGAGACCGT	TCAGTTCCGA	ATCACATCAG	GCCAAATGTA	ATGGTTTCGC	CCAGATTACT	1500
CCGATCAAGG	GCCTTACTTT	AAAGGCACAG	GCTGGTGTGG	ATATTACTAA	TACTCGCACT	1560
TCCTCTAAGA	GAATGCCCAA	TAAATCCGAT	GATTCTACTC	CTCTCGGGA	AAGAAGAGAA	1620
40 AGAGGTTATC	GAGATGTTAG	CAAGTCTTTT	ACAAATACGG	CTGAATATAA	GTTTTCATTT	1680
TGTAAGAAAC	ATGATCTTAC	AGCATTGATG	GGCATGAAT	ATATTGAATA	TGAAGGGGAT	1740
GTTATTGGGG	CATCTTCTAA	AGGATTGTA	AGTGATAAGT	TGATGTACT	GAGCCAGGGA	1800
AAAACCGGAA	ATAGTTTGTG	TTTGCCTGAA	CACAGAGTCC	CTGAATATGC	CTATTGTGCT	1860
TTCTTTAGTC	GTTTAAATTA	CGGTTTGTAC	AAATGGATGT	ATATAGATTT	CTCTGTTCTG	1920
AATGACCTAT	CCTCTCGATT	CGGATCCAAT	AATAGAAAGG	CGTGGTTCTA	TTCTGTCCGT	1980
45 GGAATGTTTG	ACATATATAA	TAAATTCATT	CAAGAAAGTA	ATTGGCTCAG	TGATCTTCGA	2040
CTGAAATATG	GTTATGGTAC	AACGGGTAA	TCCGAGATTG	GTAATTACAA	CCACCAAGCA	2100
CTCGTACTTG	TGAACAATTA	TACTCAAGAT	GCTATGGGGC	TTAGCATTTT	TACAGCAGGC	2160
AATCCCGACC	TCTGTGGGGA	AAAGCAGTCT	CAGTTCAACT	TCCGTTTGGC	TGCAGGGGCT	2220
TTCAATAATC	GCTTATCTGC	AGAGGTAGAT	TCTATCTCC	GCACTACGAA	TGATATGTTG	2280
50 ATTGATGTCC	CGATGCCCTA	TATCAGTGGT	TTCTTCTCAC	AGTATCAGAA	TGTAGGCTCT	2340
ATGAAAAATA	CGGGTGTAGA	CCTTTCTCTT	AAGGGGACGA	TCTACCAAAA	TAAGGACTGG	2400
AATGTATATG	CTTCTGCGAA	TTTCAACTAC	AATAGACAGG	AAATAACAAA	GCTTTTCTTC	2460
GGTCTCAATA	AGTACATGTT	GCCTAATACC	GCTACTATAT	GGGAAATTTG	GTACCCCAAT	2520
TCGTTCTATA	TGGCTGAATA	TGCTGGAATC	GACAAAAAAA	CCGGTAAGCA	GTGTGSGTAT	2580
55 GTTCTGTTGC	AAGTCGATGC	GGATGGTAAT	AAAGTTACAA	CAAGCCAGTA	CTCAGCTGAC	2640
TTGGAGACAC	GAATGATAAA	GTCTGTTACT	CCTCCTAATA	CAGGTGGTTT	CTCCTTAGGT	2700
GCTTCTTGGA	AAGGACTTTC	TTTAGATGCT	GATTTTGCTT	ACATCGTTGG	TAAATGGATG	2760
ATCAATAATG	ACCGTTACTT	TACAGAGAAT	GCAGGTGGAT	TGATGCATTT	AAATAAGAT	2820
AAAATGCTAT	TGAATGCCCTG	GACAGAGGAT	AATAAAGAAA	CAGATGTTCC	AAAAITGGGA	2880
60 CAGTCTCTTC	AGTTTGATAC	GCATTTGTTG	GAGAATGCTT	CTTTCCTGCG	TTTGAAGAAT	2940
CTCAAACTCA	CCTATGTACT	CCCCAATAGT	CTTTTGTCTG	GGCAGAAATG	GATTGGTGGG	3000
GCTCGTGTCT	ATTTGATGGC	GCGCAATCTG	TAACTGTGTA	CGAAGTATAA	AGGCTTTGAC	3060
CCTGAAGCAG	GGGGGAATGT	GGGAAAAAAT	CAATATCCTA	ATTCTAAGCA	GTACGTTGCG	3120
65 GGTATTCAGT	TGCTTTTC					3138

(2) INFORMATION FOR SEQ ID NO:37

70 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2607 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

75 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

15	TGGCATAGGA ATATTTTAT CTTTGCAGT ACATTAGCC CGAAAAATAT GCTCCCACTG	60
	CCATACCGTT ATGCAAAAC CGAGCACCT TTTCTCGCA AAGGATACTG CAAGAATCCA	120
	ATAACAAACA TAATTATCCT ATTTATGAAG AAAAGAATT TTTTGCTTCT TGGCATTTC	180
	GTGCTTTTC TGACTTTCAT CGGCAGCATG CAGGCACAC AGGCCAAGA TTATTTCAAC	240
20	TTTGACGAAC GGGGCGAGGC CTACTTCICA TTCAAAGTGC CTGATAGGGC CGTCTACAA	300
	GAGCTGGCTC TGATCATGTC CATCGACGAG TTTGACCCCG TAACCAATGA AGCCATTGCC	360
	TATGCCAGCG AAGAGGAGTT CGAGGCATTG CTGCGCTATG GGCTCAAGCC TACATTCTTG	420
	ACTCCTCCAT CCATGCGACG CGCTGTCGAG ATGTTGCACT ACCGCTCAGG AGAAAAATAC	480
	GAATGGAATG CTTACCCAC CTATGAAGCC TATATCAGCA TGATGGAAGA GTTCCAAACA	540
	AAGTATCCAT CACTTTGTAC TACTTCCGTC ATTGGCAAT CCGTAAAGGA TCGTAAACTG	600
25	ATGATTTGCA AGCTGACGTC CTCTGCCAAT ACAGGGAAAA AGCCTCGCGT GCTCTATACT	660
	TCTACGATGC ACGGAGACGA AACGACCCGA TATGTGGTAC TGCTCCGACT CAGAGCCAT	720
	CTGCTGTGCA ACTACGAATC CGATCCGAGG ATTAAGAAC A TCTGGATAA AACGGAAGTA	780
	TGGATCTGCC CTTTGACCAA TCCGGACGGA GCATACAGAG CCGGAAACCA CACCCACAA	840
	GGAGCTACTC GCTACAATGC CAACAATGTC GATTGGAACC GTAACTTCAA GGATGATGTA	900
30	GCCGGTGATC ACCCGGATGG AAAACCTTGG CAGCCGGAGG CAACTGCATT CATGGATTG	960
	GAAGGAACA CCTCTTCTGT GCTCGGTGCC AATATACATG GAGGAACAGA GGTGGTGAAC	1020
	TATCCATGGG ATAATAAAAA AGAAAGACAT GCAGACGATG AGTGGTACAA ACTGATCAGT	1080
	CGCAACTACG CAGCCGCTTG TCAGAGTATT TCCGCCAGCT ACATGACCTC CGAAACCAAT	1140
35	TCGGGAATCA TCAACGGTTC AGACTGGTAT GTAATTCGCG GAAAGTCGTA GGCAATGCA	1200
	AATTATTTCC ATCGCTGCG AGAAATTACC CTTGAAATCA GCAACACGAA GTTGGTGCGG	1260
	GCCTCTCAAC TTCCAAAGTA TTGGAATCTG AACAAAGAAT CTCTGCTTGC TCTGATCGAA	1320
	GAATCCTTAT ACGGCATCCA TGGTACAGTG ACTTCCGCTG CGAAGCGACA GCCTCTCAA	1380
	TGCCAGATCT TGATAGAAAA CCATGACAAG CGCAACTCCG ATGTTTACTC CGATGCTACC	1440
40	ACAGGCTACT ACGTACGTC TATCAAAGCC GGCACCTATA CGGTGAAATA CAAAGCCGAG	1500
	GGTTATCTTG AGGCAACTCG TACCATTACG ATCAAGGACA AAGARACCGT CATCATGGAC	1560
	ATTGCATTGG CCAACTCGGT TCCTCTGCCT GTACCCGATT TCACAGCTTC TCCTATGACC	1620
	ATCTCAGTAG GCGAAAGCGT CCAATTCCAA GATCAAACGA CAAATAACCC CACGAATTGG	1680
	GAGTGGAGCT TCGAAGGCGG ACAGCCTGCC ATGAGTACAG AGCAGAATCC GCTCGTATCC	1740
45	TATAGTCATC CCGGTCAGTA CGACGTTACG CTCAAAGTGT GGAATGCAAG TGGTTCCRA	1800
	ACGATTACGA AAGAAAAATT CATCACTGTC AATGCCGTTA TGCCGTGAGC TGAATTCGTC	1860
	GGTACCCCGA CGGAAATAGA AGAGGGCCAG ACGGTATCTT TCCAAACCA ATCCACCAAT	1920
	GCCACCAACT AGSTATGGAT ATTGATGGC GGCACCTCCG CTACCACTGA AGACGAAAC	1980
	CCGACTGTGC TTTACAGCAA AGCCGGCCAA TACGATGTCA CGCTCAAGGC GATCAGTCT	2040
50	TCCGTTGAAA CCGTGAAGAC GAAAGAAAAA TACATCACTG TCAAGAAAGC TCCGTTCCCT	2100
	GCTCCGGTAG CCGACTTCGA AGGAACACCT CGAAAAGTAA AGAAAGCCGA GACAGTTACT	2160
	TTCAAAGACT TGTCTACGAA CAATCCGACT TCATGGCTTT GGGTGTTCGA AGGCGGCTCT	2220
	CCTGCCACCA GCACGGAGCA AAACCCGGTG GTCACCTACA ATGAACAGG CAAGTACGAT	2280
	GTCCAGCTGA CTGCCACCA CGAGGGCCGA AGCAATGTGA AGAAAGCAGA AGACTACATT	2340
55	GAGGTTATCC TCGATGACAG TGTCGAGGAC ATAGTGGAC AGACGGGTAT CGTCATTCTG	2400
	CCGCAAAACG GAACGAAGCA GATCCTCATA GAAGCCAACG CTGCTATCAA AGCGATCGTT	2460
	CTCTATGACA TCAATGGACG GGTCTGACTC AAAACTACTC CGAATCAGCT CCGCTCGACC	2520
	GTAGATCTTT CCATCTGCC CGAAGGAATC TACACCATCA ATATCAAAC GGAATAATCC	2580
60	GCTCGCACGG AAGATGCA TATCGGG	2607

(2) INFORMATION FOR SEQ ID NO:38

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

WO 99/29870

PCT/AU98/01023

26 / 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

CTTCGTACA	GTGGAGAGAG	CGATGCAAAA	GAGTCTGATC	AGAATTGCCG	GAAATGTACC	60
TTTCATUGGT	TTGAAAAACG	AGTAAATACG	ATGCGACTGA	TCAAGGCTTT	TCTCGTGCAA	120
CTCTTACTGC	TCCCATTTT	CTTCTACAAG	CGGTTTATAT	CGCCGCTTAC	ACCGCCTTCA	180
TGCGGGTTTA	CCCCCTCATG	TTGCTCTAT	GCCATCGAAG	CCTTACGTAA	ATATGGCCCG	240
GGCAAAGGAC	TATTGCTGAG	CATCAAGCGT	ATTCTCCGCT	GTCAACCCGTG	GGGTGGAAGT	300
GGCTATGACC	CCGTTCGG					318

(2) INFORMATION FOR SEQ ID NO:39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

TTAGAGATGG	CATACGACTT	TACACAAACA	TTCCGCAACA	GCCTGGAGTA	CAGCTATCAG	60
GAAGCAACCC	GTCTCGGCGT	CGTAGCCGTG	ACGCCAAGATA	TGCTCGTACT	CGGTATCATT	120
CGCGACGGAG	ACAAATGGCGC	GATCGACATC	ATGCGGCACCT	ATGGGATCAA	CTTGTACGAA	180
CTCAAACGGT	TGATCGAGTT	GGAAGCCATC	GCCGAGAGTT	TGCTGCTTC	GCCTGAGGGA	240
TGCGCCATCT	TCACCCCTTC	GGCTCGGGAG	GCTATCGATG	ATGCCACAGA	CATCTGTGCC	300
GACATGGAGG	ACGAGGCCGT	CAGCCCGGTC	CATCTGTTGC	TGAGTATCCT	CAACTCGACA	360
CAGGAGAGCT	TAGTACAAAA	GATAITTTAT	AAACAAGGTA	TAAATACGA	CACCATCCTG	420
TCGGATTACT	TCGGACAGCG	CAACCCCTCC	GAAGGGAAGT	CTCCCTCCGA	AATGGAGATC	480
CTCGACGGGT	ACCAAGACAA	CGACTTCGAC	GACGAAGAGG	ACGAATCCTC	TCCGCCTTCC	540
GGSAATAGCG	GGACAGGCGG	AGGCTCCGGC	GACGCCCCCG	AACAGARTAC	CGGCGGAGGC	600
GATACTACCA	CCACGACACG	GAGTGGAGGC	GACACGCCCTG	CACTGGACAC	CTTCGGCACC	660
GACATCACTG	CCATGGCGGC	AGCAGGCAAG	CTCGACCCGG	TAGTGGGTGG	GGAGCAGGAG	720
ATCGAAAGGG	TGATACAGAT	ACTCAGCCGG	CGCAAAAAGA	ACAATCCGGT	GCTCATCGGC	780
GAACCCGGTG	TAGGCAAGAG	TGCCATCGTG	GAAGGACTGG	CCGAACGCAT	CGTGAACAGG	840
AAGGTGAGCC	GTATTCTTTT	CGACAAGCGG	ATCATCAGCC	TCGATTGGGC	TCAGATGGTA	900
GCCCGCACCA	AATATCGCGG	ACAGTTCGAA	GAGCGGTTGA	AAGCGGTGCT	CGATGAGCTG	960
AAGAAGAATC	CGCAGATCAT	CCTCTTCATC	GACGAGATAC	ATACCATCGT	GGGAGCAGGC	1020
TCTGAGCCCG	GATCGATGGA	TACGGCCAAT	ATGCTCAAAC	CCGCTCTTGC	CCGTGGACAG	1080
GTACAGTGCA	TCGGAGCCAC	TACGCTGGAT	GAGTATCGTA	AGAACATAGA	AAAGGACGGA	1140
GCATCGAAC	GGCGCTTCCA	GAAGGTGCCG	ATAGCCCCCT	CGACTGCAGA	AGAAACGCTG	1200
ACCATCCTGC	AAATCATCAA	AGAGAAATAC	GAGGACTATC	ACGGTGTACG	CTATACGGAC	1260
GAAGCGATCA	AAGCGGCAGT	GGAAGTGACC	GATCGCTATG	TATCCGATCG	TTTCTTCCCA	1320
GATAAGGCGA	TAGATGCCAT	GGACGAGGCC	GGCGCGAGCG	TCCATATCAC	CAATGTGGTG	1380
GCTCCGATAG	AAATCGAGAT	ACTGGAGGCC	GAATTGGCAT	CGGTGCGAGA	GAACAAGCTC	1440
TCGGCCGTAA	AGGCTCAGAA	CTACGAACCTG	GCTGCCTCCT	TCCGCGATCA	GGAGCGGCGC	1500
ACTCAGCAGC	AGATAGCGGA	AGAGAAGAAA	AAATGGGAAG	AGCAGATGTC	CAAGCACCGC	1560
GAGACCGTGG	ACGAGAATGT	AGTGGCGCAT	GTAGTGGCGT	TGATGACAGG	CGTTCCGGCT	1620
GAGCGGCTGA	GCACGGGCGA	AGGCGAAGCT	CTGCGCACGA	TGGCAGATGA	TCTCAAGACC	1680
AAAGTAGTAG	GTCAGGACAC	AGCCATCGAA	AAGATGGTGC	ATGCCATCCA	CGGCAATCGT	1740
CTGGGACTTC	GCAATGAAAA	GAAACCGATC	GGTCTTTTCC	TTTTCTCTCG	CCCCACGGGG	1800
TAGGCAAGA	CCTATTGGC	CAAGAAGCTC	GCGAATACC	TGTTTCGAGG	TGAGAATGCC	1860
ATGATCAGGG	TGGATATGAG	CGAGTATATG	GAGAAGTTCT	CCGTTTCGCG	TCTCGTGGGT	1920
CGCCCTCCGG	GATATGTGGG	CTATGAAGAA	GCGGCCAAC	TGACGGAGCG	CGTAAGACCG	1980
AAACCTTATT	CCGTGGTTCT	CTTGGATGAG	ATCGAAVAGG	CGCATGCCGA	TGTCTTCAAT	2040
CTGCTCTTAC	AGGTGATGGA	CGAAGGTCAG	CTGACCGACA	GTCTGGGACG	GGCGGTGAAT	2100
TTCAAGAACA	CCGTGATCAT	CATCACCTCC	AACGTGGGTA	CAGGCCAGCT	CAAGAGACTTC	2160

WO 99/29870

PCT/AU98/01023

28 / 490

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...897

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

TTAAAAAGG AGATAACTAT GAAACAGAAC TACTTCAAAA GAGTCTGCTC ACTGCTTTGG 60
CTGGTTTAC CCATGCTTAT TATGCCATTG GAAGTAGCAG CTCAGAGAT TATTCCGAAC 120
GAAGAGGTGT TGGAATCATT GACTTTCGTT GCACCGGTTG AGGAGACAGA CGCAATAGAG 180
10 GCAGAGGTAG AAGCTCTGCA GGAGATAGTC GCTACTGAGG AGATTGCGGA GCAGGCTGTT 240
CGTTCTTATA CCTACACGGT CTATCGTGAT GGCGTGAAGA TTGCTTCAGG ATTGACTGAG 300
CCCACTTTTC TCGATGAAGA TGTTCTGCTC GCGGAACATA CCTACTGCGT AGAAGTACAG 360
TATCAGGGAG GCGTATCCGA CAAAGTATCC GTGGACGTAG AGGTGAAGGA CTTCAAACCG 420
GTTACCAATC TCACCGGAAC TGCTTCCAAT GACGAAGTTT CTTTGGACTG GGACGGTGTG 480
15 GAAGAGAAAG CTGAAGAGCC GGCAAGTGAT AAAGCAGTCA GCTACAACGT CTACAAGAAT 540
GGAACGTTGA TCGGTAATAC AGCTGAAACT CATATATGTT AGACCGGTGT AGCCAAATGGT 600
ACATACATCT ACGAAGTGGA AGTAAAGTAT CCTGACGGTG TATCTCCGAA GGTGSGCTGTA 660
ACCGTGACCG TGACCAACAG CTCATTGAGC AATGTAGATG GACAGGCTCC TTACACATTG 720
CGAGTAGAAG GCAAGAAGAT TATTGCCGAA GCCCATGGTA TGATCACGCT CTACGACATC 780
20 AACGGACGTA CCGTGCCGCT AGCCCCGAAT CGATTGGAAT ACATGGCGCA AACCGGTTTC 840
TATGCAGTGC GCTTCGATGT GGGGAATAAA CACCATGTAT CGAAATACA AGTAAGA 897

25 (2) INFORMATION FOR SEQ ID NO:42

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

35 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS

40 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...1131

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

TTGTTAATC ATAAAAAATC ATGGTATGAA ACATTTCAAT TTTATCTCGT TGTTTCCGC 60
TCTGGCTTTA TTCTTTTGTG TGAATAATACC CTTGCACAAC AAAAAACAGA GGAGTTTGCA 120
CCTGTGTCCG ATTTACGTGC AGAAGCGTAC GGCTCTACCG TTTTCTCCA CTGGACTCCG 180
50 CCGTATGACA ATCCGATGAT TCCTCTAAGC GAGAGTTTGT AATCAGGTAT TCCAGCTATA 240
TGAAGACCA TTGACGCAGA TGGCGATGGC TATAATTGGA TGCATTGAC CAATTTCAG 300
GGACAGAGTG GTCTCTGTGT CTCTTCGGCT TCATACATAG GCGGCGTCGG AGCTTTGACT 360
CCGACAATT ATCTGATAAC ACCCGAATTA AAACATACCA CAGACGCGTT GGTGSAATA 420
ATCTAATGGG TATGACTCA AGATCTCACT GCTCCATCGG AGCACTATGC CGTTTATTC 480
55 TCTTCTACAG GCAATAATGC TGCTGACTTT GTTAATCTCT TATATGAAGA GACTTTGACT 540
GCCAAACGGA TACAATCCCC CGAGTTGATC CCGGGAATC GGACACAAGG TGTTTGGTAT 600
CAAAGAAAGG TGGTACTCCC TAACGATACT AAATATGTTG CTTTCCGCCA TTTTAATTC 660
ACGGATAATT TCTGGCTCAA TTTGGATGAA GTATCTATCC TGTATACCCC TCTTCCCGA 720
AGAGCTCCGT GTCCGCATCC GGGTGGTTAC ACTTATCTCT TATTCCTGTA TGGACAAAAG 780
60 ATAGCGAGTG GATTGTCCGC ATTGGCATAT ATCGATACGG ATGTACCGTA TGGGACTCAA 840
GACTATTGTG TCCAAGTCAA TTATCTGCAA GGAGACTCGT ATAAAGTCTG CAAAAATATA 900
GTGGTGGCAA ATTCTGCAA CATCTATGGG GCGGATAAGC CTTTTCGTT GACCGTGGTT 960
GGCAAGACCA TTGTAGCGAG TGCTTTCAAA GGAGAGATCA CTCTTATGA CATTCTGGC 1020
CGGCTGATAG CTTCCGGCTG CGATACGCTT AGGTACAAAG CGGAAATGG TTTTACCTC 1080
65 ATTAATAATC AGGTAAACGG AACTGTCTAT ACTGAGAAAA TCCAAATCCA A 1131

70 (2) INFORMATION FOR SEQ ID NO:43

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
75 (D) TOPOLOGY: circular

WO 99/29870

PCT/AU98/01023

29 / 490

(ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 5 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
 10 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2547
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43
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TTCCGGAATAT	CACCTTCAAT	GAAAAAAGT	TTTCTTTTAG	CCATAGTAAT	GCTCTTTGGC	60
ATTGCCATGC	AGGGACATTC	TGCTCCGGT	ACGAAAGAGC	GAGCTTTGAG	TCTGGCTCGG	120
CTGGCTTTGC	GACAGGTATC	CTTGCGAATG	GGACAAACAG	CAGTATCTGA	CAAGATTTC	180
ATCGATTACG	TTTATCGGCA	AGGAGATGCT	GAGAGGGGTA	TCACATCACA	AGAGGAAGGC	240
TCTCCTGCAT	ATTTTATGT	AGCTAATCGT	GGAATATATG	AGGGCTATGC	TCTTGATGCA	300
GCAGATGACA	GAATACCGAC	AATTTTAGCC	TATTCACCCA	TTGGCCGTTT	CGACATGGAC	360
AGTATGCCGG	ACAATCTTCG	CATGTGGCTA	CAAAATTACG	ATCAGGAAAT	AGGCCTGATA	420
CTTTCCGGAA	AAGCTCAGCT	CAATGAAGAG	ATATTACGTA	CCGAGGGCGT	ACCGGCTGAA	480
GTACATGCTC	TGATGGATAA	CGGTCAATTT	GCCAACGATC	CCATGCGATG	GAATCAAGGT	540
TACCCATGSA	ACAATAAGGA	ACCACTGCTT	CCTAATGGCA	ATCATGCTTA	TACCGGCTGT	600
GTTGCTACTG	CTGCAGCACA	AATCATGCGC	TACCATAGCT	GGCCGCTTCA	AGGTGAAGGC	660
TCTTTGATT	ATCATGCAGG	TTCATTAGTT	GGCAACTGGT	CCGGCACATT	TGGTGAATG	720
TACGACTGSA	TCAATATGCC	CGGAAATCCC	GACCTTGATA	ATCTGACTCA	ATCTCAAGTG	780
GATGCCATCG	CCACACTGAT	CGGTGATGTG	AGTGCACTCG	TTTCGATGAG	TTTTTATGAA	840
AATGGAAATG	GTACGTACAG	CGTTTATGTA	GTAGGAGCCT	TGCGAAACAA	CTTTGCTACT	900
AAGCGTTCAC	TGCAGCTACA	TGTACGCGCC	TTATATACCT	CACAGGAGTG	GCACGATATG	960
ATCCGCGGGG	AACCTTGCCTC	CGGAAGGCCG	GTCTATTATG	CAGGGAATAA	CCAGAGCATA	1020
GGACATGCTT	TCGTTTCCGA	TGTTTATGCT	TCGGATGGTA	CTTTCCATTT	CAACTGGGGT	1080
TGGGGAGGTG	TTTCCAACGG	CTTCTACAAA	CTAACACTCC	TCTCGCCGAC	TTCTTGGGT	1140
ATCGGAGGTG	AGGGAATAGG	TTTTACCAAT	TATCAAGAGA	TCATCACCGG	TATCGAACCG	1200
GCTAAGACTC	CCGCTGAAGC	CGGTACAGAT	GCCTTGCCGA	TCTTGGCACT	GAAGACATA	1260
GAAGCCGAGT	ATAAAAAGTGA	ATCCGGATTG	AACGTAGGGT	ATTCGATATA	TAATACAGGT	1320
GAAGAGCAAT	CAAACTTTGA	CCTCGGATAC	AGATTGAACA	AGGCTGACGG	AGAAGTCATA	1380
GAGGTGAAAA	CTTCTATCTAT	CAATATCTCT	TGGTACGGAT	ACGGAGAGCA	TCCCGAGAGT	1440
TTCTCATTTG	CACCTAATCA	GTTGTCACAA	GGAATCAACA	CCATCACCTT	ACTTTATCGT	1500
CGCACAGGCA	CCGAACAGTG	GGAGCCGGTA	CGGCATGCAC	AGGGAGGATA	TGTCAATAGC	1560
ATTAAAGTAA	ATACGACAGA	CCCGAACAA	GTCTAGTCA	CGGTAGATAA	TAACGAAGGC	1620
AAGCTCAGTA	TGCTCCCAA	CAGCTTTGTC	GCAGATCTGA	ATTCTTATGA	ACATAGTACG	1680
ATTACAGTAC	AGTTCAATAG	CGACAGCCCT	GATGAGATCC	GTACACCCGT	AGCCTTTGCT	1740
CTATCTACAG	GAGCTACTGC	GGACGATGTA	ATATCTTTGG	GCTGGGTAAT	GGCTGAAGTT	1800
CCGGGCGGTA	GCAGCAACTA	TCCGGTGGTT	TGGTCTAAAG	ACGTTCTCAC	TCTCTCGGAA	1860
GGCGACTATA	CATTGTGGTA	TAGATTTTCC	ATCAACAACC	AAAAGGATGA	ATGGAAAAAG	1920
ATCGGAAGCG	TGTCAGTAAA	AACACCGACA	GAGTATACGC	ATCCCTTATT	CGAAGTGGCC	1980
CATAATCAAA	CTTCTACCTA	TACGCTGGAT	ATGGACACAC	ACAGAGTATT	GCCCGACTTT	2040
ACACTCAAAA	ATCTCGGATT	GCCTTTCAAT	GGTGAGTTGG	TTGTTGTTTT	CCGCCAAACA	2100
CAATCCTCAT	CGGGGTCTTT	ATGGGCAGCT	CAAGAAACAG	TACATATCAA	GCAAGGAGAA	2160
ACTTTGCTAT	ATAAACCTGT	TGTCGAAGGC	CCTATACCTG	ATGGATCCTA	TCGTGCGACC	2220
CTCCATGCAT	TGTAACAGCG	ACAACAACAG	TTGTACCTCA	AGGGGAAAAG	GAATACACG	2280
GTGAAGATCG	TCAATGGTAC	AGCGGTAGAA	GCAATAGAA	CGTCAGAGA	GATCAGAGTA	2340
TTCCCTAATC	CGGCACGCGA	TTATGTGGAA	ATATCGGCAC	CTTGCAATTC	CCAAGAAACA	2400
TCTATCATTC	TTTTGATGCT	GTCAGGCAAG	ATTGTCATGA	AGAATAGTTT	ATCAGCGGGG	2460
CATGGCAGAA	TGGATGTCAG	CCGACTTCCT	AATGGGGCCT	ACATCCTTAA	GTTGGATGGA	2520
TATACGACGA	AAATAAATAT	AGTGCAC				2547

(2) INFORMATION FOR SEQ ID NO:44

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 885 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

WO 99/29870

PCT/AU98/01023

30 / 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...885

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

10 ACGAAGAAAA CACTGATGAA AAAGCTATTT CTCTCGCTCA CGAGTCTTGT AATGGTCTTC 60
GCTGTTGCAA GTTGGGATAT AATCGACAAG GATCAAACCC TCTTGCCGGC TCCGACCAAT 120
GTGACACCCG ATAATCGGGA TGACAATCCT TCGGAGATCG ACATTACGCA GACGCACACA 180
GAAAAATATG TTTTGGCTGA AGAATTTACC GGGCAAAAT GTCTCAACTG TCCGAAAGGT 240
CATCGCAAAAC TGGCGGCTCT CAAGGAGCAA TACGGTAAGA GATTGACTGT TGTGGGTATA 300
CATGCGCGCC CTGGATCTCT CGTGCCACCT CTTTCCGTA CAGAAGCCGG AGACGCATAT 360
15 TATAGCAAGT TCGCCAATTA TACCCTCTC CCTGCGTGA TGGTTTCGGC CAAAAAGTTC 420
GGCTCTTCTT ACGTTTATGA TAAGAGCTAC AAAACGTGGG ACGTGCCTAT TGCCGAGCAG 480
ATGGAGCAAA AGGCGAAGAT CAATATCTTT GCGGTGCGCC AATACACCGA TACCAAAAG 540
ATCAAGGTGA CTGTAAAGGG TAAATACTG GAGGGGAATA CACTCCCGAA GTCCATGGTT 600
CAGSTGTATC TGTGGAGGA TAAAGCTGATC GCTCCGCAGG TGGATGGCAA TACGACAGTC 660
20 GAGAAITACG AGCACAATCA CGTGTTCGGT GGAGCCGTTA ATGGTATTGG GGGCGAAGAA 720
TTTGTGAATC TCAAAGATTA TTTGTATACT TACGCCGTTG AACCGCTCTC GGGTATGTCC 780
TTCGTAGCCG AGAATTATTC GATTGTGGCT TTTGTATACG ATGTGCAGAC GTTCGAAGTG 840
TATGACGTTG TGCATGTAAA GATCAATCCG CAATCCGATG GCAAA 885

25

(2) INFORMATION FOR SEQ ID NO:45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 690 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

30

(ii) MOLECULE TYPE: DNA (genomic)

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...690

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

50 ACGAATAAAA AAGAAGAGAC AATGAAGAAA TCAAGTGTAG TAGCCTCACT TTTGGCCGTG 60
GCTCTCTGTG TCGCCGGTTG CGGACTGAAC AATATGGCAA AAGGGGGGCT TATCGGGGCC 120
GGAGTAGGAG GTGCCATTGG TGCCGGAGTA GGTAAACGTAG CCGGAAATAC GGCTGTCCGT 180
GCCATCGTCG GTACTGCAGT CGGTGGAGCA GCCGGTGCTC TCATCGGAAA GAAGATGGAC 240
AAGCAGAAAA AAGAACTGGA GCGCGCAGTA CCGGATGCTA CGATTACAGC AGTAAATGAC 300
GGAGAGGCTA TTCTGGTTAC TTTGATAGC GGTATCTCTT TTGCGACGAA CTCCAGCACT 360
55 CTGAGTCCCA ACTCAGCAC TGCGCTGACG AAGTTTGCTG CAAACATGAA CAAAAACCC 420
GACACGGATA TTGATATCGT AGGCCATACG GACAATACCG GCTCCGACAA GATCAACGAT 480
CCTCTGTCTG AGAGACGTGC AGCCAGCGTA TATTCTTTCC TGAATTCTCA GGGTGTGAGT 540
ATGTCGGGCA TGGCAGCCGA AGGGCGTGGG AGCCATGAAC CGGTTGCAGA CAATAGCACA 600
60 GTTCCCGGAC GTTCGGCCAA CCGCGTGTG GAGGTTTATA TCTTGCCGAA TGCCAAGATG 660
ATCGAACAAG CACAGCAAGG TACGCTGAAG 690

65

(2) INFORMATION FOR SEQ ID NO:46

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1026 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

70

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

75

(iv) ANTI-SENSE: NO

WO 99/29870

PCT/AU98/01023

33 / 490

GTAGTAATGA CTGCAGCGGA A

1161

- 5 (2) INFORMATION FOR SEQ ID NO:50
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 15 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION 1...585

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

GTAATGGCA	TCATTATGGA	ATTTTTCATG	TTATTCTAG	CGGCGGTTT	CGTTAATAAC	60
GTCGTGCTGT	CGCAGTTCCCT	CGGTATATGC	CCATTCTTAG	GGGTATCGAA	GAAGGTAGAC	120
ACCTCAATCG	GTATGGGTGC	AGCCGTGACA	TTCGTATTGG	CACGTGGCTAC	CTTGGTTACC	180
TTCTGTATTC	AGAAGTTCCGT	TTTGGATCGT	TTCGGATTGG	GCTTTATGCA	GACCATTTGCA	240
TTTATTTTGG	TCATTGCCGC	CTTGGTGCAG	ATGGTGGAGA	TCATATCAA	GAAAGTATCT	300
CCTCCCTCT	ATCAGGCACT	GGGTGTATTC	TTGCCCTTGA	TTACGACGAA	CTGCTGTGTG	360
CTCGGTGTCC	CTATTTTGGT	TATCCAGAAG	GATTATACCC	TGCTCCAGAG	CTTCGTCTAT	420
GCAATATCCA	CGGCTATCGG	TTTCACTTGG	GCAATGGTTA	CTTTCGAGG	TATTCGAGAG	480
CAACTCGATA	TGACCAATCT	CCCCAAAGCT	ATGAAGGGAA	TACCTTGGGC	ACTCTTGGCT	540
GCCGTATAT	TGGCTATGGC	TTTCATGGGC	TTCAGCGGTA	TCGCC		585

- 40 (2) INFORMATION FOR SEQ ID NO:51
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2628 base pairs
- (B) TYPE: nucleic acid
- 45 (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 50 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 55 (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION 1...2628

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

TACCGATCTT	ATCGTGGGAT	AGGGAGTGGG	ACACACTCTC	CTAACCTCAA	AAACCGACTA	60
AAAAGGATCG	GAATAAGGAT	ACCGAACAGA	CACTATATCC	ATATCAAGCC	AATCAAACCA	120
AAAAATAAAA	TGAACAACCT	AAACATTATC	AGCTTCATCA	TTGCTTTCCCT	ATTCTTAGGA	180
ACGAGCGCAT	CGGCTCAGCA	ATCGGGCGGA	TCCGTACAG	GTACCGTAGT	GGACAAAGC	240
TCAAAGAAGC	CTATCGCATA	CGTACAGTA	TTGGTCAAAG	GAACCACTCT	CGGAACTTCC	300
ACGGATGCAA	ACGGAACACT	CTCGATCAAG	GGAATCCCTT	CGGGTAATCA	AACTATCGTA	360
GCCCGACTCA	TGGGTACTCT	CACTTGCAG	GAAAAAGTAC	ATATAGAAA	GGGTGGTTCC	420
CGCCACGTAG	ACCTCTATCT	GACCGAAGAG	ATTCTCTCT	TCGATGGGGT	AGTGGTATCT	480
GCCAAAGAAA	ACGAGACTTT	CCGCGTCAA	GCACCTCTGT	TGGTAACGGT	ACTGTCCCG	540
GAACTTTTCC	TCAAAACCAA	CTCTACCAAC	CTGAGTCAGG	GACTTAAGTT	CCAGCCCGGT	600
CTGCGCGTGG	AGGACAACTG	TCAGAACTGC	GGTTTCAACC	AAGTTGGTAT	CAATGGACTC	660
GAAGGAGCCT	ATTCCGAAAT	TCTTATCGAC	AGCCATCCCA	TCTTCAGTTC	GCTTGCCGGT	720
GTCTATGGCT	TGGAGCAGAT	GCCCGCCAAT	ATGATCGAAC	GTGTAGAAGT	AATTCGGGGT	780
GGAGGTTCCG	CTCTGTTCGG	CTCTAATGCT	GTGGGAGGCG	TTATCAACGT	AATTACGAAA	840

WO 99/29870

PCT/AU98/01023

35 / 490

	ATCAAAGGAA	ATACTGTCGT	GTACGAAGAC	GTAGTACGCC	GAGAGCTTTA	CACAAAGCCC	1260
	GGCCAGCTCT	TTAGTCGCGA	GGATATCATT	AACCTCTATC	GTCTCATCAA	TCAGCTTGGG	1320
	CATTTTCGATG	CCGAAAATC	TATTTCCCGT	CCGATTCCCA	ATCCCGAAAC	AGGAACAGTG	1380
5	GATATAGAGT	ATGATTTGGT	GCCGCGTAGC	AGTGACCAAT	TGGAGCTTTC	TGTCGGTTGG	1440
	AGTCAGTCCG	GACTTCTGTT	CCGAGGAGCC	ATTAAGTTCA	CGAACTTCTC	TGTCGGCAAC	1500
	TTGCTCCATC	CCTCGATGTA	TAAGAAAGGG	ATCATTCCGC	AAGGGGATGG	GCAAACACTA	1560
	TCACTGAGTG	CTCAGACCAA	TGGAAAGTAC	TATCAGCAGT	ATAGTGTAC	ATTATGGAT	1620
	CCATGGTTTG	GGGGCAAGCG	GCCGGATATG	TTCAGCTTCA	GTGCATTCTA	TTCCAAGACT	1680
	ACGGCGATTG	ACTCCAAGTT	CTACAATAGC	AATGCCGGCA	ACTACTATAA	TGCCCTACTA	1740
10	AATAGCTACT	ACAACAACCTA	TAATAGTTAT	TACAACGCTA	TGTCGAACTA	TACCGGCGAC	1800
	CTCTATACTC	AGGCCAGCGA	TCCGGATCGT	TCGCTTCAGA	TGTTAGGTAC	TTGGATCGGT	1860
	TACGGTAAGC	GTTTGAATTG	GCCGGACAAT	TGGTTCCAGA	TTTATACTTC	TCTGAACCTAC	1920
	ACCTACTATA	GACTGCGAAA	TTGGAGCTAC	AATACCTTCC	AAAAATTTCCA	TCATGGCTCG	1980
	GCTAATGATC	TCAACTTGGA	GCTGCGTCTC	TCTCGTACTT	CCATCGATAA	TCCTATTAT	2040
15	ACCAGAAGCG	GATCGGATTT	CATGGTTTCT	GTTCGTGCTA	CTCTTCCTTA	TTCTTTGTGG	2100
	GACAATCATG	ACTATGCCAG	CCAGAACCTC	AGCGTAAGCG	ATCGTTACAG	ATTATCGAG	2160
	TATCAACAAT	GGAGTTTAG	AGGACGAGTT	TTTACTCCAT	TGCTCAATCC	TGCTACGCAT	2220
	AAATATACAC	CGGTGCTCAT	GATCCGAGTG	GAAGGAGCAG	TCTTGTGTTT	GTATAATTCC	2280
	AATAAGAAAT	CTCCTTTTCG	TACTTTCTAT	ATGGGAGGTG	ATGGTATGTC	CAGCTATTAT	2340
20	GGTGGCTACA	TGAATGAGAC	TATAGGTTTG	CCTGGTTATA	AGAACGGATC	TATTGCCGGT	2400
	AATAACTACG	ACTATGCATA	TGCTTATATG	CGGCTTACGA	TGGAACTACG	TTTCCCGATT	2460
	CTGTTTGAAA	ACTCATTCAA	TGCGTGGCTC	TTAGCTTTTG	CCGAAGCAGG	CAATGCCGTGG	2520
	CGCAGTATCG	ACAATTATAA	TCCCTTTAAC	CTGAAGCGAT	CGGCCGGTGT	AGGATTGCGT	2580
	GTAACTTTAC	CGATGGTCGG	AATGCTCGGT	ATCGATTGGG	GATATGGCTT	TGACCGTCCG	2640
25	GACAATTCTC	TACAGCGAGG	AGGAAGCAAT	GTCCACTTTG	TGCTCGGACA	GGAGTTT	2697

(2) INFORMATION FOR SEQ ID NO:53

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 531 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
35	(D) TOPOLOGY: circular
	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
40	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORPHYROMONAS GINGIVALIS
45	(ix) FEATURE:
	(A) NAME/KEY: misc feature
	(B) LOCATION 1...531
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

	CAATAAACA	TGAATGGCGA	TATGAACGG	TTTTTGATTI	TGATCGGCTT	TGCACTGGCG	60
	GTAGCTTTCT	COGGTTTTTC	CCAAAAGTTC	GCTTTGGTAG	ATATGSAATA	TATCCTCAGG	120
	AATATTCCTG	ACTATGAGAT	GATGAACGAA	CAGCTGGAAC	AGGTGTCCAA	GAAATGGCAA	180
	AATGAATCG	AAGCTCTCGA	AAATGAAGCC	CAATCTATGT	ATAAGAAGTA	TCAGAGCGAT	240
55	CTCGTATTCT	TGCTGCTGCG	ACAGAAGAAA	ACCCAAGAAG	AGGCTATCGT	AAAGAAAGAG	300
	CAGCAAGCAT	CCGAGCTCAA	GCGGAAGTAT	TTCCGCCCGG	AGGGGGAGCT	GTATAAGAAA	360
	CGCTCCGATC	TGATGAAGCC	TATTCAGGAT	GAGATTGGGA	ATGCTATCAA	AGAGATTGCC	420
	AAGCGTAACA	ACTATCAGAT	GGTGCTTGAT	AGAGGTACGT	CCGGAATTAT	CTTTGCCAGT	480
60	CCGTCTATTG	ACATTAGCGA	CCTGTACTG	AGCAAGATGG	GCTTTAGCAA	G	531

(2) INFORMATION FOR SEQ ID NO:54

65	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 510 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: circular
70	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
75	(iv) ANTI-SENSE: NO

WO 99/29870

PCT/AU98/01023

36 / 490

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(vi) ORIGINAL SOURCE:
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(1x) FEATURE:
5   (A) NAME/KEY: misc_feature
    (B) LOCATION 1...510

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54
10  CGAATAAATA AACACACGA AATGAAGAAA TTTTTCCTCA TGCTTCTGAT GGCTCTTCCT    60
    TTGAGCCTCT TGGCACAAA GGTGGCAGTG GTAAACACTG AGGAGATCAT TTCCAAAATG    120
    CCGGAACAAAG TAGCTGTAC CAAACAGCTC AACGAATTGG CCGAAAAGTA TCGCCTTGAT    180
    CTCGAAGATA TGGACGATGA GTTTGCCAAA AAGACAGAAG AATTGTGAAA GGAAAAAGAC    240
    TCTCTACTGG AGAACATCCG CAATCGTCGT CAGCAGGAAC TTCAGGATAT TCAAACCTCGT    300
15  TATCAGCAGT CATACCAAAC GATGCAGGAG GATTTGCAAA AGCGCCAACA ACAGCTTTT    360
    GCTCCTATCC AACAAAAGGT GGCTGATGCC ATCAAGAAAG TGGGTGACGA AGAAAACTGT    420
    GCCTACATCA TGGAGGCCGG TATGATGCTT TACACCGGAG CTACTGTAT TGAATTGACC    480
    GCAAGGTAA AAGCGAAACT CGGAATCAAG    510

(2) INFORMATION FOR SEQ ID NO:55

    (i) SEQUENCE CHARACTERISTICS:
25  (A) LENGTH: 2484 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: circular

    (ii) MOLECULE TYPE: DNA (genomic)
30  (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO

35  (vi) ORIGINAL SOURCE:
    (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

    (ix) FEATURE:
40  (A) NAME/KEY: misc_feature
    (B) LOCATION 1...2484

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55
45  ATCATGAAGG AAGCTATTCC CCGAAAGAAC AAGTATATAA AGCTCAACGG TATATACAGA    60
    TTGTCATTCA TTCTGCTATG CTGCCTGCTA TGCTCTCAGG CAGCTATGGC ACAAGGCGTC    120
    AGGGTATCGG GCTATGTGCT CGACCGTGGG GAAAAGCCGA TCCCGTTCGC CGGAGTCAAA    180
    GTGCGTGTA CCGGGACAGG CGCAACGACG AATCTGAAGG GATACTACGA GTTTCGGATG    240
    AAGGCCACGA CGGACAGCAT CACGATCGAG TTCAGCTCCA TGGGGTACCA AGGGGTAAAT    300
    CGCAGCTTTC CGTCTCTGAC CAAGGACACT CGGCTGAATG TTCGTTTGGC AGAGGCGGAG    360
50  ATGGAGCTTT CGAGCGTGAC GGTACAGGCC ACAAACGCA GACTCAACAC GATGGAGCGC    420
    GTCATATCCC GAGACCTTCG TGTCAATGCA GGGCCTACGG GAGGGGTGGA ATCGCTCATC    480
    AGTACCTACG CAGGAGTAAC GCAGAACAAAT GAACTAAGCT CGCAATACTC GGTTCGCGGA    540
    GGAAGCTACG ATGAGAATAT GGTCTATGTA AACGGAGTGG AGGTTTATCG CCGCTGCTG    600
    GTTCGCTCTG CACAGCAGGA AGGTCTGAGC TTCGTCAATC CGGATCTGAC ACAATCCGTA    660
55  CASTTCTCG CCGGAGGTTT CACGGCCGAC TATGGCGACA AGATGTCTCT CGTACTGGAT    720
    ATTGCTTACA AGCAACCGCA GGAGAAGGAA GGAGCGGTAC TCCTCGGGAT GCTACATCG    780
    AGTGCTTACT ATGGCAGCAG TGC CGGAGCC TTCAGCCAAA TCACGGGTGT ACGCTACAAG    840
    AGTGCCAAAT CGCTCTTGGG CACTACGGAC ACGAAGCCG AATACGATCC GATCTATGCG    900
    GACGACAGA CATTCATGAC GTACCGTTTC AGCCCCAAGC TGTCGGTTAG TTTCTCGGC    960
60  AATATTTGCG AACTCGCTA CAAGTTTGTC CCTCAGACCC GTGAGACGAG CTTGCGTACA    1020
    CTGAGCGATG CCAAAAAGTT GAAGATCTTT TTCGACGGTC AGGAACAAGA TCGTTTCCTG    1080
    ACCTACTTCG GTGCCTTCAG CATGAACTTC GTGCCGACG ACAAACAGCG GCATACGGTT    1140
    ACGCTTTTCG CCTTCAACAG TAACGAACGG GAGACCTACG ATATTACGGG AGAATACTTT    1200
    CTGAACGATG TGCAGCTGGG GCGGACGCGA ACTGCTTCGA TGGCTTCGGG CTCAGACAAC    1260
65  TCCAACGCTT TGGGCATCGG GCGCAATCAC GAGCATGCGC GCAACAGGCT GAGCTACCGC    1320
    GTGCTGAACA TGGGTTACAG AGGGGAGATG AAGCTGAACG AGAAGCATCG CCTGCAAGCC    1380
    GGGGTATCGG CACAGATGGA GAAAATAGCC GACCATATCA CCGAATGGGA ACGGAGGGAT    1440
    TCGGTAGAT ACAAACCTACC TCACTCGGAG ACCGTATTGC TGATGTACAA TAACCTATAT    1500
    GCCGATACGC AGATGAGGGG AACCGGCTTG TCGGCATTCT TAAGAGGATCG ATTCAACTTC    1560
70  AGCATGGGAG GAGGTACATT TTCTCTCAT CCGGGATCA GAGCTTCGTG GTGGAGCTTC    1620
    AACAAAGGAT TGCTCTGTCAG CCCACGTATC AGCGTGGGTT ATTCTCCGA AAGCAACCGG    1680
    GCTTTGTGAC TGGGTGCAGC CGCCGGACTT TATTATCAGG CACCGTTTTA CAAAGAGCTA    1740
    AGGCAGACGC ATAAGGATGC CGAAGGCAAT AACGTGGTTG TCCTCAACGA GAAGATCCGC    1800
    TCTCAGGAG CTTTTCACAT TCTCGCAGGA GCAGACTATA CCTTCGAAAT GGGGGGGCGA    1860
75  AAATACAGT TTACGGCAGA GGCTTACTAC AAGAGCCTGT TCAACATCAA CCGGTATATA    1920

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WO 99/29870

PCT/AU98/01023

38 / 490

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
15 (A) NAME/KEY: misc feature
(B) LOCATION 1...2316
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

20 CCTGCACAGC CGAAAACATA TTGCATACGA TACTTTCGGA GAGAGGTATC TCCGAGGAGG 60
CAAAACAGAAA GGACATTGTA TGCGGACAAAG ATGCGCCGSC ATATCGTCAA GTGCTGTCCC 120
TCTGCCTCCA TACTCTTGCA AGAATACTCC ACAACAGAAT TATTCATTCA TCACTTTAAC 180
ATATCAATAA TTATGAAAAA GTTTTCTTTC GCGCTACTAT CGATTGGTAT TTCAGCGCAG 240
GCTTTTGCCA AGACGSACAA CGTCCCAGCA GATTGCTAC GAGTACACAA TCTTCAGACC 300
25 GTCACGCTCT ATTCTACAGC CACGGCCGTA CCTCTGAAAA AGATACCGGC CAAGATGGAA 360
CTCATCTCAT CGCGCAACAT CAAGCAGTCC GGCTTTAACA ACATGACCGA CATCCTCAAG 420
ACGCAAAATT CGCTCGATGT CATACAATAC CCGGGCTTTA GTTCGAACAT CGGTATCCGC 480
GGTTTCAAGC CCTCCGGCAA GTATGTAACC GTATTGGTAA ACGGCATCCC TCGGGGAAAG 540
GACAAATCTT CTACGCTCAA CACGAGCAAC ATGGAACAAA TCGAGATCCT CAAAGGCCCG 600
30 TTCTCTTCCA TCTACGGCAC CAATGCCATG GCGGTGTGG TGAACATCAT CACCACACAA 660
TCCAGGACA AGATCCATGG CAACGTTTCT CTCTCGGCG GTAGCTACCA GACCATGGCC 720
GGATCATTCA ACTTGGGTGG CCGCTTCGAG GATATTTTCT CATTCGATCT TAGTCTGGGC 780
TTGGACAAGC AGAACAAGGA CTATAAGACC GGATCAAACA ATTTCTATC CCTGAGCAA 840
CTGGAAGAAG CTATAGTAGA TGTAAATGCT ACCAAAAACA AGAAATGAA GGGGAGCGAC 900
35 TATACTGTAG CAACGGGACG TCTGCGTTTC GGTATCGACT TCACGCCCA ATGGTCGCTG 960
AATCTGTATG AAAACGTATC CCTCGGAGAT GCGATCCCCG TAGGAGGATC TATATGGGGC 1020
GTTTACGGAG AATCCAAAAA AAATCTGAAT CGTCTTCGA CCTCTTCGA GCTGCTCGGC 1080
AAACATGGCT GCCACAGCTC TCATTTCTCC CCTACTTCA ACATAGAGAA ATCGGAGAAC 1140
40 TATAACAATG CCGATCCACG CGGTTTCATC AACTACAAAA GCGACTACTA CACCTATGGT 1200
GCCCTACTCC AGGACAAGAT TTCTTTTGA GGACAAAAATA TCGTACTCGG TGTCGACAGC 1260
CGAAACATGA CGATGGAGTC AGAAAGATTC GAGCAGGACG GAGTGAATAC AAAGCCATAC 1320
AACCCTGGAT ATGCCACGAA CAATATCGGT TTGTTCCGAC AGGCCAATTT CTACCTGCTG 1380
AACGATGCTC TATCGATATC TGCCGGTGCA CGTGGCGACT TCATGTTCTT TGACCTGAAA 1440
45 GCGAACGAGT ATCTCAACAA TGAAGCCAAA CAGGAAACTC ATAACTGAAT CAATCCGAAT 1500
GTGGAATCA AATATGAGTT TGTGAAAGGC CTTACAGCTC ATGGTACATT CGGTAGTGCA 1560
TTCAGTGCTC CCGATGCTTT CCAAAAAGCA GGCCCAATAC TAGGCCCGTT CGGCACGACC 1620
ATAGGCAATC CTGACCTGAA ACCCGAAAAG TCCATGACCT GGGACTTCGG TATCGGATAC 1680
AGCAATGCAC GCTGCGGGAT CCAAGCCGAC GTAACCTTAA CCTATTTCGA CACCGACCAC 1740
AAGATCTGA TCTTGCCAG CCCTGACTAT GCTAATAATA TCACCACATA CATCAATGCC 1800
50 GACAAGGCTC GTATGAGCGG TATCGAGGCC CTTTGTGCTT ATGACTTCGG CAGCCTCTTT 1860
GCCAACAAAT TCTCTCTCCG CGCATTTGCG AATGCCACGA TCATGCTCAA TTCGAGATG 1920
AAGAAAAGCC AGACCGATGC CCTTGGAGC GAAATGTACT ACGTTCGCAA GCAGAATATC 1980
ACCTTCGGTA TCGAATATCG TGGCAAAGAA GGAATGTAAG TGATGCTCAA CGGTGCTTC 2040
ATGGGACGCA GGATCGAGCA AAACCTGGTAT GCTTACTACC CCGAAGTTCG CCCCAGACTC 2100
55 CAGCAACTGC TTGCAGCAGA AGAGCCTGAA TTGGCTGCTC AGGGACTGCT CCGTCATCCG 2160
CAGCAATGG TGTTCATGC CTCTGCTTAC TACCACATGA ACAAGTATCT CACCTTCGGT 2220
GTGAACCTGA ACAACATCTT GGATGAGCTT TATACGGAGA AAGACGGCTA CCACATGCCC 2280
GGACGTAACA TCATGGGTAA GGTATGGTTC AACTTC 2316

60 (2) INFORMATION FOR SEQ ID NO:58
(1) SEQUENCE CHARACTERISTICS:
65 (A) LENGTH: 1452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
70 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
75 (vi) ORIGINAL SOURCE:

WO 99/29870

PCT/AU98/01023

39 / 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

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10  GGGCGGGCCT CTTCCCTTAA CAGGCAAATG GATGGCATAC TAAACGATGA ATATAGACAA    60
    GCATCTATGA ACAGGTTTTC AAATCATTGG CCCTGCATCC TCGTGGGGTT TGTACTCTGG    120
    TTTGTATCGG CGAGTCGGAC TGTGGCACAA AACGCTCCG AAACGACGGT ATCGTACGAT    180
    ACGGATACCG CCGTACTCTC CGAAGCCGAT GTGCTTCGSA TCGCTCTTAG TGAGAATGCC    240
    ACAGTGAAG TGGCCGATAT GGATGTGGCG AAACAGGAAT ATGCACGTAG GGCAGCACGT    300
    GCGGATCTCT TCCCGAAAGT AGACCTCAAT GGGCTTTACA GGCATACGCT AAAGAAGCAG    360
    GTCTTATATA TAGATATGCC CGGTTTCAGC AGTAGCGAAG GTATCGAAAT GGGCGGTACA    420
    CACAATACGC AAGGAGGGGT GAACGTCTCC ATGCCATTGG TGTCGGCACA GCTTTGGAAG    480
    AGCATTGCCA TGACUGGAGA ACAGCTCGAT CTGGCTCTGG AGAAAGCTCG CAGCTCCCGA    540
    ATCGATTGGG TGGCAGAGGT GAAGAAGGCT TACCTCAGTG TATTGTTGGC CGAGGACTCT    600
    TATGGCGTAT TCAAGCGCAG CTATGACAAAT GCTCTGGCCA ATTATAAGAA CATATCCGAC    660
    AAGTTCGATC GTGGACTTGT GGGCGAGTAT GATAAGATTC GAGCCAAATG ACAGGTACGC    720
    AACATCGAGC CTAACTCTTT GCAAGCGCAG AACTCCGTAG CCCTTGCTCT CTGGCAGCTC    780
    AAGGTCTCTG TGAGCATGGA AGTGGAACCT CCGATCAGAC TCTCCGGTTC ATTGTCCGAC    840
    TATAAAGAAC AAGTCTATAC CGGCTATTTT GCGCCGATA CGCTTATTTT CAACAACTCC    900
    TCCCTGCGTC AGCTCGATAT ACAGCGTCGT CTGGCTGTCA GTGCAGACAA GCTGAACAAG    960
    TACAGCTTCC TGCTACACT CAATCTGGGA GGGCAGTACA CCTATTCGCT CAACAGCAAC    1020
    GACATCAAA TCTGGGGCGA GGGACAAAGC TGGACGCTT TCTCCACCAT ATCGCTCAGC    1080
    CTGTACATTC CTATATTCAA TGGAGGCAAA CGTCTGTACA ACGTGAAGCA AAGTGCTTTA    1140
    TCGATCCGTC AGATCGATCT GCAACGACGC CACATAGAGC AATCCATCCG AATGGGAATC    1200
    AAGAACCAAA ATGACCGTCT GCGTACCTGT ATGCAGAGAT TTGTGGCCTC GGAAGAGGCT    1260
    GTCCGAAGTG CAGAAAAGGG CTATCAGATA GCACAGAAC GCTATCAGAC AGGGGAAGGC    1320
    ACTCTCGTCG AGCTCAACGA TGCCGATGTG GCTCTTTTGC AGGCTCGACT CAATTATAAT    1380
    CAGGCCATAT TCGACTTTAT GACCGCAAAG GCCGAATTGG ACAAGATGAA CGGCATGGGG    1440
    ATTCCCGAAC AA
    
```

(2) INFORMATION FOR SEQ ID NO:59

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

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60  TTTCATAACT TTGACTTCCT AAACGCTATA AAATTGTTT CGATGGCAAA TAATACTCTT    60
    TTGGCGAAGA CTCGACGTTA TGTCTGCCTT GTCGGTTTCT GTTGGCTCAT GGCATGATG    120
    CACCTCTCTG GGCAGGAAGT CACTATGTGG GGGGACAGCC ATGGAGTGGC GCCGAACCAA    180
    GTGGCGCGAA CGCTGGTGAA GGTAGCCTTA AGTGAATCCC TCCCTCCGGG TGCAAAACAG    240
    ATTCTGATCG GATTCTCTCT TCCGAAAGAA ACGGAGGAAA AAGTCACCGC CCTATATCTC    300
    CTTGTGAGTG ATTCTTTAGC GGTGCGCGAC TTGCCGSACT ACAAGGGCGC AGTCCTTAC    360
    GATAGCTTCC CGATCTCAAA GGAAGATCGT ACCACAGCCC TTTCTGCGGA TTCGCTAGCC    420
    GCACGCCGCT TCTTTTATTT GGCTGCGGAT ATAGGGCTGT TTGCTTCTTT TTCCCGATCC    480
    GATACGCTGA CTGCCCGTGT GGAAGAGGTG GCTGTGATG GCCGCCCTTT GCCGTTGAAA    540
    GAGCTGTCCG CTGCCCTCCG TCGTCTGTAT AGGGGGTATG AGGCCCTCTT TGTACCCGGT    600
    GATGGCGGAT CGCGGAACIA TCGTATCCCG GCCATTTTGA AAACGGCTAA TGGAACTCTC    660
    ATAGCGATGG CCGACAGACG AAAATATAAT CAGACGGATC TGCCGGAGGA TATAGATATA    720
    GTCATGCGGC GCAGTACGSA CGGAGGSAAG TCGTGGAGCG ATCCCGAGAT TATCGTACAG    780
    GGAGAGGGGC GCAATCATGG CTTTGGCGAT GTAGCCCTGG TGCAAAACCA AGCAGGAAAG    840
    CTCCTGATGA TCTTTGTGCG TGGAGTAGGC CTGTGGCAGT CTACCCCGCA TCGTCTCAG    900
    CGCACTTATA TATCGAAAG TCGGGACGAA GGAAGTACTT GGTGCGCTCC TCGGGATATA    960
    75  ACCCATTTCA TCTTCGGCAA GGATTGTGCC GATCCGGGAC GCACTGCTG GTTGGCCTTC    1020
    
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WO 99/29870

PCT/AU98/01023

40 / 490

5 TTTTGTGCTT CGGGACAAAG GCTTGTGCTG CCATCCGGTC GTATCACGTT TGTGGCTGCC 1080
ATCCCGCAAT CAGGGCAGGA GTACGTCTTG AACAACTATG TCCTCTATAG CGACGATGAG 1140
GGCGATACAT GGCAGCTTTC CGACTGTGCA TACCGCCGTG GCGATGAGGC AAAGCTTTCA 1200
TTGATGCCCG ATGGCAGGGT ACTGATGAGC ATACGCAATC AGGGACGGCA GGAGAGCCGA 1260
CAGCGTTTCT TCGCTCTCTC CTCCGACGAT GGCCTTACTT GGGAGAGAGC CAAGCAGTTC 1320
GAGGGCATCC ATGACCCCGG CTGTAATGGA GCTATGCTTC AAGTGAAAAG GAACGGAAGG 1380
GATCAAGTGC TGCACCTCCT GCCTCTCGGC CCGGATGGGC GTCCGATGG AGCTCTCTAT 1440
CTCTTCGATC ATGTCTCCGG CCGCTGGTCC GCTCCCGTTG TTGTCAATTC AGGATCGACT 1500
10 GCCTACTCGG ATATGACTCT GCTGGCGGAT GGAACGATCG GTTATTTCGT CGAAGAGGGC 1560
GATGAGATCT CATTGGTTT CATTGCTTC GTCCITGAGC ATCTCTTCGA TGTCCGGCAA 1620

(2) INFORMATION FOR SEQ ID NO:60

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
20 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
25 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...879
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60
AAGTCTCCGA GCGATTCCGG TTTGCCGTG GTATGGAGCG CGAATACAAT ATCTGGACTC 60
GTCGGTGGGA AACGCATTAC TTTGCTTATC CTGTATTCTA TGGCGATAAG AAGTAGTAAT 120
ATAGAATCAA TACAGTGCTT TGTGATGAAA AAAGAAAAAC TTTGGATTGC GATCGTCGCC 180
GGTTTGGCTT TCGTATTGGG CCTTTATGCT CTGGCCGCA GTGTCGCTCA GCTACGCCCG 240
TCTCAGCCTT CGGTGACTGT GACCGGTATG GCGAGCGTA ATTCAAATC CGATCTGATC 300
40 GTTTGGACTG CTTCTACCA GCTCCAGATG ATGGATCTCG AATCGGCCTA CAAGGCTTTG 360
AAGGAAAAAC AGATATTGGT AGCAGACTAT TTGAAAAACA AGCAGCTGCC CGATTCTGCT 420
TATATCTTCT CAAGCGTAGC CATCTCTAAA GAATACAACT ACTATTACGA TCCTCGGCAG 480
GAACAAAACG TCAGGACCTT TGCCGGGTAT CTGCTCAGCC AGACAGTTAC GGTGACCTCA 540
45 CAGGACATCG ALCATGTGGA GAAAAATCT CCGCATATAA CCGAGCTGAT CAATCAGGGG 600
GTAGAGATTA CCTCCGACCG TCCGGCCTAT TACTACACCA AGCTCAATGA TCTGAAGGTC 660
GAGATGCTGC GCAATGCCCT CGAAGACGCT TTCAATCGTG CTTGGGTCTT TCGGAGGGGG 720
AGCGGTTCCT CCGTGGGTAA GATGCTATCT TCTTCGATGG GCGTGTTCGA GATAGTGGGG 780
CTCAACTCGA ACGAAGATTA TAGCTGGGA GCTTCGTTC AATCGTCTC CAAGATGAAG 840
50 ACGGCAAGCA TAACGGTTAA GGCTTCTTTC GCTTTGAAG 879

(2) INFORMATION FOR SEQ ID NO:61

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 840 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
60 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
65 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
70 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...840
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

WO 99/29870

PCT/AU98/01023

42 / 490

5 TGGCTCTTGA GGGAGGATTC TTCCCGTCCG GCCGGTGCTC TGTCCGAAGT GGGATCGGTG 2220
AGCAATTTCC TGAATAGCAT CGCTCTCGGC ACCGGTGTCG GCCTTCGCTA CGATCTGGCA 2280
TTTCTCGTGG TTGCTGTGCA GTGCGGCTTC GGTCTCCACC TTCTTACAA TACGGGTAAG 2340
AAAGGTTACT ACAATATCCC ACGCTTTAAG GATGCCATCG GTTCCATTG GGTGTCGGC 2400
TATCCCTTC 2409

(2) INFORMATION FOR SEQ ID NO:63

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2349
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

30 TCTCTCTCCG CGTATATCCG TTTCTCTATG TCCTCCGATT CCGTTCGGTA TCTAATCGGC 60
ATTGCCGGCT GCTTGCTCCT CATGCTTGCT TCCTCCTGCT CGGTACCCCG TTATGTGCCG 120
GACGGTAGCA GACTATTAGA CAGGGTAACG ATCGCAAGCG AAACGGGCAG TATCGCTCTG 180
CCGGAAGATA TTCCGGGACTA TACCTCCAG CAACCCAATT ACAGACTGTT CGGGATGACT 240
35 CGCTGGCTAC TCGCGCTCTA TAGCAGCTCG AATCCGAACA CCAACAGCTG GTGGAACCGT 300
TCGCTCCGGA AATGGGCGGA ACCGGCTGTC CTCATCGATT CTGTCTCTAC CGATCGTACT 360
GCCAACCGTC TGGCAAAGGC GATGGCCGGC GATGGCTTTC TCGATGCTAC TGCTCGTGCC 420
GTGGTAGACA CCGGCTTGTA CAAGAAAGCT CGCATTTACT ATCTGATTCA GCCCGGAAGC 480
CGTTATTATA TAGCCAATAT GGCTTTGGAT GTGAAGAATC CACTCCTTCC TCCCGTTGCG 540
40 CTTGGCAATT CGCTTCCTTC GGCATACAAG GTCGGSAACA GCGAGGGTTC TCCCTTGTCG 600
CCCATCGTAC TCGATGAAGA GAGAAAGGCG ATAGCTCGTC ATATGCGCAA CAACGGCTTC 660
TGGAAAGTTCT CCGCCGAGGA TGTATTATAT GAAGCAGATA CTACCGTTTC AGGAGGATCG 720
GGTACGAAAT CTGCCGATCT GAAATTAGTG GTCAATGGCA TCGGGCGTTA TCCATATCGG 780
ATCGGCAGGG TATTCCTTCA TGCCGATTAT GATCCTCTCG AATCGGACTT CAGAGTTTCA 840
45 GAGCTGCGAC GTATCGATTG GATTTCGCGT GCGGATTACA CTGTTTACTA TGGGAGTAGG 900
GGACGTTATA TCCGGGCATC GGCTCTCAGC CGGTCCGTTG CCGTTACACC GGGAGCTTTT 960
TTCTGCGAGG ATGATGTGGA ACGCTCTTAT ATCAAGCTGA ATGCGCTCCC TATCGTTCCG 1020
AACGTGAATA TCGGATTTGT GGAGCACAAT GGTAAGGATG AGATTGCTCT GCGGATAGC 1080
TCTCGCCTTG TGGACTGCTA TATTTCTACC GTTCCGGCCA AGAGCAAATC GTTCSAAGCC 1140
50 GAAGTCCTCG GCACCAATTC CGCTGGAGAC TTCGGGCGCG CTTGTCTCTT CCGTTTCAAC 1200
GATCCGAATT TGTTCGTGGG GGCAGAGATG TTCATATCA AACTCAAGGG TGCTTACGAA 1260
GCCATTCCGA AGGTTTCGCA CAGCTTCATG GAATATGGGG TGGAAAGCTC GCTCCGTTTC 1320
CCTCGTCTCC TCTTCCCATT CATTTCTGAC GAAACGCGCC GCGGCTACG GGCATCCAGC 1380
GAATGGAAGA TCGGGTATAA TTACAGACA CGTCCGGAGT TTGATCGGGT GATTCTCTCC 1440
55 GCTCAACTCA ATTATTATG GCAGACCTAC CTGCACAATC GTCTCGCTCA TACGATCCGC 1500
CTGCTGGATG TCGATTATCT CCATCTCCG TACATCGATC CCGACTTCG CCAATCCCTT 1560
CCGCTACGGA CTGCACTGTA TAACTACAG GAGCAGTTTA TCCTCGGCTC GGCATATATA 1620
CTGAACATATA CCAACGCTTC GTCCATGGAG CGTACCGTAT CCAATCCTTT TACGGCACGG 1680
TTCAGTATCC AGACAGCCGG CAACCTGCTG CAAGCCATTT CTTATCTGAC CGATTCTCCG 1740
60 AAAGACGAAC ACGGGTTGTA TAAATGTTT GGTCTGCACT ATGCTCAGTT CGTCAAGCTC 1800
GATCTCGATC TGGCTAAAAC CGTTCTTCTC GAAAAGGACA ATACTTTGGC ACTGCATCTG 1860
GATTTCCGAC TGGCTTTCCC TTATGGCAAT GCTCGCCATA TACCTTTTGA GTTACGTTAC 1920
TTTGCCGGAG GATCGAAGAG CGTTCCGGGC TGGAGTGTCC GTACCTCTCG CCGGGGAGT 1980
ATGAAGATGA CTCCGGACAA GACCTTCTTC GATCAGATGG GTGATATTC TCTGGATCTG 2040
65 AATGTGCAAT ACAGGACAAA GCTGTTCTGG AAGTTTCGCG CAGCAGCTTT TGTGATGCTG 2100
GGCAATGTCT GGACGATAAA GAGATATGAG AATCAGGAGG ACGGTCTCTT TCGTTTCGAT 2160
TCTTCTTACA AGGAAATAGC TTTGGCCTAC GGTCTGGGGC TTGCTCTCGA CTTCGATTAT 2220
CCCTTTGTC GGCTGGATGC CGGACTGAAA GCCTACGATC CTCAGCAGAC AGGGCGTTAC 2280
70 AAATGGGCTA TCACAGCGCC AAACCTTTCT TCCATTTTCG CTGCGCACAT TGCAGTAGGC 2340
TATCCGTTTC

(2) INFORMATION FOR SEQ ID NO:64

- 75 (i) SEQUENCE CHARACTERISTICS:

WO 99/29870

PCT/AU98/01023

43 / 490

(A) LENGTH: 2625 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

10 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

15 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2625

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

25	GTGCAATCTA AATTGTTATG TCTTATGAGA AAAAGAATTC TACAACCTTTT CCTGACCGCA	60
	TTGCTGCTGG CATTAGGCTC CTCTCTCGCC ATAGCGCAAA CAGTGGTGAC CGGTAAGGTG	120
	ATCGATTGAG AAACGTCGGA ACCGCTCATC GGTGTATCCG TAAGCACCGG TCAGGGAGCA	180
	TCCCTCCGCG GTGTAACAC CGATATGGAT GGTGGCTTCC GATTGGAAGT ACCGGCCAAA	240
	TCTGTCTTGA CTTCGGTTG CGTAGGTTAT GCTACCGTAA CTCGCTCTAT AGGCAGAGGT	300
	TCTCAAGAAG ACCTCGGTAC GATTCTCCTC GATCCCCAGG CCATGGGCTT GGATGAGATT	360
	CAGTAATAG CCTCTGTGGT GCCCAAAGAC CGTATGACGC CGGTACCGGT TTCCAATATC	420
	CGTGTGGCTG ATATTGAGGC AGCATCGTTG AATGTCGAAT TTCCCGAACY GGTAAAATCC	480
	ACTCCCTCTA CCTATACGAC AAAAGGAAGC GGAGGTTTCG GTGATGGTGG TACCAATGTG	540
30	CGTGGATTGG ACACCTTACAA CTTCGGTGTA CTCATCAACG GAGTTCCTGT CAATGGTATG	600
	GAAGACGGGA AAGTATATTG GAGCAATTGG AGTGGTCTGA TGAATCAAGC CAGTACCATT	660
	CAGATTGAGC GCGGACTCGG AGCCTCCAAG CTCGGTATCA GCTCGGTAGG TGGTACGATG	720
	AACATTATCA CGAAGACTAC GGACGCCAAC ACCGGAGGTT CGGCTTATGT CGGTATGGGT	780
	AATGATGGAT TGCACAAAGA ATCGTCTCC ATTTCTACGG GTATGAACGA CGGTGGGGCT	840
35	ATCACCATTG CAGGCTCCCA TATGACGGGT CTGGGTTATG TGAAGGGGCT GAAGGGACGT	900
	GCATTCTCTT ACTTCTTCAA CGTTTCGAAG AAGTTCAATG AACGTCATAC CCTCTCTCTT	960
	ACCGGATTGG GTGCACCACA ATGGGCACAA CAACGTTCTT CCAATATATC TGTAGCCGAC	1020
	TATGACAAAT ACGGCATCCG TCACAAATCAA TCCTTCGGCT ATCTGCGAGG CGAAGTGAAT	1080
40	CCTACGGCTT ATGCTTACAA TACGTACCAC AAGCCCCAGT TCTCGCTGAA CCACCTCTGG	1140
	AAGATGGATG AAAATACCTC TCTTTATACG GCAACCTACG CATCTTTGGC TACCGGTGGA	1200
	GGTCGTCCGG CTTATGGAAA GAACAGTAAG TGGGTATTGA TCAACTACAA CACCGGACAA	1260
	CCCTATGAAC AAACAAAGGT GACTCCCGAT GGACTTATCG ACTACGATGC CGTACTGGCT	1320
	GCCAATGCTG CGGCGAGCAA TGGCTCGGAA GCAATTTTTC CCCTTGGCTC CAACTCTCAC	1380
45	AAGTGGTTCG GTCTACTCTC TTCATTCAAG AAGAAACTTA ATAGTTCGCT GACTTTGACA	1440
	CGCGSATACG ATGGGCGTTA CTACCGTGGC GACCACTATG ACAAGATCAC CGATCTGCTC	1500
	GGCGGTAGCT ACTACATAGA GGATCCCAAG ACAAGACTCG CATACCATGC GGAAGGTCAG	1560
	CAACTGAAAG TGGGTGACAT TGTAATACGG GACTACACAG GCGAAATCAT GTGGCACGSC	1620
	CTCTTCGCAC AGATGGAGCA TTCGTCCGAA TGGATCGATG CATTCGTATC AGGATCTATC	1680
50	AACTACGAAC TATACCGCAA TCACAACTAT GCGCGTAGCA AGTCCACGGG CTACCTGCCC	1740
	GGCGTATCGC CGTGGAAAAG CTTCCTTCCG TGGAGTGGCA AGGCAGGTCT GAGCTACAAG	1800
	TTCCGACACG GACACAATGT ATTCGCCAAT GCGCGTTTCT TCACACGTGC ACCACTCTTT	1860
	GGCAATATCT ATGCTGCGGG GGCTATCATT CCCAATGACA AAGCCAATAT GGAAGAGGTG	1920
	CTACAGGAG AGGTGCGCTA TGGATTACCG AATCACAAA ACTTCGAGTT CAATATCAAC	1980
55	GGATACTATA CGAAGTGGAT GGATCGCGTG ACCTCGAAGA GAATCGGAAA CGAGTATGTT	2040
	TATCTCAATG GCGTTGATGC TGTTCACGTG GGGTAGAGG CTGAGGTCAG CTATCGTCTT	2100
	ATTGCTCAGA TCGACCTTCG CGGTATGTTT TCTCTCGGTG ACTGGACTTG GCAAAACAAT	2160
	GTAAGTTACA CTCTTACGA CGAAGCCGGC AATGAGACAG GGCAGGATAT AACCTATATC	2220
	AAGSGTCTTC ACGTCGGAGA TGCAGCACAG ATGACGGCTG CTGTATCGGC AGACATAGAG	2280
60	CTGTTCAAGG GTTTCATGT CATAGGTAAG TACAACCTTC TTGGCAAGAA CTATGCAGGA	2340
	TTCAACCCCG CAACGCGTAA TGCACAGCAG TACGAAGCGG ATGGCAAAGA AATCGTGGAA	2400
	TCATGGAAGT TGCCCGATGT AGGTCTGTTT GATCTGTCTG CATCCTACAA TTTCAGGCTT	2460
	GGTTCACTCA GCACCAATT CTATTTCAAC ATGGACAACG TAGCCGACAA GCGATATGTG	2520
	AGCGATCCCG ACGACAATAT CATCGGTAAG AAACACGATG AGGCTTCGGC TCTCGTATGG	2580
65	TACGTTTTCG GCGGCACCTG GTCTACCGGT ATTCGTGTA ACTTC	2625

(2) INFORMATION FOR SEQ ID NO:65

70 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

75 (ii) MOLECULE TYPE: DNA (genomic)

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WO 99/29870

PCT/AU98/01023

44 / 490

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

15	AACAGATGTA ATCCCTCGCG TCAATACTTC CACCTATCGC AGAATGACGT TGGAAAGATCT	60
	CTCCGAGCTT TCTAATCCA TCTATCTATG AAGTTTTCAA TCCGCTTTT CCTCTGCATC	120
	ATCTTTCTCC TCTCTGCATT TATCCTGCCT GCTCTGGAC AAAAATCCAA GCAGGTACAG	180
	CGACTTGAGA AGCAACCTAA GGAGGCCCTC AAAGCCATCG AAAAAACCA TCGCGAAGCTA	240
	CGAAATACCA AGAAAGACAA GCAAGACAAA CAAAAGCATC TCAACCTCCT GAACAGCAG	300
20	GTTGCTCAAC GCAAGCAGAT GGTACAACTC TTGGACAATG AGGTCAAAGA GTTGCAATCC	360
	AGCATTGATT CCAATGACGGG TGTATGTCTAT CAGCTCTCTG TAGAAGAGAA AGCCCGATCC	420
	GATGAATATG CCCAAGCTCT ACAGTCTATG CAAAAGCGGA AACGCTCTGT GCATCGCATC	480
	CTTTTCATTT CATCGGCCAA GAGCTTTGAC GAAGGCATGC GACGATGCG TTTCTTGGAA	540
	CAATACGCTT CTGCATACAA GCTGGCATCT GTCCGGCTGC GCGATACACG TAGCAAGTTG	600
25	GAGACTGAAC GTGGGACTGT AGAAGACGCC AAAAAGSAGA NAGGACATCT CTTAGTCATC	660
	AGAGAAGAGG AAAAAAGAA ACTCGAAGGA CAGCAAGCGG AGCAACGTCG GCAGGTGCGAG	720
	GCTTTGGGAG CCAACAAAAA AGACTTGGAA GCGCAGCTGC GAAAGCAGAA AAGCAAGCC	780
	GAAGCTCTGA ACAGAAAGAT CAGAAAACAG ATTGCCAAGG AAATAGAAGC TGCCGAACGT	840
	CGTGCTCGAG AAGAACGTGA ACGGTTGGCA CGCGAAGCCA AAGCCAAGGG TAAGCCGGTT	900
30	CCTGCCGAAC CGGAACGGAA GCGGAGAC AAAGGCGGCT ATGCTATGGA TGCCTCTGAG	960
	CGTGCTCTCT CCGGAGCTT TGCACAGAAC AAAGGTGCGC TGCCCGGCCC CGTTCCGGGC	1020
	AGATACCGAA TCGTAAGCGA CTTTGGCGTG CATCAGCACA GTGAGCTGAA AAAAGTACAA	1080
	GTTAATAATG GAGGTATCGA CATGGCTGTA GCAACAGGAT CCGATGCTAC CAGCGTATTC	1140
	GATGGGTAG TGTCCAGTGT ATTCTGTGATA CCGGGTTATA ATTCCGCGCT AATGGTTCGT	1200
35	CACGGTAACAT ATATCACGGT TTATGCGAAT CTGAGCAAG TGTATGTAAA TTCCGGCACT	1260
	CGTGTTAAAA CCGGTCAGGC TCTTGGTCGT GCCTATACGG ATCCTTCCAA CAACCAAGCC	1320
	ATTATTCACT TCGAATCTG GAAAGAACGC AGCAACAAA ACCCAAGACT ATGGTTACGA	1380

(2) INFORMATION FOR SEQ ID NO:66

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1026 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

65	AGTTTTATC AAGAAATAGA CAGACTTATG AAAAAGTATT TGTATATGC CTCGTTGCTA	60
	ACGAGTGTTC TGCTCTTTTC CTGTTCAAAG AACAATCCTA ACGAGCCGGT GGAAGACAGA	120
	TCCATCGAAA TTCTATAAG GGTAGATGAT TTCACCAAAA CCGGTGAGGC AGTACGCTAT	180
	GAAAGGAATC AAGGAAGTGC TGCCGAAAGG CTCATTACCA ATCTTTACCT CTTGTTGTTT	240
	GATCAGTCAG GGGCGAATCC GGGGAAATAC TATATTACCG GTAACACTTT CACCGGAGGG	300
	AGCTGGCTTC CTGACGATAT GAAGGTGAAG TTGGATATGA CACAATCCGA GGCAGGAGAG	360
	CGCAAGTAT ATGTCGTAGC CAATGTTGAT AATGCGGTTA AAACGGCTCT TGATGCTGTC	420
70	GCTAAGCAAA GCGATTGSCA GACTGTANAG AGGACGACTG CAATGCCGTG GTCGACCGAT	480
	ATAGCCCTCTC CTTTCCTGAT GTCCGGAAC AAGACACAG ACTTCTTGGC CAATCGTCTT	540
	TTGGACAAATG TGCCCTTGT GCGTGCCATT GCCAAGGTGG AGCTGAATAT CTCGCTGAGT	600
	GAGAAATTC AGATTGTGCC GATAATTGTC AATGGTAGTT TGAGTGAGTT CAAGTTTCTA	660
	TACGTAACT TCGACAAGGA GACCTACGTA GTGAAGCCAA CAGCAAGCC GACCAATCTC	720
75	ATTAGTCTCT CTAATGGTGT TTGGCTCTAG ATTACAGATT GGACTGTATG GGGTGCTTCC	780

WO 99/29870

PCT/AU98/01023

45 / 490

5 TTAATACTT CTCCTGCTCC GGATGCGGGC ACAGGTTATA CATTGGATGC AATGGCAAG 840
GTAACGGCAC TACGGATTGT TACCTATCTG AATGAGCGCG ATAGCAAAGG GGCTACGGTA 900
GAGGTGCGAT TGCCTCGTGT GGATGATGGC ACCCTTCCTC CTCGGAATT CGGTCCGGAG 960
CTTTATCGTT TGCCTTTGCC GGACAAGATC CTGCGCAATC ATTGGTACAA GTATGAAGTC 1020
GAGATT 1026

(2) INFORMATION FOR SEQ ID NO:67

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

30 AACCTTAGGA CACAGCCTTT CTTTTGGTA GATTGCAAT CTATGATCAG AACGATACTT 60
TCAGGATATG TATCCTCGAA CTTTGGAGT CGGGGAGCTA CCTTTTTTTT CACGATTTC 120
CCGGCCTTCA TCCTCGCCGC TACTGCTTG CGGCTTGTG GAGGGGGTAC TGCTTCAGGC 180
TCCGATCGTA CGCTGGCTGT GACCATCGAG CCACAGAAAT ACTTCATCGA GTCCATTGCG 240
GATAAGTCGG TGCAGGTGGT GGCATTGGTA CCGGCCGSCA GCAATCCGGA GGAATACGAC 300
CCTTCGCCTA CGGTGATGAA GCGTTGTCC GAAGCAGATG CCTACTCTA TATAGGAGGA 360
CTGGGGTTCG AGCAAAGAAA TCTCGCTGCC ATTCGGGACA ATAACCTTAA GCTCCCTCTT 420
TTCGAAATGG GCAAAGCCTT GCGGATGCC GGAAGTGCAG ATCTCCACGG CTCCTGCACA 480
GATCATCTC ATACAGACCT GCATGCCCAT GATCCGCACT ATTGGAGCAG TGTGGTAGGG 540
GCAAGGCAC TCAGTCGTGC TGCATACGAC GCGCTTGTGG AGCTTTATCC GAACGAGAAA 600
GACAAATGGG ACAAAAGGCA CGACCGTCTC AACGGACGTA TCGACAGCGT GAAGAGACTC 660
GTGATACCA TGTTCGCCAA TGGCAAAGCA GACAAAGCCT TCGTCATATA TCACCCATCG 720
CTCAGCTTTT TCGCCCAAGA GTTCGGCCTG CGGCAGATCG TCATAGAGGA AGATGGGAAA 780
GAGCCTACGG CTGCCACCT TCGTCGTGTG ATCGATCAGG CACGTGCCGA TGGTGTCTAGA 840
45 ATCGTATTTA TCCAACCCGA ATTTGAAACG CSTCAGGCGG AGGACATCGC ACGCGAGATC 900
GGTGCTCGTC CGGTAAGGAT CAATCCTCTG CGCAGCTCGT GGGAGGAGGA AATTTTACAT 960
ATTGCTCGCG CTTTGGCTCA TGAACGG 987

(2) INFORMATION FOR SEQ ID NO:68

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2634 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 60 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...2634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

75 GCAGATTCTA TTGATATCC TCTTTACTTT TTTGGGCGGA ATCGGAAGAA ATGCTTTAGG 60
GAACCTATTG CCACCTTATA CAATAAAMAC ATGATCGGAA AAAAAATCTT TTTTATCCTG 120
CTGGCGCTCA TTGCGTTCAG TGGGCTGAAC GCAGCGACAG AACTGAGTT CAAGTACCCG 180

WO 99/29870

PCT/AU98/01023

46 / 490

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5  ACCGATGCCA ATATCATCGG TCACGTCAAA GACAGCAAGA CGGGTGAACA CTTGTGCGGT 240
   ATCACTATTG CTATCAAAGG CACTACCTTT GGTACATCTA CAGATGCAAC CGGGCACTAC 300
   TATCTTCGTA ACTTGCCTCC GGGTGAGATC ACTTTGATTA TGGGTGGCAT GGGCTATAAG 360
   AGCCAGGAGC GCGTAGTCCG CGTAGAAAAG GACAAGACTA TCGAGGTGAA TTTCGAAGCA 420
   GAAGAGGATG CCATCAATCT GGACGAAGTC GTGATTTGGG CCAACCGCGA ACTGACCGTT 480
   CGCCGCTCTG CTCTACTCT GGTAAATGTA TTGAACGAAA AAGTCTTCTC GCAAGTCAAT 540
   GCTTCTAACG TGGCTCAAGG CTTGTCAATC CAGCCGGGAG TTGCTGTAGA GAACAACCTGT 600
   CAGAAGCTGT GTTTCATCA AGTTCGTATC AATGGACTGG ATGGTCGTTA TGCACAGATC 660
   CTTCATGACA GCCGTCCCAT CATGAGTGCC CTTGCCGGTG TTTACGGTCT GGAGCAGATC 720
   CCTGCCAATA TGATCGAAGC TGTGGAGGTA GTACGTGGTG GAGGATCGGC CTTGTACGGT 780
   TCTTCTGCTA TTGCCGGAGT GGTGAATATC ATCACCAGG AACCTTCTCA CAATCTTCTC 840
   ACATTCAATG AATCTCTGAG CTTTACCGGT TTCAGCAAGC TGGATAACAA CACGAACCTC 900
   AATSCCTCCA TCGTCAGCGA TGACAACCGT GCCGGTGCCA TGGTATTCGG GCAGCCTCGT 960
   TACCGCAACC ATTGGGATGC TAACAATGAC GGTATTTCGG AATGGGTAA AATAGATGCC 1020
   CGCTCGCTGG GAGCGCATTC TTATTTCGCG TTGAGCGACT ACAGCAAATG GACGGGAGAG 1080
   TTTCACACGA TCAGTGAATT CCGCCGTGGT GCGGATCGTA TCGATTTCGC TCCTCACGTA 1140
   GTGGGTGTAG CTGAACAAAC TGACCATAGC GTATTTAGCG GAAACTTGAA ATACGATCTC 1200
   TTCTCTTCCA ACTATAAACA CCACTTCCAG GCTTATACCT CCGGACAGAT CGTAAATCGC 1260
   AAGAGCTATG ACGGAGGTAT CGGAGAGATT GACGTCAATG GCCACCCCGG TGGTACGGAA 1320
   GGCTACCCCTA TCCCTCAAGA TCAATACGGC AATAATTATG GCGTGACCAA AGGCAAGACA 1380
   TATATGGGCG GTATCCAGTA CAGCTACGAC TTGGACAAAT TCCTCTCAT GCCTTCGCAA 1440
   CTTTGTGTCG GAGCGAATA TACGGTGAT GAATCAATG AATGATGCC CATCCTTTCA 1500
   TGGCAGACCG GCGAGGATGC CAATGGGAAT ACCATTCCCC TCTATCCCGA ATTGGATCAG 1560
   AATATCAACA ACTACAGCCT ATTCCGTCAG AACGAATGGA AAAATGACAG ATGGAGCATC 1620
   CTGTGTGGCG CTCGCTTGGG CAAGCATAGC GAAGTCAAGG ATATGATTCT GAGTCTCTGT 1680
   ACCACACTCG GTTTCACAGT GAATCCGGAC ATCAACCTGC GCGCTACATA TGCAAAAGGG 1740
   TTCGCGCACC CGCAGGTATT CGATGAAGAC TTGCACGTAG CGGTTGTAGG CGGTGAGGCA 1800
   CAGAAATAT TCAACGATCC GAACCTCAAG CCTGAAATTT CTCATGCATT CAGTTTGAGT 1860
   GCCGATATGT ATCATCGTTT CCGTAACGTC CAGACCAACT TCCTTGTTGA AGGCTTCTAT 1920
   ACTCGTTTGC TGATGTATTT CACCAACGAG GAGCAGCGTG ATCAGCAGCA TGGCATCAAA 1980
   CGCTACACGC GTATCAACGG TAGCGGAGCC AAAGTATTGG GTCTCAATCT GGAAGGTAAAG 2040
   TCGCATACA AGTCTTCCA GCTCCAGGCC GGTCTTACCC TGGCCAGCAA CAAATACGAC 2100
   GAAGCACAGG AGTGGGGTCT GAATACGGTG AAAGACACCA ACGGAGCTTT TGTACCGAG 2160
   GCGAATGCAA ATGGACAACA GGAATACVAG AACGAATCCA TGACGGATAC GCAGATCACC 2220
   CGTACCCCA CGGTATACGG TTATTTTACT TTGGCTACA ATCTGCTCA CTCATGGAAC 2280
   ATAGCCCTTA CGGAGCATA TACCGGTGAG ATGTATGTAC CCGACGCTAT CGAATATGGT 2340
   GTGAAGTCTG CCGAATCGA TATTATGCAG AACAACTCCT AGATTACCGA CGAATCCGGA 2400
   AAGGCTCCCC GTATTGATGA GCTGAAGAG ACACCTGCAT TCTTCGATTG GGGCTTGAAA 2460
   GTGGGTATG ACTTCCAGGT ATTCCAGGCT ACTGAGGTTC AACTCTATGT AGGTATGAAC 2520
   AATATCTTCA ACTCTTTCCA GAAGGACTTC GATCGTGGAG CTCGACGTGA CAGCGGATAT 2580
   ATCTATGGTC CTACGCGACC GCGTACAGGC TACATGGGCT TGGTAGTGAA GTTC 2634

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(2) INFORMATION FOR SEQ ID NO:69

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45  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 618 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
50  (D) TOPOLOGY: circular

     (ii) MOLECULE TYPE: DNA (genomic)

     (iii) HYPOTHETICAL: NO

     (iv) ANTI-SENSE: NO

     (v) ORIGINAL SOURCE:
60  (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

     (ix) FEATURE:
     (A) NAME/KEY: misc_feature
     (B) LOCATION: 1...618

65  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

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   AAACAGATAG TTATGACAGT AAAGCGCGCA GTGCGAATAG CACTTCTCAC GCTGATAGGC 60
   ATTCTTTTTT CTTACCTTTC TCTTGTTCCG GCGCAAAGTC TTTTCAGCAC CGAACATGTC 120
   TTGCAACTAT ACAACAAGAT ACTCTATGGA GAGTCGGCGG CGGATACCGT CGCAGAGAAA 180
   ACGGCAGGTG AGTCGGCAAT TCCTTTTATA GACAAACTCA TCAATCTCCG CCGCACTTTC 240
   CTCGGCAAAAC CATATCGCTA TCGCGGTCCCT TCCCATGGGC CGATGGACTG CTCGGGCTAT 300
   GTGTCTTACC TCTACTCCAA ATTGACATC AAACCTCCAC GTGGTGGCGG AGCAGAGAGC 360
   CAATATACGA ATCCTATCGA GCGCGAGGAT GTTCGTCCGG CCGACCTCCT TTTTTCAAA 420
   GCGCGCAATG CACGAGCAAA CCGTATCGGG CATGTAGCTT TGGTCGTATC TGTGATGAA 480
75  GATGATATTA CCATGATGCA CAGCCGCAAT TCGCGAGGGA TCGTGATCGA AAACTCAAT 540

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WO 99/29870

PCT/AU98/01023

47 / 490

CGCAGTGCAT ACTTCTCCCG TCGCTTGGTG AGCTATGGCA GGGTACCCCG AGCCAAGAGA 600
GTGATCCAC GAAAAAGT 618

- 5 (2) INFORMATION FOR SEQ ID NO:70
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1401
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

AAAGGTACGT GGAATAGAAA AAACCGAAGA GAAGAAATGA AACGGACAAT COTCCTGACG 60
GCACTGACCG TCCTATCTTC GCTCTCCTTG CTTCGTGCAC AAAATGAATC CGAAGCATCA 120
ACCAATCCGA TGTCAGGCCT CTCCTTGGAA GACTGTATCC GGATAGCCAA GGAGCGCAAC 180
CTGAATCTGC GCAGACAGGA GATCGAACAA GAAAACCGAA TCATTAGTCT CGATGCAGCA 240
CGACACAGTT TCCTGCCCTC GGTCAATGCA GGCATCGGAC ACAACTATAG CTTCGGACGT 300
TCGAAAGACA AAACGGGAST AACCGTAGAT CGCTCCTCGA TGAATACCAA TCTCAGCATC 360
GGAGCTTCGG TGGAAATATT CAGCGGCACA CGTCGTCTGC ACGACCTCAA GCAGCAAAAG 420
TACAACGTGG AGGATGGTAT AGCCCGACTT CAAAAAGCGG GTGAAGACCT CAGCCTGCAA 480
ATCGCGGCTC TCTATATCAA TTTGCTCTTC CGTCAGGAAA TGACTCGTAC GGCAGAAACA 540
CAGTTGGCAC TGATTCGCGA GCAACGCAAT CGCACGCGCG AAATGGTTCC CGTAGGTAAG 600
TGGGCAGAGG GTAAGCTCCT CGACATAAAT GCCCAGATGG CCAAGGACGA ACAACTTCTC 660
GTACAATATC GTTCGGAGGA GGAGCTGGCT CGTCTGGACT TGGGGCAAGC CCTCGAACTG 720
GAGCACCCCG AAAGCATTCG AGTCAAGGCT CCCGACACAG ACGTTCTCGT AGCAGAAAGG 780
TTGGGATCTC TCCTTGCTCC CGAAGAGATC TATCGCACGG CTCTCGGCTT GAAACCGGCA 840
CTGCATTGCA GCGAGCTGCA AATAGCTTCG GCACGCGAAG GTCTGGCCTC GGCTCGTGCG 900
GCATACITCC CGACGCTCAG CCTCTCTGCC GGATACAGCA ACGGTTACTT CCGCGACCTC 960
GGCAAGGAGT ATGCGGCCAT CAACCCCTCC TTCTCGAAG AGTGAAGAA CAAACGGCAGC 1020
TACAGTATCG GACTCTCTT GAATATCCCC ATCTTCTCTG CCATGCAAAAC GCAAGATCGC 1080
GTTCCGGAGCA GTGCGCTGCA AATACGCTCA AGCGAGCTTC GACTCGTCTGA AGAGAAAAAA 1140
GCCCTCTATA AAGAGATCAG GCAAGCATAC AGCAATGCCG TGGCAGCCGA TAAGGCCATC 1200
GCAGCAGCGG AAAACAGCAA GGCCGCTACG CTCAAGGCAT ACGAATACCG TCGCGACAGC 1260
TTCGAGGCAG GGCCTTGTG TGCTACGAA TATGCCGAGG CAAAACAAA ATACGCCCTC 1320
AGCCAAGTGG AAGAACTTCG TGCCAAGTAT GACTTCATAT ACAAAGCCAA AGTTTGGAT 1380
TTCTATCAGG GCAAAGACTT C 1401

- 55 (2) INFORMATION FOR SEQ ID NO:71
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1353
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

WO 99/29870

PCT/AU98/01023

49 / 490

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GATCAGGTCG AATTGAATTG GACGGCTGTT CCTGCCGATC AATATCCATC ATCTTATCAG 1620
GTGGAATACC ACATATTCGG AAAATGGAAAG GAAATAGCTA CGACAAAGGA GTTGTCTTAT 1680
TCGGATGCCA TCGAGGAAAG TATTATCGGT AGCGGTATCA TTCGATACGA AGTAAGCGCA 1740
CGCTTCATTT ATCCCTCGCC GTTGGATGGA GTGGAATCTT ATAAGGATAC GGACAAGACT 1800
TCTGCCGACC TTGCCATAGS AGACATTCAG ACCAAGCTGA AGCCGGACGT AACACCTCTC 1860
CCCGGAGGAG GAGTATCATT AAGCTGGAAA GTTCCTTTCT TAAGCCAGTT GGTTCCTCGA 1920
TTCCGAGAAA GCCCCAATCC TGTGTTCAAA ACCTTTGAGG TGCCCTATGT TTCTGCCGCA 1980
GCCGCCACAA CCCCCAATCC TCCCGTTGGC GTAGTCATTG CAGACAAGTT TATGGCCGGT 2040
ACATATCCCG AAAAGGCTGC TATCGCTGCC GTTATGTAA TGCCATCCGC TCCGGACTCT 2100
ACTTTCCACC TCTTCTCAA GAGCAACACA AACAGAAGAT TGCAGAAGGT GACAACTCCC 2160
TCCGATTCGC AGGCCGGAAC ATGGTTGAGG ATCAATTTGG ATAAGCCGTT CCCGGTGAAT 2220
AATGACCATA TGCTTTTGGC CGGTATCAGA ATGCTAAHA AGTACAAGCT CAATCGTGCT 2280
ATCCGTTATG TAAGAAATCC GGATAACCTT TTCTCCATTA CCGGTAAAGAA GATTTCATAT 2340
AAACAACGGAG TCTCTTTCGA AGGCTACGGA ATACCCCTGC TCTTGGGCTA TATGGCTATC 2400
AAATATCTGG TGGTAAATAC CGATGCTCCG AAGATCGATA TGTCGCTTGT ACAGGAGCCT 2460
TATGCTAAGG GAACGAATGT GGCTCCATTC CCCGAATTGG TCGGCATATA TGCTATAAAG 2520
AACGGAACAT TTATCGGCAC ACAGGATCCA TCCGTCACAA CTTATTCGTT TTCAGACGGA 2580
ACAGAGAGCG ATGAATACGA AATAAACTG GTATATAAGG GATCGGGCAT TTCGAATGGC 2640
GTGTCTCAGA TTGAGAATAA CAATGCTGTC GTTGCATATC CGTCTGTGTT AACAGATCGT 2700
TTCAGCATTA AGAACGCTCA TATGGTTTAC GCTGCCGCCC TCTACTCATT GGATGGCAAG 2760
CAGGTTCTGT CTGGAACAA CCTCCGCAAT GGCCTGACAT TCAGTGTTCA AGGACTTACG 2820
GCCGGTACTT ATATGCTCGT TATGCAGACG GCAAAACGSCC CTGTGAGCCA AAAGATCGTG 2880
AAGCAG 2886

(2) INFORMATION FOR SEQ ID NO:73

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...2106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

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TGGAAAAAAA GTAACTCTCA ATACCGGGGC AGGACAGCAA ATTACCGAGA TCATTATAAT 60
ACAGAAAGCT ATTTAAGCCT AAGGAGGAAT CAAACAATGA AATATCTTAT CAGACTCTTC 120
TTATCATTGA TGTTACTCTC TCTCTGGACG GGCTGTACAC ACGAGGAGCT CTCATTATTG 180
GATGGCGAGA ATACGCTTGT TTTACGCGTA GAGACCGGTA AAGCCCCAAA TGCTCGTGCC 240
ACAGAACCCG GTCAGGGCAT ATACAATGAG AATAAAGTAG GCTCCATTTC TGTGCTCTTC 300
TATTTACAGG GACAACCTCG TTGGCAGGTG AAGTCTACAG ACTATCAAT CCATGAAGGG 360
GCCTATATCA TTCCGGTCAA AGAGCAATG CGACCACTAT TCAATGGCAA CAACAACCTC 420
AGCATCTATG TAGTGGCCAA TCTCGATTTC AATGCTCCGG CCACAGAAGC TGCCTTTCT 480
CAATTCTGCG TAGAGAAATC TATTGAATG TCTTCTACGA CAGCCCTGCG CGATTTCGTA 540
ATGCTTGCTC ATGGCAATAA GCAGATCAAT ATGGCTACGA CAGAAGGGAA ACTGTTGGGG 600
GATTATAAAC TCAAACGAGT GGCAGCAAAG ATTCCGATGA TAAACCCAC CATCAATGTG 660
CAAGGATATG AAGTGGTCGG AAATATACAG GCAAAGTTTC GCAATTCGGT AACGAAGGGG 720
TTCCCTTACCA CAGAAGCTCA AGAGATCCCA GCTGCTGCAT CCTATAAGAC ATCGGAATAT 780
CTTGATATTG CAGAGTCGGC ACCTGCCAAT TCTATCCATT TCTATCTTA CTATAACAAA 840
TGGACACTCT CCACACCGGA GAAGCGACCG GAATCTTCA TCATGGTCAA ATTCAAAAAG 900
ACAGGACAGC CGGACACAC AGCCAAACCG TACTACTACA GAGTGGCCCT CGAATCTCAG 960
GACAATCAGG TCAAGAGCAA TGTCCTCTAT AATCTGAATG TGAAAATCGA AATCTTGGGT 1020
TCTTTACAG AGCCGGAAGC TGTTTCTGTA AACGGCACAC TCGCAATAGA AGAATGGATT 1080
CTCCATCAGG ATGCATTCAA TCTGCCTGCC ACCAATTAAT TGATAGTGA ACAGCACGAA 1140
ATCTTCATGA ATAACGTGAA CACATACTCG GTGAAATATC AAACCTTCGA GAAACCAATC 1200
AGCATTAGCA TACAGTCAGT TACCTTTAGC TACGTCTCTT CTGATGGCAC TCAGCACAAAT 1260
CATTCTGTAG CAAGTAGTAG CGACCAGTAT CCTACGATTA CAAGCGATAA TACAAGCATC 1320
ATAATCACTT CCAAGATACC GGTAAATAAC GTACCAAGA AGATCGTTTT TGAGGTAAC 1380
AATGGGGTAG CCGGTTTGA AGAGACTGTC ACAGTACTCC AATATCCTGC ACAATTTATT 1440
GTCAATACAC TTGGCACAGC ATCGGCATGG AGACCGAAGC GATCTTTGGC TCCGGGGCTT 1500
AACAATAAAG CGATTACCA TGTGCTAGTA CTGCTTCCAC CCGAGAATTT ATTTGAAGAT 1560
GGGACACAGA CAATCATCGG TTATCCCCCC ACTGAACAA TTTCTTTTCA TAAGAAAGAG 1620

WO 99/29870

PCT/AU98/01023

50 / 490

5 AACAAATACCT ATCCGATACT ATGGTCTGAC ACAAATACGA CAAAACAGGA CCTTGAGACA 1680
TCAAGAATGA TTTCACCTTC CTTTGAGTTA GCCTCCCAAC TTGGGGCTAC TCTCCCGATG 1740
CCCTATCTCG AGTATTGSCC AGGGACATCA TATCTCCTTG ACTATTCGGG AAATAATAAT 1800
AATAAGAGAT ACCGCTTGTT TAATTGCGCT TTTTACTGG AGAAAAAGAA AGTTAATAAC 1860
GAAGAAATTA AATTGAGTGA CTGGCGTTTG CCGACAGAG CTGAGATCAA ATTGATAGAT 1920
AAGCTGCAAC ATAATGAGCA GAGTGCTGTC CAAGCTATCA TGACAGGGAA TTATTATTGG 1980
GATAGTTACT CTGCAAAATGG GTCTTATAAA ATGCAAGGAG GAGGGGGCCA AGGAAATTC 2040
TCCAAAGCCT ATGTTCTGTTG CGTGCGGGAT GTGAAAAAGC CGATTCTGTA CAAGAAGTCA 2100
GGTAAG 2106

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(2) INFORMATION FOR SEQ ID NO:74

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
20 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYRIONIAS GIUGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...3936
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

35 AAGAGGGTAG ATAGCTATGA ATGCAGACAA AAAGCTTGCA AATGTGCAAT TTGTGTGATA 60
CAAAAATTTA CTAATGTAAA ACTAAATGAT ATGCCGAAAA TTTTGAGCTT TTTGATGATG 120
TGCCTCTCTGC ATTTAGGTCT ACAATCTCAG ACTTGGCATG GAGATCCGGA CTCAGTGGCA 180
GCCCTACCTT CTATCGGTAT TCAAGAGTCA AGTTGTAGCC GAATCACGTT GGAGGTTGTT 240
TTCCCGGAT TTTATAGTGT GGAAGAACCA GAAGGCAACC AAGTCTTTCA GCGCATTTCC 300
ATGCCGGGTT GTGGCTCGTT TGGGAATCTG GCGGAAGCTG AATTGCTCTG TTTGAAAAAG 360
ATGATAGCCG TTCCGGAATT TTCAACAGCT AACGTTGCTG TAAAAATCAA AGAGACGGAG 420
ACATTCSACA ATTATAATAT CTATCCTAAT CCTACCTATG TCGTAGAGGA GTTGCCCTGAG 480
GGGGGGACTT ATCTGGTAGA GGCTTTCGCG ATAACAAATG ACTATTATAG CCAAAATGTA 540
AGCCTCCCTT CTACTACTA TGTCTATTCT CAAGACGGGT ATTTGCTC ACAAGATTT 600
45 ATGAAAGTTA CCCTGTATCC TTTTCGATAC AACCTGTCC GACRAGAAAT TCTATTGCA 660
AAAAAATCG AGTTACAAAT AACTTCCGAT AATCTCAGC CACCTTTACA AAAAAACACC 720
GGCATATTTA ACAAAGTAGC CTGCTCTGCA TTTATTAAAT ATGAAGCTGA TGGCAATCG 780
GCGATAGAAA ATGATATGGT GTTCAGTCTG GTTACAACAA CGTACATAAG CGGAAATGTT 840
GCCAGCAACC TCCCTCAGAA CTGTGACTAC TTGGTTATTT ACGATGATAT GTTCAACGTA 900
50 AATCAACAA CACACGACGA AATCAACAGG CTGTGCGAAC ATAGAGCCTT CTACAACGGC 960
TTTGATGTAG CTGCTGTAAG TATAAAGGAC GTATTGAATA GCTTCCCATC AATGCCCACC 1020
TCATACATCA ACGAAACTAA ACTGAAVAAT TTCATTGCTC CAGTTTACAA CCAAGCAAT 1080
GCCAAGAGGA CTTTAGATGG CAAACTGGGA TACGTGCTAC TGATCGGAAA ACCATTGAGC 1140
AATATTGTTG CTGACACTGA TAATACAAAA GTCCCAACT CTTTTATTCA TAATGTCTCC 1200
55 TTAATTCCAA GTCATCCAAC TTTTGGTTC ATATGCGGCT CCGACTATT TTTTAGTTCT 1260
GTTTCGCCCC TTGATACTGT CGGCGATTG TTTATCGGTC GATTAGCGT CACCAATGCT 1320
CATGAATTGC ACAATCTGAT TGAAGAGACT ATCAACAAAG AATCTCTA TAATCCTATT 1380
GCACACAAAA ATATTCTTA CGCAGAAGGG AAAGGCTGCG ATGCTCCAAT CTTACGTTTA 1440
TTCTTAAAG AAATCGGCTC TGGTTACACA GTCAACTCTA TCTTAAATC TAATCAGGTC 1500
60 TCTGCAATAG ACTCGATATT TGACTGCTTG AATAATGGTT CCAATCATT TATTTTAAC 1560
ACTCATGGAA TGCGGACTGT TTGGGGGATA GGGCAGGGAC TCGACGTCAA TACTCTAACA 1620
GCCCGATTGA ACAATACATC TTGCGAGGGA TTATGTACGA GTCTATCATG TAGTTCGGCT 1680
GTAGCAGATT CAATATTAG ATCGCTTGA GAAGTCTGA CCACATACGC ACCTAACAAAG 1740
GGATTCTCGG CTTTCTTAGG AGGAAGCAGA GCCACCGAAT ATGCGGTTA TTTACAGGC 1800
65 CCGTCTCTC CGTCAGAATT TTATGAATAT TACCTTATT CTTTATATCA CAATCTCTCG 1860
ACTGTTGTTG GCGAAATGTT GCTATCATCC ATTATCAATA CTAATTCTGT TGATACGTAT 1920
TGGAAATTC AACTCAATTT GCTTGGCGAC CCGCACTAA ACATTATGGC TCATGGCATG 1980
GAGGTTAGTA ATTGATTAC ACTACCAAC AACACCAITA TAAGCAGTCC GATAACATA 2040
AANAATGTTG GCTGCCTAAA AATACCGGAA AAAGGAGTTT TGCAATTTAC TAATATGGC 2100
70 TCCATACAA TCAATGCTCGG AGGAACCTCTG GAAATAGGCA ATCAGGCTAA AATATCCGA 2160
GAGACCGGTG CTAACCCAC CTTTATTACC GTTTACGGCG ATGGTCTTG GATTAAACAAG 2220
CAGGTAGAGA TAGACAATAT AGACCGACIT AACTTGTITT CTACCGATTG GGTATGCC 2280
AATTTTCATT TTGACAGTGT GAAATCAAC AGTGCCCGCG TGTATACAA GAACTGTATT 2340
GTGGAGATAA GCAATTGCGA ATTTACCAAT CGAAGTGACA TTATTTCAA GAATTGTGAC 2400
75 CTAAGCGTTG AAAACAGTAT GTTAGCAGT TCGGGGATAA CGGTATTCAA GCCTATGGCT 2460

WO 99/29870

PCT/AU98/01023

51 / 490

5 ACAAGCTCCA TCACCGGATT ATCTACAAA GCAAGSATT CCGACAATAC TTTTITTTGCG 2520
 ACAGGAAACT TCGCCTACCA TATCACAAC ACGCCAGGCT TAACAGCAAC CTCCAATGCT 2580
 GCCATCAAGT TAGACAATAT TCCTGAGTAT TACATTTCGG GTAATAAAAT AGTCAATGTC 2640
 GATGAGGCTC TTGTACTAAA TAATAGTGGC AACAGAACGA ACAGACTCCA CAATATCACA 2700
 CGGAATGTGA TAAAAAATG TAGGATTGGG AGCAGCCTTT ATAATTCCTA TGGTATTAC 2760
 AACCGAATA AGATCAGTAA CAATCATATA GGAGTACGTC TCCTCAACAA CAGTTGTTTT 2820
 TATTTGATA ATGCTCCTGT AATCAATGAA GAAGATAAGC AGACGTTTAT TTCTAATAGG 2880
 ACTTGGCAGC TCTATTATC AAACGGTACA TTCCCTCTCA ACTTCCATTA CAACAGCTTG 2940
 CAGGCGGGAG ATACAGATAC ATGGATTAT AACGACAGT ATACGAATCG CTATATTGAC 3000
 GTTTCAAATA ATCACTGGGG CAACATGAT TTGTTTGATC CGAATCAGGT TTTCAATACG 3060
 CCAGACTTGT TCATTGGAT ACCTTTTGG GATGGATTGC CAAATGGGAG ATCGGGCAAT 3120
 AGCTCTGCTG AAGCAGTAGA ATTCCAAACA GCATTGGACT GTATTGGCA TAGCCATTAT 3180
 CTTTCGGCAA AAGTGGCTCT CAAGATGATG GTTGAACCT ACCCGGAATC CGACTTTGCA 3240
 ATAGCTGCTT TGAAGGAATT GTTCAGGATA GAGAAAATGT CAGGCAACGA TTACGAAGGC 3300
 15 TTGAAGATT ATTTAGATC CAATCCAACC ATCATCTCTT CCCAGAACTT GTTCCCSACA 3360
 GCTGATTTC TGCTGCGCG ATCGGATATT GTGTGTGAAA ACTATCAGTC TGCCATCGAT 3420
 TGGTACGAAA ATCGCTTGAA TAGTGAAATC TCCTATCAGG ACAGTGTITT TGCACTCAT 3480
 GACTTTGGTG ACATTTATG GAATATGCAG TTAGACTCAC TCAGAGGGAC TGGTATAGAT 3540
 TGAACATAC TTTCTGTGA ACAAGGAAA TCGCTCGAAA GCCATCAAAA TGTAAAAAAT 3600
 20 TATTTGTGT CAACCTCTCC CGAATCAACA GGTACTCTCC TGCCTCCATT AGAATGCAAC 3660
 AAATCAAGCC TTGATAAATC CAAGATAATC TCTATTCTGC CCAATCCGGC GAAAGCTGTT 3720
 GTAACAAATA TCTACTATAC CGATAACCTT TCCTGTTCTG TAATAAAAT ATATGGAATA 3780
 AATGAGCCT CGGCTGATAT AACCGGGTTG CCCAACATC TATCCGAAGG TTATTACAGC 3840
 ATACAGTTCA ATACATCCAA CTTTGATCCC GGTTCATACC TGGTAACGCT AAATGTTGAT 3900
 25 CAGAAAATTA TAGATACGGA AAAATTACGA ATCAA ATCAA 3936

(2) INFORMATION FOR SEQ ID NO:75

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2814 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 35 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 40 (iv) ANTI-SENSE: NO
 (v) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 45 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2814
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

50 TCAGAAAATT ATAGATACGG AAAAATTACG AATCAAATAA TGGCTATCAT GATGAAVAGT 60
 ATTGTTTTTA GAGCATTCTT AACGATTTTG CTCTCGTGGG CAGCGATCAC GAATCCGACT 120
 GCTCAAGAGA TCTCAGGCAT GAATGCATCC TGCTGCGCTG CTCCGGCTCA ACCGGATACT 180
 55 ATCTTATATG AAAGTTTTGA GAATGGACCT GTTCCCAATG GCTGGCTTGA GATAGATGCT 240
 GATGCTGATG GTGCCACTTG GGGGAAGCCA TCAGGCTCTT TCTCTGTACC TTACGGACAC 300
 AATGGCCTTT GCACCTACTC CCAATATACG TCCGGTATCT CAACAGCGGG CAACTATCTG 360
 ATTAACCCCA ATATAGAAGG AGCCAAACGG GTCAAGTACT GGGTATGCAA TCAGTATAGT 420
 ACCAATCCGG AACATTACGC AGTAATGTA TCGACAACGG GGACTGCCAT TGAAGACTTT 480
 60 GTTTTGTGTT TTAGATATTC CATAACAGGG AAACCGACTC CTCTGTATG GCGTAGACGA 540
 ATCGTGGACT TACCGGAAGG GACCAATAT ATTGCATGGC GACATTACA AGTCACCGAC 600
 TCACACACAG AATCTTGAA ATTGGATGAT GTCACTGTGT ATAGGTGAT CGAAGGGCCC 660
 GAACCTGCTA CCGACTTCAC AGTAATCAAT ATTGGTCAGA ATGTGGGACG ATTGACTTGG 720
 AACTATCCGG AGGATTATCA ACCGGAAGGA AAGGGGAATG AAGAGTTGCA CCTTAGCGGC 780
 TACAACATCT ATCGGAACGG TACACTACTG GCACAAATAA AAGATGTCTC CATACTGGAG 840
 65 TATGTGGACA GCCTTACTC TTTGCGAGAC AATCCCTTSC AAGTGGAGTA CTGCGTTACA 900
 GCCGTTTACC ATGAAAGCAT AGAATCTTCG ACCGTATGTG CCAAGCTGCA TTACGCCACG 960
 GATGCCATCC TTTATGAAA TTTTGAGAA GTGACCTGTT CCAATGGTTG GCTTGTGATA 1020
 GACCTGATG GAGATGGATT TAGCTGGGGA CACTATTTGA ATGCATACGA CGCTTTTCCC 1080
 GGCCATATG GAGGCCATTG CTCTTGTCTG GCTTCTTATG TTCCGGGTAT AGGCCCGGTG 1140
 70 ACTCCCGACA ACTATCTGAT TACCCCAAG GTTGAAGGAG CCAACCTGTG CAACTACTGG 1200
 GTAAACACGC AGGATGCCAA TTGGGAGCG GAACATTACG CGGTGATGGC TTCGACAACG 1260
 GGGACTGCTG TCGGAGATTG CGTCATATTG TTCGAAGAAA CCAATGACAGC GAAGCCGACC 1320
 GCGCATGGT ATGAAAGAAC CATCAACTTA CCTGAAGGGA CTAATACAT CGCATGGCGG 1380
 75 CATTAACACT GTACCGATAT ATATTCTTG AAGTGGACG ATATCACTGT ATTCGGGACT 1440
 CCTGCATCAG AGCCCGAACC TGTACCGAT TTCTTGTCTT CGCTTATTGA AAACAACAG 1500

WO 99/29870

PCT/AU98/01023

53 / 490

GCGGATGTTT CATAACAAGCT GAAAAAGAAC TTGAGCCTTT ATCTCAAAAT CGATAATATG 1740
CTGGCGGAAA CGACAGAGCT TATCGGTTAT TATCCTATGC AGCCGTTCCA TTGTTTCGCC 1800
GGTTTATAGCT GGACTTTC 1818

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(2) INFORMATION FOR SEQ ID NO:77

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1071 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

AACTCCCATG CAACAGTCTC CGTTATATGT TCAATGATGG AAAAATGTAT CTTTGCTCAC 60
TATCCACATA ACCTTGTGTT CATGATTGCG AAGCATTTCG GTATCATTTT GGGATTTCCTT 120
TCTCTTGTGT TTTCGGCAGG TGCTCAACAA GAGAAGCAGG TGTTTCATTI TCTGAACCTT 180
CCGGTACTG CACAGGCTTT GGCTGCCGGA GGCAAGCTA TCACCATCGT AGACGACAAT 240
CCCGGACTGG CTTTGTAGAA TCCGGCTCTG CTCGGATATG AATCCGGTGG CCGCGCCTTT 300
CTTTCCTATT TATATTATAT GAGTGGTTCG CATATGGGCA ATGCCTGTTA TGCTCGTCC 360
GTCCGAGAGC GTGGCATGTG GGGTGTGTGG ATGCGTTTCC TGAACACGG GTCTATGCAA 420
GGATACGATC AGAATGCGAT TGGCACCGGC TCTTTTAGTG CTTCGGATAT AGCTGTACAA 480
GGATTTTACA GCCATGAAT GAGCAACAC TCCGCGGTG GAGTCAGCCT AAAAGCATTG 540
TATTCTTCTA TCGAGACGTA TAGTTCCTTT GGCCTTGGTG TGGATGTCGG TATCAGTTAT 600
TACGACGATC ACRAAGGATA TTCCGCTTCC GCTCTGTTCA AGAACGTAGG GCGCAACTG 660
AAAGGCTATA ATGAAGAACG GGAACCGCTC GATTGGGATT TCCAGCTCGG CTTTTCCTCG 720
AGTTTATATC ATGCTCCGTT TCGCTTGAC ATCACGTTGT TCAATCTGAA TCCGCACTAT 780
TTCAAGCGTC TTGTACCAGC CGATCTGTCC AAGATGCAAA AGTTCCTCCG ACACTTCTCG 840
ATAGGAGCAG AATTACTCC TTCCGAGAGG TTTTGGGTGG GGTGGGATA TACGCCACAG 900
ATTGCACAGG ATTTGAGGT GGAAGCGCGC AACAAATGGG GAGGTCTTTC GGCCGGCGTC 960
GGTTTCACTT CAGGTGTAGT ACGTGTAGGC GTATCTGCTG CCACCTATCA TCCTGCAGCT 1020
CTTTCGTTCA TGTGTTCCGT AGCTATCCGT TTGGACGATA AGAGCATCTT C 1071

(2) INFORMATION FOR SEQ ID NO:78

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1011 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

CTCAGCCCG TCGGCCTTAA AGAAATAACC ATTAACCCCA TGTGCCTCGA ACCCATAAT 60
GCTCCGATT CATCCGAGTT GCTCGAGCAG GAGCTGACTG CCGATCGTTT TCTGCGGATG 120
ACAAACAAG CCGCAATGA GATCTATGTT TTTACGGCCG AAGAAGCTCC GCATTGCATG 180
AAAGAAGTAG CCGGACTGCG AGAAGAAGCC TTTCCGGCAT ATGGCGGAGG TACTGGCAAG 240

5 GCGATCGATA TAGACGAGTT CGACACCATG CCCGGGAGCT ACAACAGCT GATCGTATGG 300
 GATCCGCAAA ACAAGGCTAT ACTCGGAGGC TACCGCTTTA TCTATGGGCG GGACGTTGCT 360
 TTCGATACCG ATGGCAAGCC TTTGCTGGCA ACGGCAGAGA TGTTCGCTT CAGTGATGCT 420
 TTTTTCGACG ATTATCTCCC CTACACAGTC GAATTGGGAC GTTCGTTCTG GTCCGCTCCAG 480
 TACCAATCGA CACGATGGG CACAAAGGUC ATTTTGTGCG TGGACAATCT TTGGGACGGT 540
 ATCGGAGCAC TCACTGTAGT CAATCCAGAG GCACCTCTAT TCTATGGCAA GGTGACCATG 600
 TACAAAGACT ATGATCGGCG AGCTCGCAAT CTGATCCTGT ATTTTCTTCG CAAGCACTTC 660
 TCCGATCCGG AAGGCTTGGT CAAGCCTATT CATCCCTAC CGATAGAGAT CAGTGCGGAG 720
 10 GCGAAGGCTT TGTCTCTC ATCCGACTTT GACACCAATT ACAAGACTCT CAATATAGAA 780
 GTGGCGAAGC TGGGTATCAA TATCCCTCCT CTCGTGAGTG CATATATAGC TTTGTCTCCG 840
 GAGATGCGTG TTTTCGGCAC TGCAGTGAAT GAGTCTTTCG GAGAGGTGGA GGAAACCGGC 900
 ATATTCTATT CTGTGGGTAA GATCCTGGA GAGAAAAAC AACGGCACAT AGAGAGCTTC 960
 ATCTCAGCC GGAACGAAAA AAAAGGTCTC GACAGTAGCA ATGCCCGATC A 1011

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(2) INFORMATION FOR SEQ ID NO:79

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1698 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

25

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

35

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

40 TACGACGGAG CGAGACTGGT CTATACCTTA TTTCCGAATA GAAACGACAT TCACCCTATG 60
 AAAACCATTT TAAGATACAG CGGCTTCCG GTCCGCTCTCT TCTTTTGCTT TTTGGGAGCT 120
 GTGCACTTGT CTGTCGAGGC GCAGATGCTC AATACTCCTT TCGAGCTGTC GGATCAGATC 180
 TCCCTGTCTC CCACCGAAG GCAATACAGG GAGATTGTG TGCAACGAA AGAAAAAAGG 240
 GGGGCCGATC TTTCCCGTT GAGCGATAAG CTGCGCGATT CGGCCCTATG TCGTTTCGGC 300
 TCGGCCATG GCGATATTG GGGCGACTAT CTTCGATACA ACGGCAATAA CTAATCCTCG 360
 45 CTCTCGCTCG AATCGGGTGG TCGCATCAGT GTCCGTAACT ATGGCAATT GCAGGGCAGT 420
 GCTTCCTACT CAGCTGGCAT GCACAAACGC ATCGGCTGSA ATGCTCTGCG CAACGCGGAA 480
 GCCTACTATC CCTATTGGT GTCCGATTGG ACGGCGGAG ACTATCATTT CGAAGACTAT 540
 CGGCTTGGCG GCTACTATT TTTTCGGGCC GGGCGCTTGC CCCTCGGTAT AGGCTTCTCA 600
 TACAGGGGCG AAGTTGCTTA TCGGCTGACC GATCCGCTGA CGACCAATAC GACCGCTGCA 660
 50 TTGGAGCTTT CTGTGTCTAC CTCTTTGACG CTGCTCCGAG AGAACAGGCT ATCGCTTTCG 720
 GCTGCGTATC TCTATCATAG ACAACACCTC ACACAGTACA ACTGGCGTCC CGGGCAGCAG 780
 GACAAATCTT TCGTCAGCTA CGGTTTCGGT CAGGTGGATG TCAGCAACAG CCTATCTCG 840
 TTCGGTATCT CCAGAAATGA CTACGTCAAC GGATGGAAGC TTAGCTCCCG TCTGGATACC 900
 CGTAGGGGCG ATGCCATCGG TCTCGACTAC AGCGGCTACT TCCTCGATAC CGAGAGAGG 960
 55 TCGTCCATCA ATCTCTTTCG TTTGCTTTAC AATCGGCTGC GACTCTATGG TAGCTGGCAT 1020
 CTGTCCGACT TCGATTTTC ATTTTCAGCC GACTATGCTC TGGGCCAAGG GATAGAGCGG 1080
 ATATACGAAG ACTACAAGCC GGATGATAAT TATCATATCT ACGACCTCCG TATCTTGGCC 1140
 ATTGCGCGCT GGTATATGCT CAATGAGTTT TCTGCCCAAG CCCAAGCCTC CTACCGTATT 1200
 CGCAGCGATA GAGGTTGTGC CCTGAGAGTG AGTCCCGSTA GTGATTCTTA CGGCTATGAT 1260
 60 GAGACGTATC GCAAGCATGG ACATCATACC ATGAGCGGAA TGCTACGTCC TTTTGCCGGT 1320
 ATAGCTATG ACCATGCCGG ATCCAAATG GATTTTGGAC TTTGCTTTC GGCTGCTTAT 1380
 CGAATGGTGC TGACGCAATC GTATAAGATT CGTACCATCC AGAAAGAGCA GCTCCACTAT 1440
 CAGCTGSCCT ATTTGCCCTA TGCTATCGT AATAGAGAAG GCGTGGAGGT GCGTCTCTCT 1500
 CTGTACGTCT CGATTCCGAT GCAGAAATACC CACCGCTGA TGACAGAGCT GCGGTTGTAT 1560
 65 GCGACCTGA TGAAAAAGAA GGACGGTATA GCCTATGGCA AAACGCCCGG TGTCATCTCA 1620
 CATATCTCTG CCGATCCGCA AGCCGAACGA ACCTCCGCGC ATACCATCGG GGCTATCTCG 1680
 AATATCTCTT ACCTCTTC

70

(2) INFORMATION FOR SEQ ID NO:80

75

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2457 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(1x) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...1596

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

10 TACAGGCGAT CGGGAAGGGT TTGTCCTCGT ATCCTCCGGA ACAACGGTTC CTACGCAGAT 60
ACTCGGTTAC AGCCGAGAAG AGCGGTTTGA CTACGAGCCG GCACCAGAAC AAAGATGAAA 120
AGAAGGTTTC TATCGCTGTT ACTGCTGTAC ATACTCTCTT CCATCAGCCT TTCTGCTCAG 180
CGGTTTCCGA TGGTGACGGG AATCGAGTTG GATACCGATT CGCTTTTCTC TCTGCCCAAG 240
CGTCCTTGGC GCGCCATCGG TAAACGATA GCGGTCAATC TGGCGGTATG GGGCTTCGAT 300
15 CATTTCATCA TGAACGAGGA CTTTGCAGAC ATCAGTTGGC AGACTATCAA GAGCAATTC 360
CAACAGGGCT TTGGCTGGGA CAATGACAAG TTTGTCACCA ACCTCTTCGC ACATCCTTAT 420
CACGGATCGC TCTATTTCAA TGCAGCGAGG TCGAACGGTT TGAGCTTCAG GCACTCTGCT 480
CCGTTTGGCT TCTTTGGCAG TCTCATGTGG GAGCTGCTTA TGGAAAACGA GCCACCGAGT 540
ATCAACGACC TCTGTGCCAC CACCATAGGC GGTATAGCTT TGGGGGAGAT GGGGCACAGG 600
CTGTGCGACC TGCTCATCGA CAATCGTACC ACAGGGTGGG AACGTATGGG GCGCGAGGTG 660
20 GCTATCGCTC TGATCAATCC GATGCGCTTT CTCAACCGTC TGACAGCAGG AGAGGTGACT 720
TCTGTCCGGG GTCCGACGGG ACAGATATTT CAGTCTGTCC CCATAACAT AGTCGTTCGAT 780
GCCGGCTTTC GCTTTTGGC AGACAAGCGG CATGCCGGA CCGGTGCCAC GGCTCTGACC 840
CTGAATCGA GATTCGACTA CGGCGATCCA TTCCGAAGCG AGACTTTCTC TCCATACGAT 900
25 TTCTTCCAAT TCAAGCCGG ATTGAGTTTC TCGAATCGC AACCTCTGCT GAGCCAGATC 960
AATCTGATCG GAATCCTAAG CGGATGCCAA CTGCTCGCAC ACGAACGAAC GGTTTGGTG 1020
GGAGGTCTCT TTCAGCACTT CGACTACTAC AATTCGGAAA AACGAATAAG CAAAATTCG 1080
GAGGAGGTAC TCGTCACCCC ATACCGTATC TCGCAAGTGG CAGCTCTGGG AGGCGGTCTT 1140
ATCTTCAGC ACCACGGAAT ATTTCGACGA CGTCTCTGG AGCTATATGC CGAGACCTAC 1200
30 CTGAATGTGG TCCCGATGGG AGCCAGTCTG TCGGATCACT ACAACGTGGA CAATCGGGAC 1260
TATAACCTCG GCAGCGGATT GAGCGGCAAG CTATACCTTG GTGCTACGTA CAATGATCTG 1320
TGGAGCTGGC TCTTGGGAGT CGAAGCTAT CGGCTCTACA CATGGATCGG GTATGAAGAG 1380
CCGACCCAGA AAAATACCGA TGTCACTCT TTTATGGTGC AGGGGGACGA AAGCAAGGCG 1440
CGCCTACTGG TGACGAGTTC CGAGTTCGCA TTTCATCCTG GCCCTGGCA TGTAGCCATC 1500
35 GTCGCTCGCC GTTTCATCGG CAAAACAGCC TATCAATTCT ACCCTAACGT ATCATTGAT 1560
ACCGGCGACA TACAGCTGCG TGTCGGATT CACTTC 1596

(2) INFORMATION FOR SEQ ID NO:82

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
45 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
50 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55 (1x) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

60 AAAAGAAGAA AAAACAGAT GAAACGACTG ATTGT'TTTC TGGCAATGGG TGGCTTGCTG 60
TTCACCCCTT CGAAGCGACA AGAAGCAAAC ACTGCATCTG ACACCTCCAA AAAGGACTGG 120
ACTATAAAG GTGTGACCGG ACTAAATGCC TCTCAGACTT CTCTGACCAA CTGGGCTGCC 180
GGTGGAGAAA ACACGGTGGC AGGTAACCTC TATTTGAACA TAGATGCCAA CTACCTGAAA 240
65 GATAAATGGA TTTGGGACAA CGGTTTGGCT ACAGACTTCG GTCTGACCTA CACAACAGCC 300
AACAAAGTGA ACAAAGTGT AGACAAGATC GAACCTCTCA CGAAGGCCGG CTATGAGATC 360
GGCAACATT GGTACGGAAG TCGGCTTTTC ACTTTCCTCT CACAGTATGC CAAAGGATAT 420
GAGAAGCCCT CGGATCACTT GACAGGAGTC AAGCATATCT CTAATTTCTT CGCTCCTGCA 480
TATCTCACTC TCGGTATTGG TCGGACTAT AAGCCCAATG AGAAGTTCTC TCTCTACCTC 540
70 TCTCTACAA CGGGCAAGCT GACTGTAGTA GCAGACGACT ACCTCTCAAG TTTGGGAGCC 600
TTCGGGGTGA AAGTTGGTGA AAAGACAATG TTGGAAGTGG GTGCTTTGGT AGTGGGTTCC 660
GCCAATATAA ATCTGATGGA GAATGTCAAT TTGATAACCA AGGCTTCATT CTCTCGGCT 720
TATACGCAAC ACTTTGGCAA CATTGACATC AATTTGGGAGG CTATGCTGGC CATGAAGATC 780
AACAAAGTTC TCACGGCTAC GATAGCCACC AATCTATCT ACGACGATGA TGTGAAGATC 840
75 AACGATGGCC CGAAAATCCA GTTCAAGAA GTTGTGGGCG TGGGTGTTCC GTACACTTTC 900

(2) INFORMATION FOR SEQ ID NO:83

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

ACGAGAGAGA	GTGTCTTACA	TTGTAGAACA	AAACTCAAAA	AAGAACGAAA	AATGAAGAAA	60
ATGATTTTGG	CAGCTACTAT	GCTGCTCGCA	ACAATCGGTT	TTGCAATGTC	TCAGAGTCGT	120
CCTGCTCTTA	GACTGGATGC	TAACCTTGTC	GGTAGTAACT	TAATGCAAAA	AGTCGCAAAC	180
ACGAGCGTGA	ACAATAAGAT	GATCGTAGGC	TTACGTGTTG	GTGCTGCTGC	TGAGTTGCGT	240
CTTAGCAATG	ATGGATTCTA	TCTCGCCCCC	GGATTGGCCT	ATACGATGAG	AGGTGCTAAG	300
ATGGAATCAC	TAAGTGAAAC	GACAACTCGC	TTGCATTATC	TGCAAAATACC	GGTGAATGCC	360
GGTATGAGAT	TTAGCTTTGC	TGACAACATG	GCTATTTCAT	TGGAAGCAGG	TCCCTATTTT	420
GCATATGGTG	TCGCCGGGAA	GATTAAGACT	AAAGTTGCAG	GCCTTACGGC	TTCTGTAGAT	480
GCCTTTGGTG	ATAACGGATA	TAACCGTTTC	GACTTGGGCT	TGGGCTTGTC	TGCTGCCTTG	540
AGCTACGACC	GTTATTACGT	ACAAATTGGA	TATGAGCATG	GATTGCTTAA	TATGTTGAAG	600
GATGCTCCGG	ATAAGACTTC	TTTGCCTAAT	CATGACTTCT	TTGTGGGTCT	CGGTGTTCCG	660
TTC						663

40 (2) INFORMATION FOR SEQ ID NO:84

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...744

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

ATCAAACGAA	TAGAAATGAA	AAGGATTTTT	ACTGTAGCCC	TTGTGCTACT	TGCTTCGGTC	60
ACTATGGCCA	TCGGACAAAG	CCGCCCGGCA	CTTCGCGTAG	ATGCCAACTT	CGTAGGCAGC	120
AATCAGAGCA	TGAAAAGAGA	CGGATATGTG	TGGGACACCA	AAATGAATGT	CGGCCGTGGG	180
GTCCGTGCCC	CTGCCGAATT	CATGATCGGA	TCAAGAGGAT	TCTACTTGGC	TCCGGGTCTG	240
AATATACGA	TGAAGGGCTC	CAAAACCGAA	TGGGATATAC	CCGAATGGT	TCCTGGTACC	300
TATATTACGA	TGGTTTCCAC	TGCTTGCAC	TATCTGCAAC	TGCCGATCAA	TGCCGGCATG	360
CGGTTCCGAC	TGATGAATGA	CATGGCGGTT	TCGATCGAAG	CGGGTCCTTT	CCTTGACATC	420
GGTATATATG	GTACATATCG	GCAGAAGTTG	GAAGGATGGA	AGCCGAACAA	CTACAGCACA	480
GAGTTTTTTG	GCCCAACGCT	TGGTGGCCCA	ACAAATATCC	GCTGGGACAT	CGGGGCCAAAC	540
ATAATAGCCG	CATTCCACTA	TAAGCGTTAT	TATATACAGA	TAGGCTATGA	ACATGGATTT	600
GTGGATATTG	TGTCAGGTGG	AGGTTCTGAT	ATTCCCCGAC	TGAACGACAA	TAGGCAATCC	660
TCTTCGACGA	CCGCTCTAAG	AGAAAAGGGA	AATAACGAAT	ACGCTTATAA	TCGTGACTTC	720
TTCGTGGGCA	TAGGTTACCG	CTTT				744

WO 99/29870

PCT/AU98/01023

58 / 490

(2) INFORMATION FOR SEQ ID NO:85

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

AAAAGAAAGA	GTATGAAAAG	AATGCTGCTG	CTTCTCGTTG	TATTATTATA	TGGAATTGCA	60
GGCCGATG	CTGCACAAGA	CGTTATCAGA	CCATGGTCAT	TGCAGGTCGG	AGCGGGATAC	120
TCCGATACGG	AGAACATCCC	GGGAGGATTC	ACCTATGGTT	TCTATTGGG	AAAGCGTATG	180
GGGAGCTTTC	TGGAAGTGGG	GCTGTCCATG	TACAACCTCA	CACGTCAAAC	AGCCAACAAT	240
GCAGACTCCT	TTGCATCGAA	CSAAGGAGAC	GGATCTTTTC	AGGTAAATAT	GTCTTCTCCG	300
AATGAGAAGT	GGTCATTCTT	CGATGCAGGC	AGTGCCAACT	GCTATATGAT	CGTCGTCCGA	360
GTCAATCCTC	TCCATCTGTT	TTGGCAGAAT	AGCCGGCACA	ATTTGTTTCT	GGCAGTACAA	420
GCCGGCCTGT	CCAATAAGCA	CAATATTCAT	TTCATCTATG	GAGACAAGGG	AGCCAAAGTC	480
AGTATCTACA	CCAATTTCGAA	TACCTACATC	GGTTACGGAG	CACGTGTAGC	CTACGAATAT	540
CAAAATCATA	AAAACGTGGG	GGCGGGTGCC	GCTGTAATGT	ACGACCACGG	CAATAAGATG	600
CTTACGGCCA	TGGCCACGCT	CTCCACTCAT	TTT			633

(2) INFORMATION FOR SEQ ID NO:86

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2859 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 45 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 50 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 55 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

ATCCGAATGA	GAGTATCCGA	TCTCTGTTC	AGACTTTCAT	GGTTATTACC	CGTAATCCTT	60
GTCCGATTGC	TCTGTGCTAC	TTTGGTGGCT	GCGGAACGTC	CTATGGCCGG	AGCAGTCGGA	120
TTGCACCAAC	GTCCGGCATG	TGCGCTGTCT	GATTCTACAG	CGAAAGACAC	GGTGCCCTCT	180
GCAAAACCTA	TTCTGTACAG	TGCTTTTCGA	GATTCCCTTC	CTGCCGATTC	CACCGGATCG	240
ATGCCGCAAG	ATAGCGTGTA	TGACGATGAA	TTGGAATTGG	AAGATATAGT	GGAGTACGAA	300
GCTGCCGATT	CCATCGTTTT	GCTCGGACAG	AATCGTGCCT	ATCTTTTCGG	CAAGAGCTAT	360
GTGAGCTATC	AAAAGAGTCG	CTTGGAGGCA	AACTTCATGT	ATCTCAATAC	CGACAGCAGT	420
ACGGTTTATA	CTCGCTATGT	CCTCGATACG	GCGGGTTATC	CGATGGCCTT	TCCTGTTTTT	480
AAGGATGGAG	AGCAGTCGTT	CGAAGCCAAG	AACTTTACCT	ACAACCTCCG	CACGGAGAAG	540
GGGATTATCA	GCGGAGTGAT	CACGCAGCAG	GGCGAAGGCT	ATCTGACTGC	CGGTAAGACC	600
AAGAAGATGC	CCGACAATAT	CATGTTTATG	CAAGGAGGGC	GTATACGAC	CTGCGACAAT	660
CACGATCATC	CTCACTCTTA	TATCAATCTT	TCCAAGGCAA	AGGTGCATCC	GGAGAAAGAC	720
ATCGTCACAG	GTCCGGTCAA	TCTGGTTATC	GCGGATATGC	CGCTGCGGAT	AGGTCTTCCT	780
TTCCGCTATT	TTCCCTTTTC	CAACAAATAC	TCTTCCGTA	TATTGATGCC	CACGTACGGA	840

WO 99/29870

PCT/AU98/01023

59 / 490

5 GAGGACAATC GCTATGGATT TTATTIGAGG AATGGTGGAT ATTATTTTGC CTTTCAGCGAC 900
TATATCGATT TGGCATTGCG TGGGGAGATC TTTTCCAAAG GGTTCATGGGG CATTTCAGGCC 960
CAATCGAAT ATAAGAAGAU GTATAAGTAC AACGGCTCGT TCGAAGCCAA TTATCTGGTA 1020
TCGAAGTCCG GCGACAAATA CGTGCCCGGA GACTACAGCA AGACCACCAAG TCTGAATATC 1080
CGATGGACAC ACAGTCAGGA TCCGAAGGCC AATCCTTTGC AAACGTTGTC GGCCAATGTC 1140
AATTTTGCCA CCGGGAGCTA TTTCAGAAAT TCGCTGAATA CCACCTATGA TGTCATGCCC 1200
CGTACTGCTA CGACACGAAG TTCGGCCGTG AGCTATTCCG CCAAGTTTCC GGGTACTCCT 1260
TTTTCGATTA CCGGTAGCAT GATATACAGC CAGAACATGC ACCTTCGCTC GCGATACGAC 1320
ACCTTGGCGA ATCTTTCGAT TAATATGTCC ACGCGTTATC CTTTCAAGCG GAAGACCCGT 1380
GTAGGACCCG AGCGATGGTA CGAGAAGTTG AGTGTGGGCT ATTCCGGTCA GCTTCGCAAT 1440
AGTATCTTGA CAAAAGAGAA AGATTGTCTC CAGAGCAATC TCGTCCGCGA TTGGAAGAA 1500
GGTATCGCTC ATTCGCTACC GATCAGTTTG ACTGTCCCTT TGTTGGATTA TATCAATCTG 1560
ACTATGGGGG TTAACATCAA TGATGGTGG TACACGAAAG GCATACGAA GTCTGGAAAT 1620
GAGGATAAGA AAACATTCCT GCCITCGGAC ACSACCTATA AATTCGCGAG ACTGTACGAT 1680
TACAGTCTGT CCGCAGGCTT ATCTACCACA TTCTACGGTA TGTTCAGGCC TTGGAACCT 1740
TTTTCTTGC GAGGCAATCT CATATGATC CGTCATCGCT TCACGCCAC TGTCAGTTTC 1800
TCCTATATCG CGSACTTCAC GAAACGCCAA TATGGCTTTT GGGAGCTTCT TGAGCATACG 1860
GATCAGAACT GCAAGCTGCA TACGCTGCTC TACTCTCCTT ATTTCGAGCA GATATTCGGT 1920
GCTCCCTCCA TGGGCAATGC AGGATCTGTC AATTCTCTT TTGACAACAA CTTAGAGGCC 1980
20 AAGATCAAT CCMATCCGA TTCGACAGG ATCAAGAAGA TCAGCCTGAT AGATCAGTTC 2040
ACATGGTCTA CATCTATAA TATGTTTGGC GATTCGATCC GATGGAGCAA TATCTCGGCT 2100
TCGCTGGCAC TTGCTCTCTC CAAGAGCTTT ACCTTGGGCT TGTCGGTCT GTTCGATCCC 2160
TATTTGACGA AGTATTATGA GGGAGAAGAT GGGAGAATCA TTCCCTATAA GAGCAACGAC 2220
CTGCGCATTT TTAACGCAAA GGGATTGGCA CGCCTGATCA GTACGGGTAC TTCTTTCAGC 2280
25 TATACGCTCA ACAAAGAGTC GCTCAGCGGA TTGATAGCTC TTTTCAGTGG CAAAAGGAG 2340
CGGAGAGATG AAAAGAAAAA CACAGGGGCT ACTCCTCATG AAGGAGACGA TGCTGCCGAT 2400
ATACTTGAGG GAGGAAGACC GCAAATGAA AGTGGGGGGT CGCTCCTCGA GCGCAACCGT 2460
CAGGGCGGAG CAGTGGATCA GATGGGTTAC TTCGATATT CGATCCCATG GAGCCTGTCC 2520
TTCGACTATA GTTGAATAT TGCTACCGAC TACAATAGGT ACATATGTC TAAGATGGAG 2580
30 CACTACTACC GGGTAACGCA GAATCTGAGC TTTCGCGGCA ATATCCAGCC TACACCGAAC 2640
TGGAGCTTGG GATTCAATGC GAATCAATC TTGACCTTGA AGAAAATAAC ATCGCTTACC 2700
TGCAACGTCA CTCGCGACAT GCACTGTCTG GCTATCTCG CCAATTTTCA CCTATAGGA 2760
GCATACAAGT CCTATAATT CGTCATATCG GTGAAGAGTT CACTCTTGCA GGATCTGAAG 2820
35 TATCAGCAGA GCAATCGTCC CATCAGCAAT ACTTGGTAT 2859

(2) INFORMATION FOR SEQ ID NO:87

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
45 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
50 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3753
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

60 AAATGGAAT TGGCATGCGC TTTGATTGCG GCGTGTGTT TCGATCCATT TGTAATACT 60
AACGAGGTAA TAATAATGAT GAAACGATAT ACAATAATTC TTGCAGTTT TCTTTTATTC 120
TGACCGGTAT TTACCTTTCA AATAAAGCT CGCCCTTATG AAAGATTTC AGATGTAGAG 180
AAGCCTTGGA TTCAGAAACA TTCAATGGAT TCTAAATTGG TGCCCTGCAA TAAGGGTAAC 240
65 TTAATTCAAG CTGAAATTGT ATACCAATCT GTTTCTGAAC ATAGTGACTT AGTTATTCA 300
CCTGTGAACG AAATAAGGCC TGCAATCGT TTCCTTCCG ATAGGAAGTC TTTTGTGCA 360
GAAAACTAC GGGCATCTCC CCCCAGTATT CCGGTTGCCG TCGACAAGTA TGCGGTACCG 420
ATTGGCAATC CAATGGATCC TGAAATCCC AATGCCTGCG ATGTGACGCT AAAAATCACT 480
ACTAAAGCGG TAACAGTACC TGTCGATGCG GTGATGGTTA TCGACCAATC TTCTGCAATG 540
70 GAGGGCAAAA ACATTGCCAG ATTAAGTCT GCCATTGCAAT CGGGACAGCG TTTTGTGAAA 600
AAAATGTTCC CTAAGGGGAC GGCTACAGAA GGGGTGCGTA TCGCTCTTGT GAGTTATGAC 660
CATGAGCTTC ATCGCTTATC TGATTTTACC AAAGACACTG CTTTCTCTG TCAAAAAATC 720
CGGGCTTTGA CTCCTATTG GGGAAACAT ACCCAGGGGG GGCTTAAAT GCGGAGAAC 780
ATTATGGCCA CTTCTACTGC TGTGGATAAG CATATCATAT TGATGTCTGA CCGGTTAGCG 840
75 ACGGAGCAGT ATCCTGTTAA AAATGTAAT ACTGCAGACT TCATTGGCAA AACTGGAAT 900
GCGAATGATC CCATTGATTT GGTATACAAA GGAGCAATTA ATTCCTTAC AAATTATGTT 960

WO 99/29870

PCT/AU98/01023

60 / 490

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TCCAACAATC CATCTACACC TCTTACCCCA AATTATCCAA CTCATTCTTC TAAAGTTGGA 1020
 CGGAGAAATC TGCCGGAATC CAAATTCGAT TATAGTAATC TGAGTGCAAG GATTACTTTT 1080
 GATGGGTGTG CTGGCGCATT GGTCTATGAA CCGAGGTTTC CTCATCCCTA TTATTATTAT 1140
 TTCCCTTGTA ACGCTGCTAT CAATGAGGCT CAGTTTGCGA AAAACTCTGG TTATACAATC 1200
 CATACTATTG GCTATGACCT GGGAGATTTT GCCTTGGCCA ACAATTCTGT GAAACTAACC 1260
 GCTACAGACG AGAATCACTT CTTTACGGGG ACACCGGCCA ATTTAGCTGC AGCGTTTGAT 1320
 AATATTGCCC AAACATTTAA TATAGGTATA CAGAGGGGGG AGGTGACGGA CTTTGTAGCT 1380
 CCTGGTTTCA TCGTTAAAAA TCTGACGCAA TCGGGAGATG TTACTCATT GCTAAATGTT 1440
 TCAAAATGGA CGGTGCACTA TGATGTCTCT ACTAAAAAAC TGACATGGAC TACTGGTACT 1500
 ATCCTGAGCT CATCAGAAGC TACCATAACT TATCGTATTT ATGCCGATT GGATTATATA 1560
 CAGAACAATG ATATTCCGGT AAATACTACT TCTGCTATCG GCCCGGATCT TGGTGGATTC 1620
 GATACCAATA CCGAGGCCAA ATTGACCTAT ACCAATTCCT ATGGCGAAC GAATCAGCAG 1680
 TTAATTTTCC CACGTCCGAC GGTAAAGTTA GGTATGGTG TTATTAGCG GCACATATGA 1740
 TTGGTAAATA AAGAGGTCA ACCATACAG GCAAAATGGA CAGTTGTAG TTCCCTAAGC 1800
 GAGGCTCATG TTCTACATC ACRAAGTTTC TTTTGCCTC CAGGTGGAGG TCATATTGTT 1860
 CCCAAATGGA TAAAGTTGGA CAAACGACC GAAGCATTAC AGTACTATT CGTACCCCGG 1920
 ACTAACACCG TCATCACTAC TGCCGATGGT AAACGTTATC GTTTTGTGGA AGTCCACAGC 1980
 TCCACGCCGA ATCCGGGCCA AATCGGTATC AGTTGGAAAA AACCGGCAGG AAACGCTTAC 2040
 TTCCGTTTCA AGCTCCTCAA TTATTGGATG GGAGGAACAA CAGACCAACA GAGTGAATGG 2100
 GATGTGACCT CCAATTGGAC AGGAGCCCAA GTACCGCTCA CAGGAGAAGA TGTAAGTTT 2160
 GCAACGACAG AAAATTTCGG TTCTCCGGCG GTAGCCGATT TGCAATGTCC GACAAACCAAC 2220
 CCAAAATTA TCGGTAACTT TATCAATAAT TCCGACAAGG ATTTAGTTGT TACCACAAGC 2280
 AGTCAATGGA CGATCAACGG CGTGGTTGAG GATAACAATC CGAATGTCCG TACGATCGTC 2340
 GTGAAGTCGT CGAAGACAA TCCTACGGGG ACATTGCTTT TTGCCAATCC GGGCTATAAT 2400
 CAAATGTGAG GGGGACCGT CGAGTTTAC AATCAGGCAT ATGATTGTGC CGATTGTGGT 2460
 ATGTATGCGA GGAAGTGGCA GTATTTCGGT ATCCCTGTCA ATGAATCAGG TTTCCCAATT 2520
 AATGATGTGG GCGGAACGGA GACCGTCAAC CAATGGGTG AGCCTTTCAA TGGCGATAAG 2580
 TGGCGGCCAG CACCTTATGC ACCTGATACA GAGCTTCAAA AATTCAAGGG CTACCAGATC 2640
 ACCGAATGAG TGCAGGCACA GCCTACGGGA GTTTACAGCT TCAAGGATAT GATTGTGTG 2700
 TCGGATGCGT TCCTGAATCT GACACGCAGG TCCGGTGTCA ACTACTCGGG CGCCAACTTG 2760
 ATCGGCAACT CATACACTGG AGCCATCGAC ATCAAGCAGG GTATTGTCTT CCCGCCGGA 2820
 GTCGAGCAGA CGGTGTATCT GTTCAACACG GGAACACCGG ACCAGTGGCG TAAGCTTAAT 2880
 GGAAGCACCG TTTCAAGGCTA TCGAGCCGGT CAGTACCTCT CTGTACCTAA GAATACAGCG 2940
 GGTCAAGACA ATCTTCGGA TCGTATTCCA TCGATGCATT CCTTCTGGT GAAGATGCAG 3000
 AACCGAGCGT CTGTACGTT GCANATCTTG TACGATAAGC TGCTCAAGAA CACGACTGTA 3060
 AACAAACGGA ATGGTACGCA GATCAGATGG CGATCCGGCA ACTCCGGATC GCGGAATATG 3120
 CCGTCACTTG TGATGGATGT TCTTGGTAAC GAGTCCGGCG ACCGTTTGTG GATCTTTACC 3180
 GATGGGGGCT TTTCTTCGG ATTTCGCAAC GGCTGGGATG GTCCAGAGT GACTGAAAAA 3240
 GGTTTGTGAC AACTTTATGC GATGTCTGAC ATCGGTAATG ATAAATTCCA GGTTCGAGGG 3300
 ATCCCGGAGT TGAATAACCT GCTGATCGGC TTCGATCGCG ATAAGGATG TCATATACAG 3360
 TTGAGTTTGG CTCTTTCGGA TCATTTTGGG AAAGGGGCTG TTTACCTGCA CGATCTTCAG 3420
 TACGGAGCCA AACACCGTAT TACGAATCT ACCTCGTATT CATTCGATGC CAAGCGGGGA 3480
 GATTCCGGGG CTGCTTTCGG CTGTGATAT GGATGTGATC AGAACGTAGA TGATTCGCAT 3540
 TCGTGTGAGT CAAATGGCCG TGAATTTATA ATTCTGAATC AAGATGCTCT TGACTGCACT 3600
 GTAACTTTAT TCACAAATGA AGGTAAGCTT CTTCGCCGCT TGAAGTATT AGCTGGTCT 3660
 AGAGAGTCA TGAAGTGCA GACCGGAGGG GCCTATATTG TGATCTTCA AATGCTTTC 3720
 ACTAATGATG TGCATAAGGT GCTTGTGAG TAT 3780

50 (2) INFORMATION FOR SEQ ID NO:88
 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (11) MOLECULE TYPE: DNA (genomic)
 60 (111) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 65 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1278
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

ACTATGGAAG TGAAGAAAA CACAGTGGTG CTACGCCCTC TGATTGGGTT CGTGGCCATT 60
 CTCTCTTTC ACTCTCAGG GCTGTGGGGA CAGGAAGGGG AGGGGAGTGC CCGATACAGA 120
 TTCAAAGGAT TCGTGGATAC CTACCATGCC GTACGCAGCT CTCTCTCTT TGATTTCATG 180

WO 99/29870

PCT/AU98/01023

61 / 490

	AGCTCGGTA	CGAGAGTGAG	AGGTGAGCTG	GAGAGGTCGT	TCGGTAATTC	GAAAGTAGCC	240
	GTATCGGTCA	ATGCCACCTA	CAATGCTCTA	CTGAAAGACG	AGACCGGCTT	ACGTTTACGT	300
	GAAGCCTTCT	TCGAGCATCA	GGAAGAGCAT	TGGGGGTTGC	GCCTCGGACG	ACAGATTGTC	360
	ATTTGGGGGG	CTGCCGACGG	TGTGCGCATC	ACGGATCTGA	TCTCCCCGAT	GGATATGACC	420
5	GAGTTTCTGG	CACAGGATTA	CGATGATATT	CGTATGCCGG	TCAATGCATT	CGGTTTCTCT	480
	GTCTTCAACG	AATCGATGAA	AGTGAAGTC	GTGGTACTGC	CIGTATTCGA	GGGGTACCGT	540
	CTGCCGTGTG	ATCCTCGCAA	TCCTTGGAAT	ATCTTCTCCC	TTTCGCCCAT	TGCTCAGGGG	600
	ATGAATATCG	TCTGGAAAGA	AGAAGCCGGC	AAACCGGCCT	TCAAGGTTGC	CAATATCGAG	660
	TACGGTGUCG	GATGGAGCAC	TACGCTCTCC	GGTATCGACT	TCGCTTTGGC	TGCATTGCAT	720
10	ACATGGAACA	AGATGCCUGT	CATCGAAGTA	CAGGGCATTG	TGCCGACGGA	AATCATCGTT	780
	AGCCCTCGCT	ATTATCGTAT	GGGATTTGTC	GGCGGCGACC	TCTCGTACC	CGTCGGACAG	840
	TTTGTTTTCA	GGGGAGAGGC	TGCGTTCAAT	ATCGACAAAC	ACTTCACCTA	TAAGAGTCAT	900
	GGCGAGCAAG	AGGGTTTCCA	AACAATCAAT	TGGTTGGCCG	GAGCCGATTG	GTATGCTCCC	960
	GGTGAATGGA	TGATCTCAGG	ACAATTCTCA	ATGGAAAGCA	TATTCAGGTA	TAGGGATTTC	1020
15	ATCTCCCAAA	GACAACTTC	TACCTGATT	ACTCTCAATG	TTTCCAAGAA	ATTCTTCGGC	1080
	AGTACACTCC	AACTTTCGGA	CTTCACCTAC	TACGACCTTA	CGGGCAAAGG	ATGGTTCAAT	1140
	CGCTTTGCAG	CTGACTATGC	CTTGAACGAT	CAGATACATC	TGATGGCCGG	ATATGACTGG	1200
	TTCAAGTAGTA	AGGGCAGCGG	TATATTGGAT	CGGTACAAAG	ACAATTCGGA	ACTCTGGTTC	1260
20	AAAGCCCGCT	ACAGCTTC					1278

(2) INFORMATION FOR SEQ ID NO:89

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1392

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:89

45	TACGGCAAAA	GAAGAAAGCT	CGGAACCTCC	GTCCGACCTT	CGGTTCTAAC	CCAAATCAGA	60
	TTTATTTTGG	ACTTACACCT	TATTACTGAT	TTTTTTGAAG	GGCTTCGGGT	CAATCCTATC	120
	GGTGACGACG	CCATAGTGGC	TTTCATTATC	GACCTGCTTC	TTCTTTGCTG	TTCCGGCTTT	180
	ATGTCCTCCT	GTGAGGTGGC	TTATTTTCA	CTAAAGCCGA	TCCATCTGCA	GAACATCCGC	240
	GAACGGAATC	ACTCTTCCGA	CATCGCGCTT	TCCAATTTAT	TAGACATTC	GAATCAGCTA	300
50	TTAGCTACTA	TTCTGATCGG	GAATAATGTG	ATTAATGTAG	CCATCGTTAT	CCTTTCCAT	360
	TATGCCATCG	AGCAGACATT	CGTTTCTCT	TCTCCGATCA	TTGGATTTCT	GATCCAGACG	420
	ATACTCCTGA	CCACTGTTCT	TTTGCTGTTT	GGAGAGATTG	TGCCGAAAGT	GTATGCGCGG	480
	AAGAATCCGC	TGCAATACTC	GCGCTTTTCT	GCTGCAGCTA	TGTCGGTTAT	CTATAAGATA	540
	TTGTCAACCGT	TTTCAAAATT	GCTGGTCAAA	AGTACCGGCA	TGTTACCAAG	AGGTATCAGC	600
55	AAGAAGAAAT	ACGATATGTC	CGTGGATGAG	CTCTCGAAAG	CGGTAGCCCT	CACCACTACG	660
	GAGGGAGAGC	CGGAGGAGAA	AGAAATGATT	AACGAARTCA	TCAAATTTCTA	TAATAAGACA	720
	GCCTGCGAAA	TCATGGTTCC	GCGTATCGAT	ATTGTGGATG	TGGATCTGAG	CTGGCCATTT	780
	CGTAAGATGC	TTGACTTCGT	TGTTTCGTGG	GGTTATTCCA	GACTTCCCGT	TTCCAGAGGGG	840
	TCAGAAGACA	ATATCAAAGG	GGTGATTTAC	ATCAAAGATC	TAATCCCA	CATGGATAAA	900
60	GGCGATGAAT	TCGACTGGCA	TCCTCTGATT	CGTAAAGCAT	ATTTTGTCCC	CGAAAACAAG	960
	CGCATAGATG	ATTTGCTCGA	GGAGTTTACA	GCCAAATAGG	TGCAATGCTC	CATCGTTGTG	1020
	GATGAGTTCC	GTGGCACTTG	CGGACTGATC	ACAATGGAGG	ACATATTGGA	AGAGATCGTC	1080
	GGCGAGATTA	CGGACGAGTA	CGATGAGGAA	GAATCCCTT	TTAAGGTTTT	GGGGGATGGC	1140
	AGTTATCTTT	TGGAAGGAAA	AACGTCTCTC	TCCGATGTTT	GACACTATCT	TGACCTTCCG	1200
65	GAATATGCTT	TCGGTGAATT	GGGGGACGAG	GTAGATACGC	TAAGTGGGCT	CTTCTTGGA	1260
	ATCAAGCAGG	AACTCCCCCA	TGTGGGCGAT	ACAGCAATGT	ACGAGCCATT	CCGCTTTCAA	1320
	GTGACCCAAA	TGGACAAGCG	CCGAATCATC	GAAATCAAGA	TTTTCCCTTT	CGAGCGCACT	1380
	TGGGAGGTGG	AA					1392

(2) INFORMATION FOR SEQ ID NO:90

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 798 base pairs
 (B) TYPE: nucleic acid

WO 99/29870

PCT/AU98/01023

62 / 490

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(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)
(ii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc feature
15 (B) LOCATION 1...798
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

20 ATAATTTATA GATCAACAAT GAAACTATTA CTTTATCTCC TATTGGTCTT GTCGACTCTA 60
TCCCCGATGT ATTGCGCAAAT GCTCTTCTCA GAGAATCTCA CAATGAATAT AGACAGCACC 120
AAAACCATAC AAGGAACGAT ATTGCCCGTA CTGGATTICA AAACCGAAAA GGAAAATGTG 180
TTCACCTTCA AAAAATCTGC CAATCTCAAT CTGCTGATAA AGCAGCGTCA AGTAATCAAC 240
TTAATTAATA AGCTTGAGTT TTCTACCTAT GGCAATAAAG TAACCGTAAG TGGAGGATAT 300
GTACACACCG AATACCGCTA TTTGTTGCAT CATGTTTTTG AGGTTTATCC TTATGTCGAG 360
25 TCGCAATGGG CAGAAAGTAG AGGAATGAAA TATAAGGTTT CTACGGGATT ACAGTCGCGT 420
TATCGGCTGG TAAATAGTGA TAACTGTCTC ATGTTTGCAA CATTGGGGGT ATTTTTCGAA 480
TTCGAAAAGT GGGAACAGCC AGCCACTAGC CTCTTTGCGA GAACGTATGC ATACAGCCGA 540
AGTATCAAAA GCCACCTGTC TATCAGTTTC AGACATCGGT TGGGTGAACA TTGGGAATTT 600
ACAATACGG CTATTCACCA GGGAAAGCCT GACAGTTATT TTAAGAAGGC ACGTTTTCGA 660
30 GGAGCTATCG ACCTCAATA CCAATACACA CCTACGATAG GAATACGGG GGCCTATCGG 720
ATCATCTACG ATACTGCCCC TATTGTACCT GTGCGGAAAG ATTACAACAC CGTIGATGTT 780
GGTATCGATA TTTGTTTT 798

35 (2) INFORMATION FOR SEQ ID NO:91
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2721 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
45 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc feature
55 (B) LOCATION 1...2721
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

ACTATATGCG TTGCCTTCTT ATCCGCTCCC GTTGGGGCAT TGCGCGAGTC GCCGCCAATG 60
GGGGCGGAGC GGAAGACTCC CTCTCTCCTA CCCCTTCTTT TCGAGCATTC TGATAAAGGA 120
AAGGGGTTTC ACTACAGACT ATTCACAAGC AATAAACTTA AAGTGTGTC CACAGGTAAC 180
AGCCGATACA TACACAATA ACCAACAATC ATCCAAGCAA TGAACGAAT CGTTTATCA 240
TCTTTCTGT TCGTTCTGTC CATACTTCT TTAGTGGCAC AGAACATAC CCTCGATGTA 300
CACATATCCG GTACGATCAA GGATGCCCTCC TCGGCGGAAC CAGTGCCCTA TGCCACTGTA 360
AGCATCCGCG TGACAGGAGC AGATACCACA CAGGTGTTCC GACAAGTGAC TGACGGCAAC 420
65 GGCTACTTCG TCATAGGCTT GCCGGCAGCT CCTCTCTATC ACCTGACAGC TTCGTTTCGTA 480
GGTATGAAAA CCCATACCAT GCAGATTAGT CGGGGAAATG GACAGCAGCA CATCAATCC 540
ATCGACATTT CTCTCGAATC CGAGGACAAA CAACTCTCCA CCGTCACCGT ATCGGCAGCA 600
CGACCACTGG TGAAGATGGA GATAGACCGC CTGTCTCTATA ATATGAAGA TGACCCGCA 660
70 GCGCAAGACA ACAACCTGCT CGAAATGCTG CGCAACGTTT CTTTGGAATC GGTGGATGGT 720
CAGGCAATA TCCAGGTGAA AGGATCTTCC AACTTCAAAA TCCACCTCAA TGGCAGGCC 780
TCGACCATGG TGACGAGCAA CCGAAGGAG GTCTTTCGCT CCATTCTCTC CCATACGATC 840
AAACGGGTGG AGGTCATCAC CGATCCGGGT GTAAAGTACG ATGCGGAAGG CACAAGTGCC 900
ATCCTGACCA TCGTCACGGA AGAAGGTAAG AAGCTGGAAG GATATTACAG TTCCATCAGC 960
GCCAGTGTCA GCAACAATCC CACAGCCAAC GGTAGTATCT TTCTGACGGC AAAGTCCGGC 1020
75 AAAGTCGGGC TGACTACCAA CTATACTAC TACGGTGGCA AAAACAAGGG CTCTCGCTAC 1080

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WO 99/29870

PCT/AU98/01023

63 / 490

5 TTTACCGAAC GTACTACATC CATGCTCCAA ACGATAGAAG AAGGCAAAGG GCAAGAAACC 1140
 TTTGCGGGAC ACTTCGGCAA TGCCCTCCTC TCATTGAGGA TAGATTGCGT CAATCTCTTT 1200
 ACGGTGGGCG GCAATGTACG CCTTTGGGAG ATGACCACCG ACCGGAACAG CGTAGAAAAA 1260
 AGCTTTGGCG GCAGCAACCT CATGTCTTAC ATAGACAGAA AACTCAAAAC ACAGATGGAT 1320
 GCCGGATCAT ACGAGCTCAA TGCCGACTAT CAGCACAGCA CTCGCCCTGCC GGGCGAATTG 1380
 CTACCGGTTT CCTACCGCTT CACTCACAAT CCTAATAATA GCGAGACCTT CATTGACCAA 1440
 TGGAAGCGCG ATCCGCTCAA CACAGCTAAT ACGATCCAGT ACGCCGGCCA GCACTCCAAA 1500
 TCCGATGCGG GCATGGACGA ACATACGGCA CAAGTGGACT ATACACGTCC CTTAGGACAA 1560
 GCACATCTCT TGGGAAGCAGG GCTGAAGTAC ATCTATCGTC ATGCCACGAG CGATCCTCTC 1620
 TATGAGATAC GACCATCCGA AGATGCTCCG TGGCAGCCCG GCTCTCTATA TGCACAGAAT 1680
 CCGTCGAACG GAAAGTTCGG CCACGATCAA TACATCGGAG CAGCCTATGC CGGTACAAAC 1740
 TATCGTAAGG ATCAGTATTC TTTGCAAACC GGCCTCCGAG TGGAAAGCAG CAGGCTGAAA 1800
 GCACTCTTTC CCGAAAACGC AGCAGCAGAT TTCTCCACA ACTCGTTCGA CTGGGTGCCA 1860
 CAGCTCAGCG TCGGCTATAC CCCCTCGCCC ATGAAGCAGC TTAAGCTGGC CTATAACTTC 1920
 CGAATCCAAC GTCCTGCAAT CGGCCAACTG AATCCCTACC GGCTACAGAC CAACGATTAT 1980
 CAAGTACAGT ATGGTAATCC CGACCTAAAG TCGGAGAAGC GTCACACAGT CGGTCTCTCC 2040
 TATAATCAAT ACGGAGCCAA GGTATGCTT ACAGCATUGC TCGACTACGA CTTCTGCAAC 2100
 AACGCCATCC AGAATTACAC CTTCTCCGAC CCGGCCAATC CCAATCTGTT CCACAGACC 2160
 TATGGCAATA TCGGACGAGA GCATTCTTTC AGCTTGAATA CCTATGCCAT GTACACGCCG 2220
 GCCGTATGGG TCAGGATTAT GCTCAACGGA AATATCGATC GCACATTCCA AAAGAGCGAA 2280
 GCACTCGGCA TTGATGTCAA TTCATGGTCC GGCATGGTAT ACTCAGGCCT GATGTTCAAC 2340
 CTGCCGAAGG ATTTGGACTGT GAATCTCTTC GGAGGTTATT ATCATGGGGG AAGAAGCTAC 2400
 CAGACGAAGT ATGATGGCAA TGTATTCAAC AATATCGGTA TAGCCAAACA GCTTTTCGAC 2460
 AAAAAATTGA GAGTCTCGCT GAGCGCAAAC AACATTCATG CGAAGTATTC GACATGGAAG 2520
 25 AGCCCGACCA TCGGCATATG ATTTACTATT TATTCGGAAA ATGCCGGTAT ACAACGGAGT 2580
 GTTTCCTCA GCCTCACCTA CAGCTTCGGT AAGATGAATA CACAAGTGGC CAAGGTAGAG 2640
 CGTACGATCG TCACGACGGA CCTCAAGCAA ACCTCATCCC AAGGACAGCA GGGTGGCGGA 2700
 CAAGGAAATC CTACCGGCAA T 2721

(2) INFORMATION FOR SEQ ID NO:92

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1350
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

55 TGGTGCCAAT CCGACCCAAT ACCTCATTGC CATGCAGTAT ATCGAAACGC TCAAGGACAT 60
 CAACAAGGGC GATCAGACCA AGACCGTTTA CCTCCGTTTC GAGGCTACCG GTATGCTCGG 120
 TGCCCTTGGG GGTATGAAGG ATTTGGTGAA AGGATGAGAC TCTCTGCCAT TCTTATCGCT 180
 TTGATTGTGA TGCTGCCTGC TGTGCTTAGC GGGCAGCATT ATTATTCCAT GCGGGGAGAG 240
 CGACTGGAGA CGGACAGCAT TCGTCCGAAC GAATCTCTGG CATCGATCCG AAGTGCCTT 300
 TTCTTTCGGA ACAAATGAATA CAATGCCAGT TCGGTCAAAG GTTATACGTT GCGGGGTGCA 360
 60 CGGGTTTCCG CTTTTGCTTC TTAATCGCTG CCGGCAGCAC ATGGGTGTAA GCTTTGCTC 420
 GGAGTATCTA CCTGAACTA CTGGGGGGCA AGTCGCTATC CGGCCGGTAT CGCTTATTC 480
 GATTTACCTT ATTGGACGGA CTATAACGAC TATGTACGCT TGGGTATCCT GCCTTATGTA 540
 CAGGCCATGC TGAAGCCGAC GGCACGACT GCTCTCATGC TGGGCAATAT AGCCGGTGGT 600
 ACGGCTCAGC GACTGATCGA ACCGATCTAC AATCCTGAGT TGGATTGAC GGCTGATCCT 660
 65 GAAGCCGGTG TGCAATTTCC GGGTGATTGG ACAGGTTTCC GAATGGATGT TTGGGTCAAT 720
 TGGATGAGCA TGATTTTCAA AAATGACAAT CATCAGGAGT CGTTTGTCTT TGGCTTCTC 780
 ACTACTTCGA AATTGTTATC GGGTGAAGGC AAATGGCGAC TCGAACTGCC CTTGACGGCT 840
 ATTGCCAGC ATCCGCGCGG GGAATACAAC TGGGCGCAGC AGGATACCGT GCATACATGG 900
 70 GTCAATGGAG GTGTCGGACT TAAGCTTTCG TATCGCCCTC GTACCGACAA ACCCATGCAG 960
 ATTTGGGGAT CTGCTTATGG TGTGGCAGCC TTGTCAAGCG GAGGATACCT CTTTACGAA 1020
 AGACGGTGGG CCGGTTATCT TTCTCTCGGA ATGGAAGTGG AGCACTTCGC TTTTCGTACC 1080
 GACTATTGGT ACGGACGGCA TTACGTTTCT CCCTTTGCTG CACCTTTCGC CAATCCCTG 1140
 ACGTATGACA AACAGCCTCT TACGAACGGT TGGGGCGATT ATATTGCTCT CTATGCCGAC 1200
 TATTCGTGGC GGATGGCAGC AAGTGTTCG TTGGCGGCTG TTGCTGGGT ATGGTTCCAG 1260
 75 CCTTCGGATC GTTTTGGCAT GAGCCACGCC TTGGAAGTGA CGATCGGTAT CGATCCCAAA 1320

WO 99/29870

PCT/AU98/01023

64 / 490

TTCCCAATAG CTTTTCTGAA AGGCAATCAT

1350

5 (2) INFORMATION FOR SEQ ID NO:93

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1341 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...1341

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

CCGTTTTCAC CGCCATGGGT ATGTGCTGGA GCGGCTTCCT CAGTACGCAC ACGGCCATGC 60

TCCGACAGTCT CAAGTACCGC CGCCTCATCA CACAGGCGAT CGGAGCACAT GCGATCGGCG 120

30 GACTCGTGGC CGGCATATTC GCCCATTTGGC TCTTTGTCTT CATCTCACTC ATTTGATTTCG 180

ATACCCGACC AAGTATGAA CAAATCGCTA TTATCATTGG CATGGCTCAT CCTGTGCGGT 240

ATGCCGGCCA TCGCCCAACA GACAGGACCG GCCGAACGCA GCGGCGAGCC TTCTCTGGCC 300

GAACGTGTAT TCGGTCTGGA GCAGAAGCAG AAAAAGCTGA AGGTGTACTT AGGCATACAG 360

TCCGTTCTAG ACCAGCCGCT TGTGATGAC GAATCCCTATA TCGGACACTT CAAGGTACAG 420

35 GAGCTGCGGA TGTCTGCTCA TGGCGAATCG AACCGCCACC TCAGCTTCGA CTGGCGACAA 480

CGTCTCAACC GTGCCGCGGA CGGCCTTCG TTTGCCGACA ATCTCTCCAA TGGCATCGAC 540

ATCGCAGGTG TGGACTGGCA CCCGAACGAC AAGGTGTCTT TCTCTTCGG ACCTCAGTAC 600

GCGCGTTTCG GAGGGATAGA ATACGACATG AACCCCGTAG AGATCTACCA GTACAGCGAC 660

CTTGTGGATT ACATGACCTG CTATACTTCG GCGGTGAATC TCGCATGGAA CTTCACCCCC 720

40 GAACAGCAGC TGCAGCTACA GGTACTCAAT GCTTACAACA ACCGCTTCGC CGACCGCTAC 780

CACGTGACAC CCGATGTCGC TACCGCCACG AGCTACCCGC TCCTCTACTC GGCACAGTGG 840

AACGGTACCC TCCTCGGAGG AGCACTGCAT ATGCGTTACG CCGTGTGAT GGCTCATCAG 900

GCCCAAGAGC GTAATATGTG GTACTTCACT GCGGGCAACC TGTTCATCC GGGCAAACGG 960

ATCAACGGAT ACCTCGACCT CACCTACTCG ATCGAGGGAT TGGACGACAA AGGCATTATG 1020

45 ACTGCTCGCT ACGGCAAGGG CAAGACCCCTC ACGGACGTCA AGTACTATGC TCTGGTATCG 1080

AAGTGGAACT TCCGCAATTT CGATCAGGTC AATCTCTTCC TCAAAGGCAT GTACGAGAAC 1140

GGCTATGCGC CTGCCAATA CGGCGAGAGC AGCCACACGC GCCACTCCTA CGGCTATATG 1200

GGAGGGGTGG AATATTACCC TACGGAGACC AACTTCCGTC TGTTCCTCAC CTACATAGGA 1260

CGGCATTACC GGTACAGTGC GACCGAGACG GAAAGCACCA ATGCTCTTCG CGCCGGTCTG 1320

50 ATCTATCAGA TACCTTTCTT A 1341

(2) INFORMATION FOR SEQ ID NO:94

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 681 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

60 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

65 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

70 (A) NAME/KEY: misc feature

(B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

75 TATAAGCAAG CTATAATGAA ACATTTGTTT AAGTCGACAT TAGTACTTCT TTGTGCTCTT 60

WO 99/29870

PCT/AU98/01023

65 / 490

5 TCTTTTTCGG GTACCTATAC CTTTGCACAA GAAAATAATA CAGAAAAGTC ACGATTGAT 120
TTTTCTGTGA GGCCTGGGACA GGGATATATT GCAGGTTCAA CTACCAACCT GATGTATGGG 180
TATACATCTG CTAACGATAG ACTTTGTCT GGTGCAATTT ATCTGGGCTT GACACCAAGT 240
AAGAAAGAAA ATGCAACCGG CGTAGCATTT CGTTTCTTAT CCCCCTCTCC GGGTTATTAT 300
GTCGATATAT CCGGCAAGA AAATACCTTG AATTATGCGT TTACGTTGT CGGAGCATAT 360
AATAGAATAG CCATTCTTAT ACGCCCTATC AAAAATTTTA ATTCTACTT CTCTACAGAA 420
GTCGCAATGG CTTGGATGAG TCGTCATGAG CAAATTTACA ATTCTACTT GCAGACTTGG 480
GATAAGCAGC GCAAGTCGAG GTCGGGACTG GATTTTGGTC TCGGGATGCA TCTGCAATHC 540
CACATTAATA AGACCGTTTA CTTTATGGCA GGAACCGATC TTACGTTCTG CATGTTGGGA 600
10 AAAAGGATCA ATGACTACCA GCAAAAGGAT CGAACCTTCA TTGCATTTAT CGACACAGT 660
ATTGGCATAG GATTAAACCT C 681

15 (2) INFORMATION FOR SEQ ID NO:95
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1218 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
25 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...1218
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

ATATTTCATAG ACCCGCATAA GAATACAAAA CAAAACGAAC GAAATATGAT TATCAAGAAA 60
ATGCTGAAAA ATAAATGGGC CCCCTTGGCC ATACTGTTC TTTTGTCTCC AAAGGCTATG 120
AAGGCTCAGG AGCAACTGAA TGTGGTACAC ACCTCTGTGC CATCGCTGAA TATCAGTCCG 180
40 GATGCACGTG CGGCCGGTAT GGGGGATATA GGTGTGGCAA CGACGCCGGA TCGGTATTCA 240
CAGTATTGGA ATCCGAGTAA ATATGCTTTC ATGGATACGA AAGCCGGTAT TAGCTTCTCA 300
TATACACCCCT GGCTGTCCAA GCTGGTCAAT GATATTGCC TGATGCAGAT GACCGGTTTC 360
TACAAATTGG GAACAGACGA GAATCAGGCT ATTAGTGCTT CTCTGCGTTA TTTCACATTA 420
GGAAAGTTGG AGACTTTTCA GAATTTGGGC GAATCCATGG GAGAGGCCCA TCCCAATGAA 480
45 TTTGCTGTGG ATTTGGGCTA TAGCCGCCAG TTGTGGGAGA ACTTCTCCAT GGCTGTTCGA 540
CTGGCTTACA TCGGCTCAGA CCAAAGCACT CACAACACCG GAGAGATCA GGCCGGAAT 600
GCCTTTGCGG CGGATATAGC CGGTATTTC CAGAAGTATG TGCTACTGGG TAATGCGGAG 660
AGCTTGTGGT CGTTGGGTTT CAACGTAAAG AATATCGGAA CGAAGATCTC CTATGACGGA 720
GGTGTACGA CTTTTTTCAT CCTTACTTCG TTGAATCTCG GGACGGGGCT GTTGATCCG 780
50 ATCGATGACT ATAACAGCAT CAATTTC AACCTTGAAC GCAAGCTGCT GTTACCCACT 840
CCTCTATCA TGGATCAAAA CGATCAGGCC GGGTATGAGG CTGCACTCAA GAAATATCAG 900
GAAACTTCTT CGATCAGCGG TATATTCTCT TCTTTCGGTG ATGCGCCGGG AGGACTCAAG 960
GAAGAATTCC GTGAGATTAC ATGGGGACTT GGGGCTGAAT ATAGCTATGA CGATAAATTT 1020
TTTGTTCGTG CGGATATTTC ATACCTGCAC CCCACCAVAG GCAATTTGCA GTACTTCAG 1080
55 GCCGTGCCG GCTTCAAAAT GAACATATTC CGTATCGATG CTTCCTACCT GTTGTCTACG 1140
ATCCAGAGTA ATCCGTTGGA TCAGACTCTG CCGTTTACGC TTGCTTTCGA TATGGATGGA 1200
TTGCCAATT TGTCCAC 1218

60 (2) INFORMATION FOR SEQ ID NO:96
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1356 base pairs
(B) TYPE: nucleic acid
65 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
70 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
75 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

WO 99/29870

PCT/AU98/01023

66 / 490

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1356

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

CTAATAATCG	AAAAGGAAAT	GAAAACAACA	GTTCAACAAA	TTATTCTGTG	CCTGGGCTTTA	60
ATGATGTCAG	GTGTATTGGG	CGGAAACGCA	CAGAGCTTTT	GGGAAGAAAT	AGCTCCTCCT	120
TTTATCAGTA	ATGAGCCTAA	CGTCAAGTAT	ATAATTCCCA	ATATGGGCAT	TGATTCAAAAG	180
GGAAACAATCT	ATGTAACCGT	GACAAAAAGG	ATTCAGCAGG	GAGCAAAATTA	TACTTCTGAG	240
CAATTGGGCTA	TGTACTATCG	ACCAATTAGG	GATAATGAAC	AGTGGTGGAA	ACATGATCCG	300
TATTTTGATG	ACAAGATAGT	TGCGGATATT	CAGACAGATG	CATATGGCAG	AGTTTATGTA	360
TGTACGACTT	CTTCTCGACA	TCAAGAGTAT	CAACTTTATA	TAAACGAGCA	GAACGAATGG	420
AGGTGTATAT	TCAAAACTTC	TGTGTCTACA	TATGAGCATG	GTATGGCTGT	TTTTCGCTCT	480
TCGACAGGGG	TGACTTATAT	AGGTACCAGG	CATCAGATCT	TCGCATCAGG	TGTAATGAT	540
TTCGAGTTCA	ACACTATCTA	TGAAGACTCT	ACACCTATGA	GCTGTGCTTT	TGCAGAGGCT	600
ACGAATAGTG	GCACCATCTA	TCTGGCATTG	ATGCATGAAA	CCACAATGTC	TACGACTATC	660
CTTACTTATC	AAAACGGTGA	CTTCGTCGAT	ATCTCGGAAA	GTGAATTGAG	TAACTCGATT	720
ATTGCATCCA	TGTGCTCTAA	TAAAGAAGGT	GATATAATAG	CTCTTGTTAC	TTCATATACA	780
GGATTTATGA	GTGGAACCTT	TGCGATCACA	AAAGCAGATG	AAGGCAAAAT	GCAACTTGTT	840
GGCGGAGATA	TACAGAATGC	GATCGTTCAA	AATATATGCA	TGATGGACGA	CAACAAGATT	900
GCTTGTGAAG	TCTTCGGGAC	TCCTAACCGA	GTAGATGGTC	GGACAAGGGT	TTGTGTTTCT	960
GACGCATCTG	TCTTTGATTT	TGAGTGGTAT	GAAGATGAAA	TATACGGAGG	CCTGATATTT	1020
GACACTTTCT	TCTATAGCCC	TTGGGACAAA	CTTCTTTATG	CGAAATTTGG	TGGGATTATG	1080
CTCAGAGATA	AAGAGTCTTT	TATAACCTCT	TTCAATTTCT	CGACAGTTGT	ACAAGGAGTG	1140
GATGCTATA	CTTTGCCGGG	GAAGATAAAG	ATCGAAAGTG	AAACTCGGGT	GTCTGAGGTG	1200
TTGCTTTTCG	ACCTGGCTGG	CAGGATGGTA	CTTCGGGCAA	CGATTGATAA	TAAATCTAT	1260
TCGGACATAG	ATACTAACGG	ACTAAAGCGA	AGCGGTATTT	ACGTAGTCTC	GGTGCGGCTC	1320
TCTTCCGGAC	AGGTATTTCG	TGATAAGGTG	CAGGTA			1356

(2) INFORMATION FOR SEQ ID NO:97

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 993 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...993

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

GGCCTGTACG	GTATGCTGCT	TGTACCTATA	ATTAATTTATC	TTTGGCGTAT	ATCAAATTAT	60
GCAAGACTCA	TGATAATCCG	GTGTCTTATC	CGTCGTCGGA	GAACCGTCCT	GTTCGGGTTG	120
ATATTCTGTG	TAGGTCTTTT	CTCTGCGATG	GCGCAAGAGA	AAAAGGATAG	TCTCTCTACG	180
GTTCAGCCAG	TGCGGAATAG	CAGCATGCTG	GAGCAGACCC	CTCTCTCTCT	CATTGATCAC	240
CCCGTCCTGC	CCGCTTCTTT	TCAGAATACC	CGTACACTGA	AAAGGTTTAG	AGACAAACAT	300
CTTTCGATG	CTTTGCTCAA	TGGATTGAAG	CCTCATCGCT	CATCTTTGCA	ATTGAATGAG	360
GAACCTCACT	TGCGGCGAGA	GCGTCGGGAT	TTCGTTTCTC	CCCTCTTGCA	AACTCGCCAC	420
GCTGCCGGTG	TCCTTTGATG	GCGACCGACC	GATAGGATGC	ATTTTATATC	ATCGGGCAAT	480
ATCGGCTCTG	GCCATGATTT	ATTGACCGGT	GTGCGCAAGG	ACTTCGGATG	GAATGCTGGT	540
GCCGACTTCT	TGCTGAGTCA	AAATCTTACG	GCACATGTCC	AAGGCGGTTG	GCAGCAGAAAT	600
TTGCGCTTTA	TACCTATGAC	GGCTGTCAAT	GGCCAACTGC	GTTCGGCAAGC	CACCGAGAGA	660
TTGAGTTTGA	CCACCGGTAT	CGATTATCGA	CAGGTACAGT	GGATGCTTTT	CGATAATAGA	720
ACGTTCTCGC	TTAAAGGAAG	TGCTCGATAC	GAGTGCATGG	ACAAATGCTT	TGTCAATGGA	780
TTTGGCAGCT	ATCCTCTCTA	CAGCAGTACG	CGCTCAGGAC	TCAATATGGC	TGTTCCGATG	840
CATGGATTTC	GCCCTCAGTA	CGGTGGATCG	CTTGAGCTGA	AAGTCTCCGA	CGGATTCGGC	900
TTTGGCGTCG	GTATGGAGCG	CGAATACAA	ATCTGGACTC	GTCGGTGGGA	AACGCATTAC	960
TTTGCTTATC	CTGTATTCTA	TGGCGATAAG	AAG			993

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(2) INFORMATION FOR SEQ ID NO:98

WO 99/29870

PCT/AU98/01023

67 / 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 987 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

GAGACGAACT	CTTGGGTATC	CAGCGATTGC	AATTGACGGA	CGATGAAAC	GAATAGACGA	60
TACGCATTTC	TTTGGCCGCT	CTGCTACTC	ACCGGATTGT	TGGCATGGGG	GCAGGATTCT	120
TCCCACGGTA	GCAATACAGC	GTTTGCAACT	GATTCTTCGA	GTAGAGAGTT	GCCCACGGAG	180
CAGTCCGCCT	ACCGCATTCA	TTCTGGCTAT	ATGGTCGGTG	GTGGCGGAAG	CATAACGGCG	240
GACACCTATT	TGTCACCCCT	TCGTTATGGA	GGATGGACAC	TCAATTGTGT	GGGAGAGAAG	300
ACGTTCCCTC	TCAAAGCCCT	CGATTCCCGT	TGGATGATCC	GTACCGGGCA	TGAGCTGGAT	360
TTTGGCCCTG	TGGACAATCC	GGCCAATAAT	GCTCATTTC	ATTCCCTGCT	GTATAACGGT	420
TCCGCTGGCG	CTCTTTACCG	CCTTGGCGCT	AAGCATCTGC	GAGCCGCGTG	GATGGACAAT	480
CTGCGCTTGG	CATTGGGCCC	GGGCTTGGAA	ATCGGGCTTG	GAGGAATTTA	TAGTACACGC	540
AACGGCAATA	ATCCTGCGAC	ATTGAAGCTC	TACACCAATG	CCATCGCCCA	AGCCTCGATA	600
GGATACTAGC	TCCCTCCCGA	AACTTTTCCC	CTGTATTTTC	GGTTGCTCTC	CCAGATCAAT	660
CTCTTCGGTA	TAGCCTATGG	AAATGGTTTT	GGTGAGAGCT	ATTACGAGAA	TTTTTTGCTC	720
AAATACGGCA	TTCAGGGCTC	CCTGCATTTC	ACTTATCCGG	GCAAGTTTAC	TCGGTTCACG	780
ACACTCATAA	CGGCGGATAT	TCCCATTCCG	AACTTCTGTA	CGCTTCGTGT	CGGTTATCGC	840
TATTCCCAAT	TGGGCTCTTC	GCTTAACGCA	TGGGATACTC	GAATCCACAG	TCATACGGCT	900
TTTATCGGTT	TCGTACGGGA	GTTTTACCGA	TTCCGTGGGC	GCAAGCCAT	GAATACCGGT	960
CGGAGAACCA	GTCTTTACTA	TCATGAT				987

(2) INFORMATION FOR SEQ ID NO:99

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 957 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

TTTACGTCCG	GTACGATATT	CGTCCGTATA	GCCATATCCG	GCCGTGTAGT	GTGCCGTGAG	60
GTTAGGGATA	ACGGAAGGAG	AGAAGCTGTG	CGTCATGATG	GCATGGTAGT	GACGCTGCTC	120
GTAAATGTGC	GTATTGTGGT	AGTAGTGCGG	TACTCCTTGC	GCGTCCACGT	ACATAAGACC	180
GGCACTGTTC	TATCGGCGGC	CATATTTGGC	TTTCATCTCC	TTGGAAAGAC	CGTTCCATGC	240
GATACCGGTA	ACTTCTTTTC	CTCCGAAAGT	GATGAACCTG	AGAGCCGTGT	TGCTACCGAA	300
ATAGCCCAAC	TGTGCGAAAT	AGGATTTTCG	ATCCACGCTT	CCTCTATCCA	CGTAGCCGTC	360
CGAACCGATT	TTGGACAGGC	GGGCATCCAC	TGCCCAATGG	CGACCGATGC	GTCCGCTACC	420
GAGTTTGACC	GATCGGCGGA	ATGTGCCGAA	CGAACCTCCG	CTCAAAATCG	CACGGCCATA	480
AGGAGCCACT	CCCAAAATAT	CCGTACGCAT	ATTGACACTT	GCCCCAAAG	CTCCGCAACC	540
ATTGGTGAA	GTACCCACAC	CTCGCTGCAC	CTGAAGGTCT	TCGATGGGAG	AGGCGAAGTC	600
GGGCATATTC	ACCCAAAAGA	CGSACTGAGA	TTCCGAGTCC	TTGAGGGGTA	CTCCATTGGT	660

WO 99/29870

PCT/AU98/01023

69 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...729

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

TCGACAATAA	TGAAAAAAGC	TATTCTTTCC	GGAGCGGCCT	TGCTCCTCGG	CCTATGTGCC	60
AACGCCACAA	ACGTGCAGTT	GCACTACGAT	TTCGGTCATT	CCATCTACGA	CGAACTAGAT	120
GGACGTCCCA	AACTGACTAC	CACAGTGGAA	AACTTCACAC	CCGACAAATG	GGGAAGCACC	180
TTCTTCTTCA	TCGACATGGA	TTACACGGGC	AAGGGTATCC	AGTCGGCCCTA	TTGGGAGATT	240
TCGCGCGAAC	TGAAGTTTIG	GCAAGCTCCC	GTTTCCATTG	ATTTGGAGTA	CAACGGAGGC	300
CTCTCCACAA	GCTTTACTTT	CGGACACGAT	GCTCTAATCG	GTGCCACCTA	CAACTACAAC	360
AACCCCTCCT	TTACACGTGG	ATTTACGATC	ACGCCCATGT	ACAAGCATCT	GGGTGCGCAC	420
GACTTCCACA	CCTATCAGAT	CACCGGCACT	TGGTACATGC	ACTTTCGTGA	CGGTCTGCTT	480
ACCTTCAACG	GCTTCCCTGA	TCTTTGGGGT	TTCCCCAAG	AGAACCCAAT	CGGGGGCCCT	540
GTGCTCAAAG	AAGGGCATAA	GTTCGTATTC	CTGTCCGAAC	CGCAGTTCTG	GATCAACCTC	600
AAATCGCATCA	AAGGCATCGA	CAAGGATTTC	AATCTCAGCA	TAGGGACAGA	GATGGAAATC	660
ACCGAGAACT	TGCTCGCAT	GGACAAATTC	TCTTGATATC	CTACTCTTGC	GGTCAAATGG	720
ACTTTCAAC						729

(2) INFORMATION FOR SEQ ID NO:102

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

ATGAAAACAA	TTAGTAAGAA	CCATGCGGCA	CGGATCTGTG	CCGCCATTGC	TTTGTTTGCA	60
GTGTGTAACG	GCCGGATAGC	TGCTCAGGAT	TTTCTCTATG	AAATAGGAGG	AGGTTTGGGT	120
GCTGCTCAGT	ATTTTGGCGA	TCCAAACAGA	GGCTTGTTCG	GTTTATCCGG	AGTAGGTTTG	180
GAGTTGGTCG	GACGTTACAA	TTATAATTTT	CGCTGGGCTT	TCAGTACCAT	GTGGGATTGG	240
CGTACATTCA	GAGGCGATAC	CGATAAGTCC	GGGAATGTCT	TCCCCGATT	TGCTCAAGCG	300
GATTTTAAGG	TCGGCTTGAC	TCAGCTCCAC	GTTAGAAGCG	AATTTAACTT	TCTCCCTTAT	360
AGCGATGSGT	ATAAGTATCT	TGGTACAGCT	CGGCTGTCTC	CTTATGTAGC	GGCCGGGTTG	420
TCTTTGGGTT	TTGCTTCGGG	TGCTAAAGCT	TCGGCTTTTG	CTCCCGGGAT	TACTGCGGGA	480
ATGGGAGTGA	AGTATAAGCT	TAAACCGCGG	ATCAATGTCT	GTATCGAGTA	TTCTTTCACG	540
GGGTTACTTA	ATGACTCCTG	GGTCAAAAAC	AAGGATGCTA	CAGGGGCCCT	AGTGCTTAGG	600
ATTACGTATG	ACTTCGGCCT	GCGTAAGACT	TTTTGTAATA	AACAA		705

(2) INFORMATION FOR SEQ ID NO:103

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

WO 99/29870

PCT/AU98/01023

70 / 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1308

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

AATATAATGT	ATAAAGACTA	TAAGGGTTTG	TATGCGTCGC	TTCCGGTGGTA	TGCCCTGATC	60
ATTGGGGTTG	TATTTGCAGC	ACACGGTATA	CAGGCTCAGA	ACAACAACCT	TACCGAGTCG	120
CCTTACACTC	GCTTCGGCCT	TGGCGGTCTC	GGAGAACGGA	CGACTATTAG	TGGGCATTCC	180
ATGGGAGGAC	TGGGCGTCGG	TCTGCGTCAG	GGCACATACG	TCAATGCCGT	CAATCCTGCT	240
TCATACTCGG	CTGTGGATTG	GATGACGTTT	ATCTTCGATT	TGGGTGCATC	TACCGGAATT	300
ACGTGGTATG	CCGAGAACGG	GAAAAAGGAC	AATAGGAAAA	TGGGAAACAT	TGAGTATTTC	360
GCCATGGCTT	TTCTTATTTC	CAAAATCCATT	GCTATGAGTG	CGGGAGTGCT	TCCTTACTCC	420
GCATCCGGGT	ACCAGTTCGG	ATCCGTTGAT	CAAGTGGAGG	GAGGCGAGCT	CCAGTACACC	480
CGTAAATACT	TGGGGACAGG	CAATCTGAAC	GATCTCTATG	TGGGTATAGG	TGCACCCCGC	540
TTCAAAAAC	TCTCAATAGG	AGCCAATGCT	TCATCCCTTT	TTGGGGGATT	CACACACAGC	600
AGGCAGGTAA	TCTTCTCCAC	GGAGGCTCCT	TACAATCCCG	TACATCTCTC	GACGCTGTAC	660
TTGAAGGCTG	CCAAGTTCGA	CTTCGGTATG	CAGTATCACC	TTCTTCTCAA	ATCAGATCGT	720
TGCTCTGTTA	TGGTGCCCGT	CTATTCTCCG	CGGGTGAAGA	TGCATAGCGA	GCTGACTCAG	780
ATAAAGATC	AGGTTGAGAA	CGGTGTAGTA	GTGGAGAGCG	AAACCCAAAG	ATATATCAAG	840
GGAATGGACT	ATTATACCTT	GCCTCATACA	TTGGGGATAG	GTTTCTTTTA	TGAAAAGAAA	900
GATAAACCTT	TCTTAGGAGC	AGACGTCCAA	TATAGTAAAT	GGAAAGGCGA	GAAATTTTAT	960
AAATCCGATT	GCAAAATCCA	GGACAGAATA	CGGGTATCTC	TGGGCGGAGA	GATCATACCG	1020
GATATRAATG	CGGTGGGAT	GTGCGCTAAA	GTTCGCTATC	GCTTCGGTTT	ACATGGTGAA	1080
AATCTCTACC	TGAAAGTGCC	GACTAAAGGC	GGTGATATAT	AAGGATACCA	TATCGTAGGT	1140
GCTGTATTCC	GTATAGGAAT	CCCGCTCAAT	GACAGACGTT	CGTTCGTAAA	TGCTCTCTTT	1200
GAATATGACC	GATTGATCCC	GAAGGAGGGT	ATGATCAAAG	AAAATGCTCT	GAAATTGACC	1260
TTCCGGCTCA	CGTTCAACGA	GTCATGGTTT	AAAAAGCTGA	AACTGAAC		1308

35 (2) INFORMATION FOR SEQ ID NO:104

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

40 (ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2835

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

AATACCATTT	CGGAGAATGG	GAACGATAGC	ACCTATTTTT	CTTTTCAAAC	TTTTCTTATG	60
CGATCGATTT	ATCAATTACT	GTTGTCAATA	CTCCTTGCTT	CTCTTGGTTT	CGTCGGGCTG	120
GAAGCCCAAC	AAGCCGGAGT	AGCAGGTAGA	GTATTGGACG	AAGAAGGCAA	CCCCATGATT	180
CAAGCCCAAC	TACAGCTTGT	ACAGAGTACC	GGCCAAGTAG	CCGTTGCCGC	AGGTGCCACT	240
AATGAAAAAG	GGTTGTTCAG	CCTGAAAACG	TCACAGGAGG	GTGACTACAT	TCTGCGCGTT	300
TCATATGTAG	GTTACACTAG	CCACGACGAA	AAAATATCTC	TTAGAAACGG	GCAAAACATT	360
ACGCTCAAAG	ATATATCCAT	GAACGAAGAT	GCCCGTCTTC	TACAGAGTGT	GACCGTGCAG	420
GCTAAAGCGG	CACAGGTGCT	GGTACGCAAC	GATACGCTCG	NATTCAATGC	CGGATCCCTAT	480
ACCGTAGCAC	AGGGAGCTTC	TATCGAGGAA	CTGATCAAGA	AGCTACCCGG	AGCAGAGATC	540
GGATCCGATG	GGAAAGTAC	CATCAACGGC	AAGGACATTA	GCAAGATCCT	TGTCGATGGC	600
AAAGAGTTTT	TCTCCAAAGA	TCCACAGGTG	GCAATAAAGA	ATCTTCCGGC	CGATATGGTC	660
AATAAAGTAC	AGGTACTGAA	CAAACTGAGC	GAGCTCTCGC	GGATGAGCGG	TTTCGATGAT	720
GGAGAAAGAG	AGACCGTAAT	CAACCTGACG	TGAAGGCCCG	AAAAAAGAAA	AGGCCCTCTC	780
GGAAACGCTC	AGGCCGGCTA	CGGTACCGAC	CAACGCTATA	TGGCCGGAGG	GAACGTCAAT	840
CGGTTCGATG	GAAATAAGCA	ATGGACATTG	ATCGGTAGTG	CGAACAATAC	GAACAATATG	900
GGCTTTAGCG	AGATGGACAG	CGAGATGGGA	TCCATGACCT	TCTTCTCTCC	CCAGGCGGCT	960
GGTCGACGCG	GCTTCGGCAA	TAGTGGAGGT	GTTACGTCTT	CGTCGATGCT	GGGCGGCAAC	1020

WO 99/29870

PCT/AU98/01023

71 / 490

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TTCAGTGTG AATTCCTCTC TGCCCTTAAT ACAGGAGGCG ATGCACGCTA CGGATAC/MC 1080
GACAAGGCCA TAGAGACGAC CAAACGCGTG GAAAATATCC TCGCCGAAGG GAATACTTAT 1140
ATGAGCAAAA ATATATTGGA ACGCTCTTTC TCTCACAATG GTGAGGCGCG ATTTAGGATG 1200
CAATGGAAAC CGTCCGAACG TACCGAAGTG GTATTGAGC CGGATCTTTC GATATCCAAG 1260
ATCGATGGGT TCTTTAACGA CACATACGAG ACGAAAGATG CCACCGGAAT CTCTATCAAC 1320
AAAGGTTCTA TCCACCAAAC TACACAAGGA AACAACTTCA GACTGAACGG AGAATTGGAT 1380
ATCAGTCACA AGCTCAACGA CGAAGGCGGT ACGATCAGTG CCTCCGTGAG TGGCGGTCTG 1440
ACCGACGAAG ACGGAGATGG CATATATCAG GCTGTGCTCC AAGCGGTGGA GACGAATCAA 1500
AAGCAATTCA ACGACAATC CAACCTGCAA TATCGGCTTC GCCTCTCGTA TGTGGAACCG 1560
TTGGGTAATA ACTACTTCGC ACAAGCGATT CTGAACGAGC GTTCTCTCCG TCGCAATTCC 1620
GATCGTGAGG TGTACCGACT GGGCGATGAC GGGCAATACT CCATATTAGA CAGTCAGTAC 1680
GGACTCTCCT ACAGTAACGA GTTCACCCAG TATCGCATCG GACTCAACCT CAAGAAGATT 1740
GCCAAAACGT GGGACTACAC CGTAGGATTG AATGTGGATC CCAACAGAAC TCTCAGCTAT 1800
CGGAGCGTAG CCGAGTAGA GCAGGACAAA CTGGCTTTCA ATCGTGTCAT TCTCTCCCG 1860
ATGCTCCGAA TCAACTACAA ACCGAGCAGG ACTACCAACC TCCGAGTGGG CTACCGAGGA 1920
CGCACGACAC AACCTCCAT CAATCAGATG GCTCCCGTTC AGGACATCAC GAATCCGCTA 1980
TTCGTGACCG AAGGCAATCC CGGTCTGAAG CCGAGCTATT CCAACAATGT GATGGCCATG 2040
TTCTCGGACT TCGATGCCAA AAGTCAGCGA GCTTTCAACA TTGTTTCTT CGGCAACTAT 2100
ACATTCGAGC ACATCGTCCC CAATACGAC TACGATCCGT CTACAGGGAT CCGTACCACT 2160
CGTTACGCC TAACGCTTCC CTATGGATTG CGGAATCTTC ATGGGACACT ATCGCTTCCA 2220
CTCAAGAACT GGGCATTTTC TTTCAGGATG TCCTTGTTCA ACAGGTTGGC CGAAGGACAA 2280
AGCTTCATCA ATGACGATAA GAACAAAGCT CTCTCTTTCC GAACGAGGGA ACGCTGAGC 2340
CTCACCTATC GCAACAATTG GATCGATACG AGTATCGGTG GCAATATCGG ATTCTATATG 2400
GCCAATAATA GTCTGAGCGG ACAGAAAGAT TCTCGCACAT ACGATTTTGG CGGCAATTAT 2460
CAAGTTGCC TAACGCTTCC CTATGGATTG CGTATCGACA GCGATGTTGA ATACAATACG 2520
AATCTCGGTT ACAGCGGAGG ATTCAGTCTG GACGAATGSC TTTGGAATGC TTCGCTTTCA 2580
TACAGCTTCC TCCGTGACAA GGCCGGTACA CTGCGTGTCA ATGGCTATGA CATCTCGGT 2640
CAGCGGTCAA GTATCAGCGG TTCTGCTTCG GCCATCAATA TAGAAGAGAG CATGTCCAAT 2700
ACGATCGGAC GCTACGTGAT GGTGGACTTT ATCTACCGAT TCAACGCCCT CAGTGGTGGT 2760
GGATCTCGCA CGGATCATCA GCGTGGCAAT ATGAATCGTC CGGGCCCAAC TTTGCGCGGT 2820
GGCAGACGAC CGTCC 2885

35 (2) INFORMATION FOR SEQ ID NO:105
40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
45 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1236
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

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GGAGAGTATC CTGCAACAG TAACGACAAA AAAGAGATGG TTATGAAGCT GATTAAAGA 60
AGTTTGTCTC TGCTTGGAGC GGTACTGTG ATTACGCTTC CTGCGTACTC GCAGAATGAT 120
GACATCTTCG AAGATGACAT CTATACATCG CGAAAGAAA TACGTAAACA AAACCAAGTT 180
AAAGACTGGC AAAACCAAGA GGACGGATAC GGCGACGATA CGGAATATAC AGTGGCTTCC 240
GATCGGGACA TTGAGCGCTA CAATCGTAGA GATGGCCAST CCTACGATGG GAAAAAGTTG 300
TCCAAAGACA AGAAAAGAGA CTCCACTCGT TCTTCTGTTC CCGGTGCTA TAGTCGCCGC 360
TTGCTCGAT TCTATAAGCC GAATACGATC GTCTTTTCAG GTGCCGACA TGTATATGTA 420
ACTGATGATG GTGAGTATTT CGTCTATGGA GACGAATACT ATGATGACGC GTCGTCTGTA 480
AACATTTACA TCAACAGTCC TTGGTGGGAT CCGTTCCTT ATACGTCATG GTATCCATCT 540
TTCTCCGGCT GGTACAACAT TACGTGGAAC TATCCATGGT TCTACTACGG TAGCCATATC 600
GGATGGGGCG GTTATTACCC CGGATATAAT TGGTATTGGA GCTACTACTA TGATCCTTTC 660
TACATCCCT ATGGNAATCG TATGGGTTGG GGATATCCCT ATGGCTGGGG CAGCTATTAC 720
GCTTGGGGTG GCTATCCGG AGTGATACAT CACTACCACC ACTACCCCAA GAAGACCTAT 780
TCCAAATGGT AGCATTCGG AGCTTACTAT TCTATGSCC GACCGAATCG TATCAAAGGT 840
GGAAAGTCCG GTGCCAAACT TGGGACAGGA CGCTACGATA GAATTCAAAA TTCCTCTTCG 900
CAAAAAATA AGTTCGGATT GCAGTCGAAC AAACCCAAATA ATATCTGCA AAATGTCAAG 960
TCGGGACGTA CCGGCCGAGC CAATAGAGAC CGAAATATAG AAACGGTAAC TCCAAACAC 1020
GGGCAAAAGC AAGATCGTCC CGTATTCAG CAGATCAAT CCGGCAATGA CCGACCGACC 1080
GGACGGAATA TCCGCAGCGA GAGACAGGGG GAAAATACG ATAGGACATT TTCGACTCCT 1140

WO 99/29870

PCT/AU98/01023

72 / 490

TCCTCGTAGCA ATAGTAACGG TGGCTTCTCC ACGCCTTCTC GCTCTTCTTC CGGCTCTATG 1200
ACCGGAGGTG GCGGACGTAG TGGCCGGGGA CGCAAT 1236

5 (2) INFORMATION FOR SEQ ID NO:106

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1803
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

AGTAATAGCA GCTCCACAA GTGGTTAATT TATTATCATA TAGAAAAGAC TAAAAGTATT 60
ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG 120
GTACCAACCG ACAGCACGGA ATCGAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC 180
TCCTTTGAATA GGGATGATGC TCCGGATAAA TGGC/ACCTA TGCATGCCAA TTTCAGTATT 240
CAGAGCGATA TGGTGCTTTC TACTGCCCCA AAGTCCAASA ACACCTGGTT CGGCAACTCC 300
TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC 360
TATAAGCCCC TGCCCGGACA TGAACCCGAG ATGGGGCGTG GCGTTCCTCA CATGTATGTG 420
AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC 480
GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGGCGC 540
GGACGTATAG TACTCACTCC TTTTGATGGA GTGCGTGTCA AGGGTATTGC AGGACAGCAG 600
CGTAACACT TCGACCCGAC GGGCAAGGTA TTCGAATCCG CCGCAGGCTA CCTACTGGGT 660
TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGCGCGACAA TGAATATCAT 720
TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT 780
GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCGC 840
ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT 900
CCCTCGGCAG ACAATGACTA TATCTACCAC GACGACAGG CTGCACTCCT CTCTGCCTCA 960
TACTCCAAA AAGGGATGAG TATCCTGTTG CAGGCCAAAC GTTGTGAGAA CTTTGTCTTC 1020
CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC 1080
CAAGCTCACA CTTATACGCT GCGCGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA 1140
TGGGCTTTCC AAGGTGAATC GCGTTACAA TTTGCTCGCC GGACAGCTCT CGGTGGACGC 1200
TACGCTACCG GCTTGGGTAT CAACGTTTCG CATGTGCGTG GTCTGGACAA AAAGATGCTC 1260
AAAGAGAATC CCGACGMACT GATCGGAACG GATGGCTACA CCGTTTCTTT CTTCGGCATG 1320
GGCGACCTCT ATTATTCGGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC 1380
AACTTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC 1440
GGAGGAAGC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG 1500
AGTAATAAGG TAGCCCTCG TACCGAATG CAATATTGTC ACACGAAGCA GGATCAGGGT 1560
GACTGGATCT ACGGCTGGC CGAGCTCTCT ATCCTGCCTT CTCTGATGCT TTCCCTCTG 1620
GAGCASTATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT 1680
CACGGAGCAC ATCGAGTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGGAT GAACTGCTCG 1740
GGAGGTGTAT GTCGTGTGGT CCCTGAGACT CAGGGATTCT ACCTTTCTTA TAGCACAAT 1800
CTG 1803

60 (2) INFORMATION FOR SEQ ID NO:107

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 756 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

WO 99/29870

PCT/AU98/01023

73 / 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...756

5

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:107

10	AGGGGGTCGA GTTCGGGCAT TTCAGCCCGT GGACGCGACA TGGGTTCTTT ATTTTGTAGC	60
	GCCTTGGCGA GCTCCTCTCT CCATGGTTCA GAGCGACGCA GTCCGATAAG TTCTTCTGTA	120
	GTCTATGTCAA TAAGGCAGAA AATAAGGTTA TTCCATCTCT CGGTATGCGC CCAAACGCAT	180
	GATCATCTCA TCGAAATCCA CTTGGTGTGC ATCGAATTCG GGGCCATCGA CACAGACGAA	240
	TTTCGTCTGT COTCCGACGC TTATACGACA AGCCCCACAC ATACCGGTGC CATCCACCAT	300
	AATTGTATTG AGAGAAGCTA TGGTCGGTAT CTCGTAACGT TTGGTCAGGA GAGAAACGAA	360
15	CTTCATCATC ACAGCCGGCC CGATCGTAAC GCAGAGGTCT ACCGTTTCCC GTTTGATAAC	420
	GCTTTCCACT CCATCCGTTA CGAGGCCCTT CGTCCCATAA GACCCATCGT CTGTCATGAT	480
	GATCATTCA TCGCTATTGG CTCGCATTGG TTCTTCRAGG ATAACCAGAT CTTTAGTTCT	540
	GGCAGCCAAT ACGACAATTA CACCGTTGCC TGCTTTGTGG AAAGCCTCCA CGATCGGGAG	600
	CAAAGGAGCC ACACCCACAC CGCCTCCGGC ACAAACTACT GTGCCGACCT TTTCGATATG	660
20	CGTACTCTGT CCCAGCGGAC CTACCACATC CGTGATATAG TCGCCGACTT CGAGTTCGGC	720
	CAATTTCTTG GAAGATTTGC CCACGGCCTG AACCAC	756

(2) INFORMATION FOR SEQ ID NO:108

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

30

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

40

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...2370

45

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:108

50	CTCTTGTTTT TTCTCCTTT ACCCGGAATG GATCGTCTTA AGCCTTCATA TATTGTTGGA	60
	ATAGCAGCCA TTCTCTGCTT GTTTGTGCGC AGGCCTTTGT TTGCGCAGAG CTATGTGGAC	120
	TACGTGATCG CCGTATCGCG GACGCTAAGT TCTTTTGAGC TGAGTGCGGG CAATACCTAT	180
	CCGGTGATCG GTTTACCGTG GGGAAATGAAT AGCTGGACAC CGATGACCGG TGTACCCGGT	240
	GACGGCTGGC AATATACCTA CTCGGCACAC AAGATTCGCG GATTCAACA GACCCACCAA	300
	CCCACTCCTT GGATCAACGA CTACGGCCAA TTCTCCCTTC TTCCCTTAC GGCACCGCAG	360
	AAGCCATCAT CGAACGACTC CATAGCTCTG ACTAAATGGT GCAAGCAACT CTTTTCGGAC	420
	GAACAGACCT CGTGGTTCTC GCACAAAGCG GAGACGGCGA CGCCATACTA TTATAGTGTC	480
55	TATTTGGCCG ATTACGACAC ACGCGTGGAG ATGGCTCCGA CCGAGCGTGC AGCTATCTTT	540
	CGCATACGTT ATTCCGGCAA TACCGAAAGT GGCTCCGGTC GATGGCTTCG TCTTGATGCC	600
	TTTACCGGTG GTTCGGAGAT TAGCATCGTG GATCCTCACA CCGTAGTGGG CATATCTCGC	660
	AAGAAATAGCG GAGGTGTGCG GGCTAACTTC GCCTGTTATT TCATCTCGCA GTCCGATACT	720
	CCTATGGCCG ATGTCTGTCT TGAGACAGAT ACCGGCPAGT CAGACGAAGG CACAAGGGCA	780
60	TGGGCAGCCT GTCCGTTGCA TTCGCAAGAA GTTACCGTCC GGTGGGCATC TTCTTTTATC	840
	AGTGTGAGGC AGGCCGAAAG AAATCTTGCG GAAGTCAAAG GGCAGAGTTT CGACCGGATC	900
	AGACTTGCCG GTCGCGAAGC TTGGAATAAG GTGCTCGGAC GCATACATGT GGAAGGAGGA	960
	ACGAAGGATG AGCGCACTAC ATTCTATTCC GCACTCTATC GCTGTCTGCT TTTTCCCGCT	1020
	CGCTTCTATG AGGAGGATGC TTCCGGCAAT TTTGTGCATT ACAGCCCTTA CAATGGAGAG	1080
65	GTACTTCCCG GTTATCTCTA TACCGATACC GGAATTTGGG ACACITTTTC AGCCCTTTTC	1140
	CCCTTGCTCA ATCTGCTGTA TCCCGATGAA AACATTAAAA TTCAGGAAGG TCTGCTGAAT	1200
	GTATATCGCG AGAGTGGCTT TTTCCCGGAA TGGGCCACTC CGGGCCATCG GGATGTATG	1260
	ATAGGCCAACA ACTCTGCTTC TGTTCTGGCG GATGCTTACC TCAAGGGGTG TCGGGTAGAA	1320
	GATACCCGTA CACTGATGAA CGGACTCTTG CATGCTACGA AAGCCGTCCA TCCGAAATC	1380
70	TCCTCCACGG GTCCGAAAGG TTGGGAGTGG TACAACCTCT TAGGTATATG TCCGGCTGAT	1440
	GCAGGCCATG ACGAAAGTGC TGCCCGTACG CTCGAATATG CTTATAACGA TTGGTGCATC	1500
	CTCCGACTGG GGGCCACATT GGGTTGGGAT AGAGCTGCAT TGGACACGTT GGCTCATCGT	1560
	TGATGAACCT ATCGTCATCT GTTCGATCCG GAAACCAAC TCATGCGCGG TAGAAATCAG	1620
	GATGGTAGTT TCCGGACACC TTTTCCCTT TTCAAATGGG GAGATGTATT CACGGAGGGC	1680
75	AATGCCGTCG ACTACACTTG GTCCGTCTTT CATGATGTGC AGGGGCTTAT CGACCTGATG	1740

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

74 / 490

5 GGAGGAGATC GCGCGTTCGT GTCTATGCTC GATTCGGTAT TCAATACTCC TCCTATGTTC 1800
 GATGAGAGCT ATTACGGATT TGTCTATCCAC GAAATCAGAG AGATGCAAAAT AGCGGATATG 1860
 GGCAATTATG CTCATGGCAA TCAAGCCATA CAGCATAIGA TATATCTGTA TAATCATGCC 1920
 GGTCTATCCAT GGAAGGCTCA GGAGAGACTA CGCGAAGTGA TGGGGCGGCT CTATCGTCCT 1980
 ACTCCGGATG GGTATTGCGG CGATGAAGAC AACGGACAGA CTTCGGCTTG GTACGTTTTC 2040
 TCTGCTTTAG GCTTCTATCC TGTACACCC GCTACGGATC AGTATGTGCT CGGTCGCGC 2100
 ATTTTTCCTA AGGTAATACT CTCTTTCCC GACGGACACA AAACGGTGTT GCATGCTCCG 2160
 GCCACAGTG CCGATACGCC TTACATCCCG TCGATCAGCG TAGAAGGAAA AGAATGGAGC 2220
 TGCAATTACC TGACTCAGCA ACAGCTTCGC TCTTCTGCAT CCAATCAATG GATGATGGAC 2280
 10 ACGAAACCCA ATTATAATCG TGGTATGAAG GAAAGTGACA GACCTTATTC CTCTCCAGC 2340
 GAGCAACAGC GTCGCGCTAA TCACAGTAAT 2370

15 (2) INFORMATION FOR SEQ ID NO:109
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 858 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...858
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109
 40 ATTTGTGGCA GTAAATGAA TCTATCGGGA TTACAATCTT TCACTATGAT GAAATCCATG 60
 CGCAGCGTGC TGTGCTACT CTTTCCATTG TCTTTGATCA CTGCTTTGGG CTGTAGCAAT 120
 AACAAAGCTG CCGAATCGNA GTCTGYCTCT TCGATTCCGG CCTATCTCGA ACGCTACATC 180
 CCTCTGCGGG CAGACATAGA TACGCCATCG CTGCATGTGA TGATCAGCTA CGTCTATGCT 240
 TCGGGAGATG ATATGCTCAC AGAGATTTTC AACGGTTTGC TCTTCGGCGA CAGCCTGATG 300
 GATTCTCTTT CCGCGGAGAA TGCCATGGAA GGCTATGCAC AGATGCTGGG AGAAGACTAT 360
 CGCTCTAACA ATGCCGAAGC CAATCTGCAA GGGCTTCCTT CTGACCTTTT GGACTATATC 420
 TACAAGCAGG AAAATACCAT CGCTTATTGC GATACGGGAT TGATCTCCAC GCGCATCAAT 480
 45 ACATATACTT ACGAAGGCGG TGCCATACCG GAGAATACAG TCCGGTTTGC CAACATCCTT 540
 CGCACCCCG GCAAGGTGCT CGAAGAGCGA GATATATTCA AGATCGACTA TCGGGAAGG 600
 CTGTCCGCAC TCATCATAGG ACAATTGGTG CACGATTTCC GCAAGACCAC ACCTGCCGAA 660
 TTGGATGCAA TAGGTTTCTT CAACGCAGAA GAAATACAGC CCAATGGCAA TTTTATGATC 720
 50 GATGACAAAG GTCTCACATA CTGTTTCAAT GAGTATCAGA TAGCTGCTTA TGCCAGAGGT 780
 GCTGTCTATG TCCGTCTCGG ATATGACGTA TTGGCTCCTT TGCTAAGGGA TGATTCGCCA 840
 CTAAGCGTT ACTTGCCG 858

55 (2) INFORMATION FOR SEQ ID NO:110
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1134
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110
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WO 99/29870

PCT/AU98/01023

75 / 490

5 GGGATAATAT CTGTTCTTTC ACATGTGGTT GACCGTCCAC AATGGGGTGC TTCTCCCGAA 60
GCTGCTGGCA CGCATAGTGT GTATTGCAAT CTACATCCCT CGCCCGGTAT TATCCGGATC 120
AGGTCTATGG GTATTATCTC AGCCTGCCGT ATCGCAATTC TTGCCGGCAA GCACCCCGCT 180
AGCGTCTGTG CGAGGGGCAA TGTAGGTATT CTTTCGTACA ATCCAGAAA CACGCCCGAG 240
AAAAAGAGAA AACTGCAAGA AAAAATGTT TTCCTCCAAA TCCGGCTCCG TCAATCATT 300
AATAATTGA TACCTTCGCT CCCATTAGA ATCGATAACA CAAAAAAT CACTGAAATG 360
AAAAAACTA CTTTGACAGG ATCGATATGT GCTTTACTCC TGTTTTGGG TCTCTCGGCC 420
AATGCCCAAT CGAAGTTAAA GATCAAGAGC ATTGAGGCAG CTACCACTT CAGTTCGGCC 480
ACGGCCGAA ATGGTTTGG TGGCAATATC TTCGGCATGG ACATGAGCAT ACGGATGAGG 540
GTACACCACA GCATTCTGCC CGAAGGGTGG GATTTTTCGG TAGGAATACA TGAAAGAAGA 600
GCACACTGGG AAGAGGCCGG AAGTCCGAAG CTCATGTATA CGAATGTCCC AAGTATCATT 660
GGTATTGTTG AAAAGGTAAT AGTCTTCGAA GACGCAGAAG ACTTTTGA CAAAAAGCT 720
CTCGGCCGCT TCCTCATCAG TTTCGGGATA TCCTATACCA AGCATCTGGG AGCGTATTGG 780
GGATGGACCA ATGACGCCCA TATCTTTTC TCACCGATAC CCAAGAGCAA GGTCCACTAT 840
GACACCTACA CAAGAGCTGG CAGTGACCTT GTACTTCAGT CCGAAGATGT TGCCACAGTG 900
AGCAATGGT TTTACCGGG GATCGGACTC AAAAGTTCTA TTTGGTGGAA AATGCCCATC 960
AAGAGCAAT ATGATTTTCG CCTCGGTTTC AGCCTGGGCT ATGAGTATCT GAACCTGCTA 1020
TATCCGTATC GTAAATTTCAA GCTGGATGGA AATAAGCCGC TTTCAGCACT ATCTCTCGC 1080
20 ATGAACCACA TCGGCCATGT GGCCTTCAAC TTTACCGTGG GTCTTTGGAC TAAT 1134

(2) INFORMATION FOR SEQ ID NO:111

25 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3807 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
30 (11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
35 (1v) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
40 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...3807
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

45 GTAAATGTA TGGGCAAGTA TAAAGAGCT AAGTACCGCT ATTGGCTTTT TCCTTTCTGT 60
TCGGATTATT ATACCTTTGA GGGAGTTACT TTTTATGCG CATCTGACGA TATGACAACC 120
AAGAAACCCC AAGCCATTTT AGACTTAGAG AAGGCCTATA ACATTGAAAT TCCTGATCTC 180
TCCTCACAA AAGGGATAAG CTGCTCGGTA AATAGATATT TCAAGCAAGA TTCCTCCGGT 240
50 GCAGTCTGTG AGCTTTGCTT GCGAGAATGT CAGATAGAAA GCATGACTTG GCTTATTGAT 300
TTTCCTGCTC TAAAAAGCT TGATCTATCG TATAACCAAA TCAGTAAGCT AGAGGGTCTA 360
GAACGTCTTA CTGTTTAACT AAAACTTCGT CTAAGTAGTA ACCAAATCCG TAACTAGAG 420
GGCCTGGATA GTCTCACCTC GCTAACAAA CTTTCTCTCT CCGATAACCA AATCAGTAAG 480
CTAGAGGGTC TGGAACTGCT CACCTCGTTA GCGGAGCTTT ATCTTTTGGG TAACCAATC 540
55 AGTAATCTAG AGGGTCTGGA ACGTCTCAGC TCCTTAGCAA CGCTTGAATC ATCGGGTAAC 600
CAAAATCCGT AACTGGAGGG TCTGGAAAGT CTCACGTCTC TAGCAACGCT TGAAGTATCG 660
GGTAACCAAA TCCGTAGCT AGAGGGTCTG GAACGTCTCA CTTCTTTAAC AAAGCTTCGT 720
CTAAGAAGTA ACCAAATCAG TAAGCTAGAG GGTCTGGAAC GTCTCAGTCT CTTAGCAACG 780
CTTGAACTAT CCGGTAAACA AATCCGTAGG CTGGAAGGTC TGGAACTGCT CACCTCTCTA 840
60 GCAACGCTTG AACTGTGGGG TAACCAATC AGTAAGCTAG AGGGTCTGGA ACGTCTCTCT 900
TCGTTAACA AACTCTCTCT AAGAAGTAAC CAGATCAGTA AACTAGAGGG CTTGGAACGT 960
CTCACCTGCG TAACAAAATC TTCTCTCTCC GATAACCAAA TCAGTAAGCT AGAGGGTCTG 1020
GAACGTCTCA CTTCTTAGC GGAGCTTTAT CTTTGGGATA ACCAAATCCG TAAGCTGGAG 1080
GGCCTGGAAC GTCTCACCTC GTTAACAAAG CTTCTCTTAA GAAGTAACCA AATCAGTAA 1140
65 CTAGAGGGCC TGGATAGTCT CACCTCGCTA ACAAACCTTT CTCTCTCGA TAACCAATC 1200
AGTAATCTAG AGGGCTCTGA ACGTCTCAGC TCCTTAGCGG AGCTTTATCT TTTGGATAAC 1260
CAAAATCCGT AACTGTGGGG TCTTGTGGT CTTGCTTCTT TAACAAGGCT TAGTCTAAGG 1320
QSCAACCAAA TCAGTAAGCT GGAAGGACTA GACAGACTAA AGGTTTGGAG AAACTTGAT 1380
70 GTTTCGGGCA ATGATATCA ATCTATTGAT GATATTAAGC TATGGCTCCG GATTCTGGAG 1440
CAAACTTTAG AAAAATGAG AATCCATGAC AATCCATTTG TTGCATCATC AGGCTTGATA 1500
CTCTCTCTCT ATGATAATCA TTTGCCGGAG ATTAAGCTCT TTCTTGAATA AGAAAAAGAA 1560
AAACAGAAAA AGACTTCAGT TGAATATCAC CCATTTTGCA AAGTAATGCT ATTGGGAAT 1620
CATCTCTCGG GTAAACCAAC ATTCTTAGT CAATACGATA CAAATTATAC GTATCAGAAA 1680
AATACCATG TGTGTGCGAT ACATCGAAGC AATAACCCTA ATGCGATCTT TTACGACTTT 1740
75 GGGGGACAGG ACTATTATCA TGGGATTAC CAAGCTTTT TTACCACCCA ATCGTTATAC 1800

WO 99/29870

PCT/AU98/01023

76 / 490

CTTCTCTTTT GGGATGCTAA GAAGGATCGA AACTTTGTGA GCGTAGATGA TAAAGAATAT 1860
CAGACTCTTA ATTTCATCG CCCCTATTGG TTAGGACAGA TAGCCTATGC CTGCAATCGT 1920
TGTATGTCGG TTGGAGGAAA TCCTGATGGC AAGGACACAC CACAGACCAC AGACGATACA 1980
ATTATCATTC AGACTCATGC CGATGAAACG GCGGCTAAGC AGCAAACTT AGGCTGTGCA 2040
5 GCGGAGAAATG GAGTATTGGA AGAAATCTAT GTATCCTTAG AGCCCAAGGC GAATAGTGCC 2100
GTACATGCGC TCAACTATCT GAATGAGCGG GTGCGAGAAG TTGTCGCAAG CAGGAGTAAA 2160
TCAATTGAGA TCACAGAAAA AGATAAGGGA TTGTACGAAG CTCTTCCAC AATCGCCGGT 2220
GATAATAAAC ACATCCCTAT CTCTCTCGAA GCTCTTGGG CTCMAATTGA TAAGGGAAGA 2280
GCTGAAAATG ATCTTTACAC CATAGAGTAT CTACAGACCG AATTGAACCA GCTTAGTCTG 2340
10 CCGAGGGGAGG TGCTTTACTA TCGTGAGANT GAGAAGCTGA ACAATTATGT CTGGTTAGAT 2400
CCGGCAGCTT TTGTCCAAAT GATTCAATGA GAAATCCTCC AAAAAGACAA CATCAATAGA 2460
GGAACAGTTC CTAAAGACAT TTTTGAATGC AAATGCATA ATCTAAGTTC CGGAAGTATA 2520
TTTGAAGAAG ATGGCCAAAA TGGAATATG ATCTTGACGC TATTATTGGA AGAGCTGATC 2580
GTATATGAAG ATAAGGACTG CTATGTGATA CCGGGCTATC TCCCTTTGCA TTCCGATGAC 2640
15 GAAGCCTATA AATGGCTTAC TTTGGGATTC GAGAGGCCCA ATTTGTCTCT CAAATTGAA 2700
CGTTTTATCC CTTTTGGCCT GATCAACCAG ATTATAGCCT ACTATGGCCG GGAAGAAGGT 2760
GCTCTAAGC GGTATTGGCT AGATCAGGTC ATCTTACAG CAGGCGGTGA GATGGATAGG 2820
CAAAACGCTTG AGCAAGAAGA AGAGAAGAGG GGTTTGCCCA AGACGAATGC CGAGGATTAT 2880
CAGATCTGGA TCAAGCTCGA CTTTACCGAC TTGGCCATAT CCGTATTCAT CAAAGAGCAG 2940
20 AGAAAGACAT CAGCTAAGGA TATGCAGCGG AAAGAGGCTA CTATCCTCAG TGATATGTTG 3000
GATATGATT GGAACAATAT CCCTCCGAGG GAGCAAAATG GAGATAAGGA TACGGAGCAA 3060
ACGAGAAGCA CTATTCTGTA AACAAACAGA AAGAAGAGAC CCATCCAGGA TCTCTACCTC 3120
TCCTGTGCCA AAGCGGATAA AGATTGACG GAGTCTCATT ATATCCATTT GGGCAGCCTG 3180
GACGATGAAA GCAAGACTAC GCGGAGGATT SCAGCCTATC CTTTGAAGAA CGGCGTTATC 3240
25 GATAAAGAGC GGGTGGGAGA AGTATCGACT CGTCCCTACA AACATCTTTC CGTCAATAAA 3300
AATCTGGCTA CTGCAAAACA GATCTTTATT TCCYATTCCA AAGAGGATCA GACTGAACTG 3360
GAGACCTGTC TGCAATTITT CAAACCCCTG GAGAAGAATG GTCAGATCGA GATCTACTAT 3420
GATAAGTTGA CTAAGTTTGA AACACCTATT CACCTGAAA TAAGAAAGCG TATGTGCGAA 3480
GCGGACTGTA TAATCGCTTT GATCAGCCAA CGCTATCTGG CCACGGATTA CATCCTGGAT 3540
30 CATGAGTTGC CTGTATTTCG GGAGTATAAC AAGACCATAG TGCGGATATT GATCAAGCCT 3600
TGTCATTTG AAGACGATGA GTTCTTCCG GAGAAATATT TTGCTCAGAA AGCTCAAATA 3660
ATCAATCTTG GAAAGAGGG AAAAACCATT AAGCTTATG ATAGTATTAC GGCATCAGCC 3720
CATCGTGATG AAAATTGGGT GGCAGTAGTC AGAGAGTTCA AAGAGAAGAT ATTAAGAATA 3780
35 ACAAACAGG AGGTAAATAC AGATGAA 3807

(2) INFORMATION FOR SEQ ID NO:112

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 693 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
45 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
50 (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
55 (A) NAME/KEY: misc feature
(B) LOCATION 1...693
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

60 AAGTTTATGA TGA AAAAAGC ATTTGTTTC GTACTACTGG TTTGCCTATT CTCTCGTTC 60
AGCAGTTCCG CCCAAACAAC GACGAACAGT AGCCGGAGTT ATTTTACAGG ACGAATCGAG 120
AAGGTGAGTT TGAACCTAGG GGTCCCCCCC GTAAGCACAG AGGTTTGGGG AATGACCCAT 180
GATGCGAAGG GTCTCCCTTT CGAAATACCT ATCTCTTTCA GTCTTTTCAA CAGCCAGGGA 240
GATATAGCTA CCACTTATTA CATAGCSAAT AGCGAGGCAA CTTTGAATGA ATGGTGGGAC 300
65 TATGCACACC CGGGCGGCAT CGTAGSGGTA GAGGTCGTT TTTGAAATAT GACTTACAAC 360
ATACCAACCT ACAATGCAGT CTGCCCCCGG ATTACATTGG AAAATCAAGA AATAGAAGGA 420
ACGATCGTCT TGATACCCAA GCGCAAAAGTC TCGCTGCCTC ATGTGTGCGA ATCGGTGCCT 480
TGCTCCGAAA CCGAAGCCCG GAGGGAATTT ATCCTTTGCG AAGAAGACGA CACTTTGTG 540
TCTCAGATG GTAACGAAGT AACGATAGGC GGTAAACUUT TCTTGCTCAA TACCAACGTA 600
70 AAGATTGTGG GGGACGTATC TCAAAAGTAT GCCGTGGGGG TAGGAGAAAT TCGATTCTCTG 660
CAGATTTTGTG CCCAAACAGT ATCACAACAA AAA 693

(2) INFORMATION FOR SEQ ID NO:113

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WO 99/29870

PCT/AU98/01023

77 / 490

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1689 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1689
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113
- | | | | | | | |
|------------|------------|-------------|------------|------------|-------------|------|
| TCGCTAATCA | ACAAATTCAG | AGACTGGAGG | GCTCCTGTCC | GATTGAGTCT | CAAAAAAAG | 60 |
| ACAAAAACTA | TGAAGACAAA | AGTTTACGC | AAATTCGTGG | TGGCGGCTTT | CGCGTCGCA | 120 |
| ACCTCTGTGC | CTCTCGCCCA | AGCGCAGACG | ATGGGAGGAG | ATGATGTCAA | GSTGGTCCAG | 180 |
| TACAATCAGG | AAAAACTGGT | ACAAACGAGG | ATGAGTGTGG | CGGACACCGG | ATGGATCTAT | 240 |
| GATTAACCCC | ACAGTGGATA | CGACACCGGC | AATAGCAATG | TGAAGATCTT | CCGCTCCAAA | 300 |
| GACCAAGGTG | CCACATACCA | AAAGTTGAGG | GATTGSSATC | CATCGGATGA | TTATCAGTTT | 360 |
| CAAGACTTCG | ATATCGTGGT | AACGGGTAAAG | AATGAATCCG | ACATCAAGAT | TTGGTCGGTA | 420 |
| GAGCTCATGA | ATAAGCCCCG | AGGATATAAG | AGTAGAGTTG | CGGCTTTCAG | TCGCGATGCC | 480 |
| AACGGCGAGA | ATGCGAAACT | CGTGTATAAG | CAAGACTTCT | CCAATGTGCA | GTTGTACGAT | 540 |
| GTGGATATAG | CCTCCAACTA | TCGTTCCGCT | TCTTCTCTTA | ACAATGGTGG | CAACCCCTTTT | 600 |
| GCTTTGGCTT | TCGCTTACAC | CGGCTTCAAC | AATACGCACA | AAATAAGTTT | TGTGGACTAT | 660 |
| GTGTTCTCTC | TGAATGGAGG | GCAAAATTTT | AATAAAAACT | TACTCTTCAG | TCAAGATGGA | 720 |
| GAGAAGAAAA | TTGACAAGGT | GGATCTCTCA | TTGGGTAGCA | CCTCTGAATC | CATGGGTCAC | 780 |
| AATGCTTGGC | CGCTAATGGG | TGTGGTATTC | GAAATGAATA | AACAAGGGGG | AAAAAGCGAT | 840 |
| ATCGGTTTCT | TGTCGAACCT | TGTGACAAAT | GATCCCGAAT | TTCAAGTGGT | AGGCCCTATA | 900 |
| AAAGTGAGTG | AAAGCGACAT | GTCGTTCCAG | CCCAAAATCC | AAATGTTGCT | GGACGAGGAT | 960 |
| AACAATACGA | TCAATGGGGA | GAGTTGCCAC | AACTTCAATG | TTACGTACAG | CGATTATGAT | 1020 |
| TCTGAATATT | CGGATTGGGA | CATTGGGTAT | GTATATCCCA | AGAAATCGTT | CAAGTATGAA | 1080 |
| AAAGGAAAAA | CTCCGACTAT | GGATGATCTG | GTGGAGGCTT | TCCTTACAGC | TTGCTACCCG | 1140 |
| AGTGAGACCA | ACTCGGGGCT | GGGTATGAC | AAGAAGGCCA | ATCACTACCT | GATTACATAT | 1200 |
| GCCAAVAAAG | AAGAGAACGG | TACGAACACG | CTGAAATACC | GCTGGGCCAA | TTATGACAAV | 1260 |
| ATTCATAACA | AAGATTTGTG | GAGCGACACA | TTACGTATA | CATCATCTGC | CAATGCTCTC | 1320 |
| TACACACCTC | AAGTAGACAT | CAATCCGACC | AAGGGTCTCG | TGTGCTGGTC | ATGGGTGGAA | 1380 |
| TATCTGCCGG | GCAAACGGAT | CGTTTGGTCT | GATACGCAGT | GGACCATATC | CAACGGTGTA | 1440 |
| GAAGACATCG | TAATGCCAAG | AGGCAGCATG | AAGCTCTACC | CGAATCCGGC | TCAAGAATAT | 1500 |
| GCTGTGATTA | GCCTGCCGAC | GGCAGCAAAC | TGCAAGGCTG | TTGTTTACGA | TATGCAGGGC | 1560 |
| AGAGTAGTCG | CTGAGGCTTC | TTTCTCGGGC | AACGAATACA | GGCTGAACGT | GCAGCACTTG | 1620 |
| GCTAAGGGTA | CGTACATACT | CAAGGTCGTA | TCCGATACGG | AGCGTTTCTG | AGAGAAGCTC | 1680 |
| ATCGTGGAA | | | | | | 1689 |
- (2) INFORMATION FOR SEQ ID NO:114
- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2358
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

WO 99/29870

PCT/AU98/01023

79 / 490

5 GCGGAGCTAT TGCCTCTCTC CTCGCGCGAT TCACGACTGT ATGTGACGGA TCGTGGTCTG 900
TTCATCTGTG CCGAGAATCG AATTTATTTT ATAGAAAAAG CTCGCAAAAC GACACAAATT 960
CCTATAGCCG ACGTCTCTGG TGTGCGTGCC ATGAACGAA GCAATAOCCG ATACATAGCA 1020
TTGGGAGAAG AAGSTTTGGC TTCCTTTCTT CTCGCGAGAG GAAGTACGCC CGAAGCCATG 1080
10 CCTGTAGCAT TCGACGGACC GGGGGACAAT GATTTCTACG AGATGCGGTT TAGTCAGGGA 1140
CGTCTGTATG CAGGACGCGG ACTCTGGGGA ACAAACCTGA TGGGACATGC CGGTATGGTG 1200
AAGCTATACG ACGGCAACCG ATGGACTAAC TTCGACAAGA AGACCGTACA GGAACAGTTG 1260
GGCGGCGGAT TCAGTTTCAA TGATGCTATC GATATAGCTG TTTCCAAACG AGACCCCGAT 1320
CACTTTTCTG TCGGTACATG GGGAAACGGT CTGTTGGAAT TCAAGGATGG CAAAGCGATA 1380
GCTCGCTATT CCGGAAACGA AACTGCTATC GCAGAATGTA ATCCCGGAGA TGCCCGTGTG 1440
15 AAAGCGATTG CCTTTGACAA TAAGGGCAAC CTCTGGGGGA CGCTCGGTGC CGTAGGCAAG 1500
AACATCTTCA TGTACGATCC GCAGAGTAGC ACATGGCAIT CTTCAGCTA TCCGATGTA 1560
GCCATCTGCG CCTCTCTCGG CAATATGATT ATCCTACCCA ACGGAGACAA ATGGGTAAAT 1620
ATCCTTCACC GTAGTGGCGG ATCCACGCGC AAAGGTGTCT TGATCTTCAA CGATCGGGGT 1680
ACACCGGAAA CGACTTCTGA CGACAGCCAT CTTTACGTCG AGCAGTTTGT CAATCGCCTC 1740
20 GGGGAGGAAA TAGGACATAA GACTATCTAT GCAATGGCCG TCGATCATAA CGGCTCTGTC 1800
TGGATGGGAT CCGATATAGG CATTTCGGGC GTCTACAATG CAGCCGGAGT ATTCTCCTCG 1860
ACTTCTACCC CTATCGCTGT TCGCCCGGTC GGAGGAGAAG AACCCAAATT GTACTATGTG 1920
CTGGACAAAG TGACGGTGAC AGACATCGTC GTGGACAAAC TCAATCACAA ATGGGTTGCC 1980
ACCCAAAGGA CAGGACTCTA TCTCCTTTCC GAAGATTGTA GTAAGATCCT CGCGCAATTT 2040
25 ACGGTAAGAA ACAGCCCTTT GCTTTCTAAC AACATACTAT CCCTGGCCTT AAATGACGAT 2100
AACGGACTGC TGTACATCGG TACGGCGGAC GSACTGATGA CGTTCCAAAC GGSTACGGGG 2160
AGTGGATCAG CTTCCGAACG GGACGGCGTC TATGTATACC CCAATCCGCT AAGGCCGGAA 2220
TATCCCGATG GCGTCACCAT TGCCGGAGTG CAAGCCGGCT GTAGTGTCAA AATCACCGAT 2280
ACCAACCGCA GACTGCTATA CCACACTGAG AGCGTAACCA CCGAAGTCAA ATGGAATGCT 2340
30 CGAGGTGCGG ATGGCAATAG GGTAGCTTCG GCGGTATATG CCGTTGCACT GTACGATCCG 2400
GTATCGAAAA AGTCCAAACT AATTCGCTTC GCAGTGATTC GC 2442

(2) INFORMATION FOR SEQ ID NO:116

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3486 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO
45 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
50 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3486
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

60 GCTATTCTC AGATGAAACG AATACTTCCA ATAGTCGGAT TCCTTTCTCT CTTCCTTGCC 60
CTTGCTTTGC CTGCGAAGAC GCAACGAGCT ATGGGGAAGA CGGCCGACCG TTGCTTAATG 120
GCTTCGGGAC ATTGGGTCAA GATACGTGTC GATGCAAGTG GAGTGTATCG CCTTACGGAC 180
GAACAGCTCC GTGCCAATGG CTTCCTCGAT CCGTCCAAAG TAGGTGTGTT CGGTTATGGT 240
GGAGGGGTGC TTCCCGAAGA TCTGAGCCGG ATCAGCAGAG ACGATTTGCC TCCGGTACCG 300
GTACTCCGTC AGGGCAATGC GCTGTATTTT TATGCCGTGG GCCCGGTGAC ATGGTTCTAC 360
AATCCGGCCA AAACCAACAT GGAGCATACG GTGAATACAT ACAGTACGCA TGGCTACTAC 420
TTCTGTGCGG ATGCTGCCGG AGCACCTTTG CAGATGTCTT AATATACGGG TGGAGGTGCG 480
65 TCGGCCGAGG CTTTGATCGA CTACTACGAT GAGCTGATTC TCCATGAACA GGAATTGTAT 540
TCGCUCAAAG AATCGGGACG AGATCTGTAT GCGSAGTCTT TCASTGCCGT CAATACCGGT 600
ACGOTCAAAT TCCCTTTGAG GGGCAACACC CGTGTGCTG GCGAACTCGT TACCGTATTC 660
TCATACATAG CCAAGGCCAG ATCGGCCGGT GCGGCGCTG AGATGTGCTC CTGCGCGAAT 720
GGCATTCTGA TCTTACGCGA TCTTTTTC ATGACATGSA ATGAAGTCTC CAATTCTAT 780
70 TTGGCGCGCA AGAAGCGTGG TCTCTATCAC AGTACGCCGA TGAACAGCTT GGTCAATGAG 840
TTGCGCTTGG ACGCGAACTA TAGCATGACA GGAGATGCGG TCAATCTGGA TTTCTATAGAG 900
GTGGCTACAC AGAACGACCT CCGGTACGAT GGCGCACCZA TGCATATCAG GCGGTTTTC 960
AATTGCCCCG TTTTGGGGGG CGAGTCTGTC CGGTTCTGTA TCAGTGAGGT GCGGGAGTCT 1020
75 TTGTTGGTTT TGCAGGCCAA TTCTTCCCTG ACAGCATCGC TTGTTCCGCT TAAGACTGTC 1080
GGGGATAAGA CCATTGAGTT CGTGGCTCCG CCGAAGGGTC AGGATCGTAG GACTATCAAT 1140

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

80 / 490

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ACGTTTATG CCGTGGACTT GTCACAGGCT TCTGCTCCGG AGATCCTCGG AGCGGTACCC 1209
AATCRAAACC TGCATGGAGA GGAAATCCCT GATCTGATCA TTGTCTCTAC TCAGGCGCTC 1260
CTCCTTGAGG CTGATCGACT GGCCACCTAT CGTAGAGAGA AAAACGGGCT GAAGGTTTGG 1320
GTCTGTGTGC AGGAACAGGT GTTCAACGAG TTTTCGGGTG GAACTCCCGA TGCTACAGCA 1380
TACCGCCTCT TTGCCAAAT GTTCTACGAC AGATGGAAAG CAAATGCACC TGTGGGAGAC 1440
ACCTTCCCGA TGCAAAATGCT TCTCTTCGGT GATGGGCTC ATGACACAG GAAGGTCTCC 1500
GTAGCTTGGC AGAAACCGTA TCTCCAACAA ACGGAGTTCT TGCTGACATT CCAAGCCGTC 1560
AATTCCGAGA ACGTAAACAG TTATGTGACG GATGATTACT TCGGCTTGCT GGATGATCAG 1620
CCGGCCTCGG TCAATATCGG TTGGCGCAAT TATAATATGG CTGTAGGGCG ATTCCCGGTA 1680
CGTACTCCGG CCGAAGCTCG CATCGCAGTG GACAAGACCA TCCGATATGA GGAGGATCGA 1740
GAGAGTGTGT CCTGGCGTAT TCGTGCTGT TTTGCGGCGA ACAACGGGGA CAAGCAOGCA 1800
ACCGAGACTT CCGGTTTGAT CGATACCGTC AAGCGTTATG CTCTGCCAT CATGCCGGTA 1860
CGCGCCTTTC AGGACGTATA TCCGCATGTC ATCGAGAACG GGTTCACAG CATTCCGGGT 1920
GCAAGAAAA AGATGCTGGA AACCTTCAG TCGGTAITA TCCTGCTTAA TTATGCTGGT 1980
CATGGCGGTC CTGCGGATG GTCGGACGAG CATTGTCTGA CGCTCAACGA TATACACAAA 2040
TTCAATATA AGCATATGCC CATTGGATT ACTGCCACGT GCGACTTTGC CAACTATGAC 2100
AGTCAGAGA CCTCGGCAGG GGAGGAGGTT TTCCTCCATG AGAAGAGTGG CACTCCGATC 2160
ATGTTCTCGA CTACGCGTGT CGTTTACAA ACGCAGAAAT AGAAGATCAA TGGTTTTATG 2220
CTTCGGCGTA TGTTCGAGAA AGCTAAGGAT GGGCGTTATC GTACGATGGG CGAGATTATC 2280
CGATCGGCCA AACAGGGGAT GCTCAGTACT GTTTTCCCGG ATTGATCAA CCAGTTGAGT 2340
TTCTTTCTGA TGGGTGATCC GTCGCTGCGT ATGAATCTTC CTACCCACAA AGTGCAATTG 2400
ACCGCAATCA ACGGGCAGGA TCCCGAAGGG CAGTATGGAA CTATTATGCT CAAGTCTTTG 2460
GAACGGGTAG CTCTGAAGGG TAAGGTAAAC GATGAAAAGG GUAATTGCA CGAGACATTC 2520
AGTGGCAAGG TTTTCTCGAC CSTCTTCGAT GGCAGAAAGA AAATGCACG TTTGGAAGAG 2580
GAGGGAACG ATCTCTCTCT TGTATATTAT GACTATCCTA ACGTGATGTA TCCCGTATT 2640
GCCGAGGTGA AAGACGGACT CTTCGAAACT TCGTATATCG TACCCAGGA TGTGAACAT 2700
TCCGAGCCAG AAGGCCGGAT CAATCTTTAT GCTTATAACG AGAGCACAAA GCGCGAAGCC 2760
ATGGGGGTAG ACTTCTCCAT CAGAGTCCAA CCGGTTATTC CTGATGAGT AACGGAAGAT 2820
AATACACCGC CTGAAATCAT AAGCTGCTTC CTCAATGACA GTACATTCG ATCGGGAGAT 2880
GAGGTTAATC CTACTCTCTT GTTTATGGCC GAAGTATTCG ACTTGAATGG AATCAATATC 2940
ACGGGTAGCG GAGTAGGSCA TGATATTACG CTTTGTATCG ATGGCCGTGC CGAOCGTACC 3000
TACAACCTCA ATGCATATTT CACAAGTTCG GCTACGGATG CAGGTGTGGG CACTATTCTC 3060
TTCAATGATC CCGCTTTGGC CGAAGGAGAT CATACTGCCC GACTGACGGT TTGGGACATT 3120
TTCAATAATG CCGTCCATCA TGACTTTTCA TTGAGAGTGG TAGATGGCAT TCGTCCGGAT 3180
TGGGGTGATG TGATTCTATT CCGGAATCCG GTACGCGAGA GTGCTACGTT CCGAATCTTC 3240
CACAAATCCC CCGGAAGCGA TTTGAACGTG GCGCTGGAGA TCTATGACT CACCGGTCGT 3300
CTGTGAACA GTTTGCCAGT CAAGACCTAT TCGTCTTCTT ACGGAGAAC TATAGAGATC 3360
AAGTGGGATC TGACCTCCAA ATACGGAGTG AAGATCGGAA ACGGATTCTA CCTCTATCGT 3420
TGTGTGGTGA ACTCTCCCGG AGGACAGACG GCCTCCATGG CCAAGAAAAT GATCSTGGTA 3480
GGACAA 3486

(2) INFORMATION FOR SEQ ID NO:117

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2919 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

60 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...2919

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

TTTTACCCG GAATTGACTT GCATATAGAA AGCCAAATGA AGAAACTTT CCCATTATTA 60
TTACTCATAT TGTGATTTT GGTCCGATGT GGAAAAAAG AAAAACAATC TGTAACTGAA 120
ATCGCCCGAG AGAAAAAGCG TATTACTGCA TTGCTGTACG AAAAAGAACT CCCCACTGAT 180
TCTGTTAAAC AGCTTTACGA GAACAGCGTA CAGAACAGA ACCTTGTTGG ACAATGTGA 240
TTCGGGATCG AGGTCCGCAA ACGGATGCGT AATATGTCCC AATACACAGA TCGGATGCTA 300
TATCACCAAA AAGGTTGAA CGCTGCAATG AATCTAAGGG ACACCATCGT AGCCGCACAA 360
GCATGGAATC ATCTCGGAAC GGATAGCCGT CGTATCGGTG CTTTGGCAGA AGCTTCGGAT 420
TATCATTACA AGGCTCTTTC CTGTATAGAA TCTTTTAGCG GAAACAGAA TAGGCTCGG 480
ATCAAAGCCA GATCGGCGGC CCTGAACGCG ATCGGCACAA TCAATCTTGA GTTAGGATAC 540
CATGATGAGG CCGAAAAGAA TTTCTTGAAA GCACTGCAAG GTGAGAAAGA ACTCGACAGT 600

	CCTCTCGGGC	AAGCTATCAA	CTATGCGAAC	CTCGGACGTA	TCTATCGACA	ACGCAAGAA	660
	TACGACAAGG	CTCGTACCTA	CTTCCTCTTG	TCTCTGGAGC	AGAACAATAT	GGCAGAGAAT	720
	CTGATGGGTA	TCGGGACTCTG	TAGCATCAAT	CTCGGAGAAG	TAGACGAAGA	AAAAGGGGAT	780
	TATCAAAAGG	CTTTGCAAGA	GTATGCCACG	GCATACAAAC	TGATGGAACA	GTTGTCCGAT	840
5	CGATGGCACT	GGCTGAATTC	CTGTATCCCG	ATGGCACGTA	TCAATCTCAA	ACAAGGTAAC	900
	GAAAGGCTCT	ACCAGCATTT	CATTCTCTTG	GCGGAAGGGA	CTGCGAAAGA	AATTAATTCG	960
	ACTTCACATC	TGATAGAAAT	ATACAATCTT	CAATACGAGA	ATCTCGAGCG	TAAAAAAGAA	1020
	TACAAACAAG	CCCTCGAAGC	ATTCTGTCTG	AGCAAGACGT	TGAGCGACAG	CATGTCCATT	1080
	GCGCACAAGG	TCAGCAGCAT	ACAGAAACG	CGATTCAACT	ACGAACGAAA	CAACTCCCAA	1140
10	AAAGAGCTTG	AAGAAATACA	GCAAGTAAGC	AAGGCAAAAC	AAGAGAAATC	GAAGTTTATC	1200
	CTCTTGAGCA	CTCTTTTTCG	CTTTTTCATC	TCGATTCTTT	TGATTTCTGT	TCTGACATAT	1260
	GCATACCGTC	AGGGCAAGAA	GCATAACAAG	CTGATCAAAG	AGACGGATAA	ACTTCGCTCC	1320
	GGCTTTTTC	CCGGTATTAC	ACAGGAATTT	CGTAGCCCTA	TCACCGTCAT	ACAAGGTTTG	1380
	AATGAGAAAA	TGAGTTCAAG	TCCTGATCTC	CAAGCATCGG	ACAGAACCAG	GCTGCACAAG	1440
15	ATATAGACA	GACAGAGTAG	CCATATGCTG	AATTTGGTGA	ACCAGCTGTT	GGATATTTCG	1500
	AAGATCAGAA	GCGGAGTATC	CACGCCCGAA	TGGCGCAATG	GCGACATCGT	CTCCTTCGTA	1560
	CAGATTCTCA	TGCAATTCGT	TGCACCATAC	GCACAGGCTC	AAGACATAAC	CTTGGAGCTA	1620
	CAACCCGAGA	GCAAACTTAT	TGTCGTGGAC	TTCTGCTCC	CCTACTTGCA	AAAAATCATA	1680
	TCCAATCTTT	TGTCCAATGC	CATCAAGTAT	TCTTTAGCCG	GAGGGAGAGT	GGTCATATCT	1740
20	CTGGCAAAAA	CCAAGAAATGA	AAAAAATCTG	ATCATACGCG	TGCGAGACAA	TGGCATAGGA	1800
	ATAGATAAAA	CTGATCAGGC	TCATATCTTC	GACATCTTCT	ATCGAGGACA	GTCCGCTACC	1860
	GAAAGCATTG	GATCAGGCGT	CGGACTCTCG	TTTACCAATA	TACTGGTCGA	AAACCTTCGA	1920
	GCTACGATCA	AAGTGGAAAG	CCAGCCGGGG	AAAGGAAGTG	CUTTCACCAT	CAGTATTCCT	1980
	ACACAAAC	AGTCTCTTTC	GGCAGAGATT	CTTCCTTGGC	TACCTCTCTC	CGATGACATT	2040
25	GTCTGCTCGT	TCCACATCGC	GCCCGATGAC	TCACCGACAT	CTCCGNTGGT	AGCAGCTCTG	2100
	AATCATCGCT	TCGAGGACGA	ACGTCCGACC	ATACTGCTCG	TCGAGGACAA	TAAGGATATC	2160
	AACCTGCTCG	TCAAACTACT	CCTTTGCGAT	CGCTACAATG	TGCTATCCGC	CGCAAAACGGA	2220
	AAAGAGGGA	TAGCCCTCGC	TACCGAGCAT	ATTCCCGACA	TTATCATTAC	GGATATTATG	2280
	ATGCCGATAA	TGGATGGGAT	AGAAATGACA	ATCCGGATGA	AGCAATCGCC	TCTGCTCTGT	2340
30	CACATCCCA	TGTGCTCTTT	GACGGCCNAG	AGTACCGAAC	AGGACAGATT	GGTAGGAATC	2400
	AAAAGCGGTG	TAGTCTCTTA	TCTATGCAAG	CCATTCTCTC	CGGAGGAGCT	TTTGATGCGG	2460
	ATCGAGCAGC	TCTTGAAAGA	CCGTGAGTTG	CTCAAGAAAT	TCTATATGCA	AAAACCTCAT	2520
	CTGGATCGGA	AGCCGGAGGA	GGAGCCTCAA	CCGATAGATG	ACAGCAGTAT	GCAGTTTCTC	2580
	CTTGCTGCCA	AAGATGCAGT	GTCCGGTGGA	ATCAAAACAA	ATCCGGATTT	TTCCGCTCAA	2640
35	GACTTGCCCG	AAAAAATGTG	CATGAGTCCA	TCCCAACTCA	ACAGAAAGCT	CACGATGTGC	2700
	GTAGGTTGCT	CCACCATCGG	CTACATACAG	CAGATCAAGA	TAAATTTGGC	CTGCAAGCTC	2760
	CTTGCCGATG	AGAGCAAAAA	CATCTCCGAC	ATTAGCATTG	AGGCAGGCTT	TTCCGATCCG	2820
	GCTTACTTCT	CTCGCACCTT	CAAACGCTAC	ATGAAGTCTG	CTCCCTCCCA	ATATCGGCAA	2880
40	AAACTCTCTG	CCATGCCGGG	GAGCGACAAG	GAGACAGTT			2919

(2) INFORMATION FOR SEQ ID NO:118

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
- (A) NAME/KEY: misc feature
- (B) LOCATION 1...1689
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

65	CATCATAAAA	CATATCAAAC	AATGAAAAAG	CTTTTACAGG	CTAAAGCCTT	GATTCTGGCA	60
	TTGGGACTCT	TCCAATGCCC	CGCAATCGCC	CAAAACGCAA	TGCAAGCAGA	CCGAACAAC	120
	GGTCAATTTG	CAACAGAAGA	GATGCAAGCA	GCATTCCAGG	AAACGAATCC	CCCTGCAGGT	180
	CCTGTGCGTG	CTATCGCTGA	GTACGAACGC	TCTGCAGCCG	TTTTGGTACG	CTACCCGTTT	240
	GGTATCCCGA	TGGAATTGAT	CAAGAGCTG	GCCAAGAACG	ACAAGGTATG	TACCTTTGTG	300
70	GCGAGTGAAA	GCCAAAAAAA	CACCGTTATA	ACCCAGTACA	CCCAAGCGGG	TGTGAATCTC	360
	TCTAATTGGG	ATTTTCATCAT	TGCGAAAACT	GACTCTTACT	GGACACGCGA	CTATACCGGT	420
	TGGTTGCGAA	TGTACGATAC	GAACAAAGTA	GGTCTCGTGG	ACTTTATTTA	TAACCGCCCT	480
	CGTCTTAACG	ATGATGAATT	CCCCAAATAC	GAAGCAATAT	ATCTGGGCAT	CGAGATGTTC	540
	GGGATGAAGC	TCAAGCAGAC	CGGTGGCAAC	TACATGACGG	ACGGATATGG	ATCCGCTGTG	600
75	CAGTCACATA	TCGCATATAC	GGAGAACTCC	TCTCTGTCTC	AAGTCAAGT	AAATCAAAAG	660

WO 99/29870

PCT/AU98/01023

82 / 490

5 ATGAAAGACT ATCTGGGCAT CACACATCAT GATGTGGTAC AAGATCCGAA CGGGCAATAT 720
ATCAACCATG TGGACTGTTG GGGCAAGTAT TTGGCACCAG ACAAAATCCT CATCAGGAAA 780
GTGCCTGACA ATCACCCTCA GCACCAAGCC CTGGAAGATA TGGCAGCCTA CTTCGAGGAA 840
CAGACTGGCG CATGGGGAAC GAAGTACGAG GTATATCGCG CTTTGGCCAC CAATGAACAA 900
CCGTACACGA ACTCTCTGAT TCTGAACAAC AGGGTATTGG TTCTGTCTAA TGGCCCCGCC 960
TCCGTGGACA ACGATGCTCT GAACGCTCTA AAGACGGCAA TGCCCGGTTA CGAAATTATA 1020
GGTGTCAAAG GGGCTTCAGG AACACCTTGG TTAGGAACAG ATGCCCTGCA TTGTCGTACT 1080
CACGAGGTAG CGGATAAGGG CTATCTCTAT ATCAAGCACT ACCCGATACT GGGCGAACAG 1140
GCAGGCCCTG ATTATAAGAT CGAAGCAGAT GTCGTCTCAT GCGCCATGCG TACTATCTCG 1200
10 CCGGTACAAT GTTACTATCG TATCAATGGT TCCGGTAGCT TTAAGGCTGC TGATATGAGG 1260
ATGGAATCAA CAGGTCACTA TACTTATAGC TTTACAGGTC TTAACAAGAA TGATAAGGTA 1320
GAATACTATA TCTCTGCCGC TGACAATAGT GGTCCGAAAG AGACTTATCC CTTTATCGGC 1380
GAACCTGATC CTTTCAAGTT TACGTGTATG AACGAAACCA ATACATGTAC TGTGACCGGA 1440
GCTGCCAAAG CTCTTCGTGC ATGGTTCAAC GCCGCTCGTT CAGAACTGGC TGTTCGGTA 1500
15 AGTTTGAATA TTGCGGGCAC ATATCGGATA AAGCTTTATA ACACCGCAGG AGAAGAAGTC 1560
GCTGCAATGA CCAAGGAATT AGTAGCAGGG ACGAGTGTCT TCAGTATGGA TGTGTATTCT 1620
CAGGCTCCGG GCACATATGT TCTGGTTGTT GAAGGAAATG GAATCCGTGA GACAAAGAAA 1680
ATTCTCAA

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(2) INFORMATION FOR SEQ ID NO:119

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

45 ACCACAAATA GAAAACCAAA TACTAATATG AAACITTCAT CTAAGAAAAT CTTAGCAATC 60
ATTGCATTGC TGACGATGGG ACATGCTGTG CAGGCACAGT TTGTTCCGGC TCCCACCACA 120
GGGATTCCGA TGTCTGTAC TACAACCAAG GCCGTAGGCG AAAAAATCGA ATGTGTTGGT 180
CATTCATAG AGAAGAAAGG CATCTGGATC GATCTCAATG GGGATGCCAC TTACCAACAA 240
GGAGAGGAAA TAACCGTATT CGATGAGGCA TACCACGAAT ACACGATCGG GACGCAAAAC 300
CTCACTATCT ATGGTAATAC GACCGGATTG GGCTGTCGAT CTACCGGTGC AACGGCTGTC 360
50 GATGTAAAGA AAAACCTTAA TCTGACCTAT CTCGCATGCC CGAAAAATAA TCTGAAATCA 420
TTGGACTTGA CGCAAAACCC AAAGCTGCTG CGAGTTTGGT GCGACTCTAA CGAAATAGAA 480
AGTTTGGACC TGAGTGGCAA TCCGGCTTTG ATCATCCTCG GCTGTGACAG GAATAAGCTG 540
ACTGAGCTGA AGACCGATAA CAACCCCAAG TTGGCCTCTC TTTGGTGTTC TGATAATAAC 600
CTGACGGAGT TGGAACTCAG TGCCAATCCT CGTCTCAATG ATCTTTGGTG CTTCGGTAAT 660
55 CGGATCACGA AACTCGATCT GAGTGCCAAT CCTCTATTGG TAACACTTTC GTGCAGTGAC 720
AATGAGCTTT CGACCTTGGG TCTTTCCAAG AATTCGGACG TTGCTTACCT TTGGTGTTC 780
TCGAACAAC TTACATCCTT GAATCTGTGC GGGGTGAAGG GACTGAGTGT TTTGTTTGT 840
CATTCCAATC AGATCGCAGG TGAAGAAATG ACGAAAGTGG TGAATGCTTT GCCCACACTA 900
TCTCCCGGCG CAGGCGCTCA GAGCAAGTTC GTCGTTGTAG ACCTCAAGGA CACTGATGAG 960
60 AAGAATATCT GTACCGTAAA GGATGTGGAA AAAGCTTAAA GTAAGAACTG GCGAGTATTT 1020
GACTTCAACG GTGATTCTGA CAATATGCTT CCATACGAAG GAAGTCCGAC ATCGAACTTG 1080
GCAGTAGATG CTCCCACTGT CAGGATATAT CCAATCCCGG TAGGAAGATA TGCGCTCGTC 1140
GAGATCCCGG AGTCTCTTTT AGGCGAGGAA GCTGCTTTAT ACGATATGAA TGGGGTAAAG 1200
65 STCTATAGTT TCGCGGTAGA STCTCTTCGT CAGAACATTG ACCTGACACA TCTTCCCGAC 1260
GGCACTTATT TGTTCGCTCT CGATAACTAT ACCACTAAGC TCATCAACAA G 1311

(2) INFORMATION FOR SEQ ID NO:120

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 954 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

75

WO 99/29870

PCT/AU98/01023

83 / 490

(ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 5 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 10 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...954
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120
 AATCATTTGA AGACAAATAT CAAGATGAGA AAAACAATAA TTTTCTGCTT GTTGCTCGCC 60
 CTATTTGGCT GTTCTTGGGC ACAAGAAAGA GTCGATGAAA AAGTATTCTC CGCAGGAACA 120
 AGTATTTTGA GGGGCATCCT TGAAAAGGTG AAAGCACCGC TTATGTATGG AGATCGTGAG 180
 GTATGGGGTA TGGCTCGTGC GAGCGAGGAT TTCTTTTCTA TACTTCCCGT TACGGATGAC 240
 20 CTCACTCCCG TGCTTTTCTA TAACCGTCTT ACAAACGAAC CCTGCTTTGT GTCAGACCAA 300
 GGAATAACTG AGTATTTCAA ATTCGCTCAA GAAGGTGATT ACATTGAAGT CGAAGGAAGC 360
 TCTGTATTCA TGGCGAATCT TTTGTACTAT CGTTTTTCC CGACAAGAA TACCTCCTAT 420
 AATGCTCCCA TTGAAGGTGT TGTGAGCAAG ACGGGAAATC CTGCTTTTAC AATCCGATG 480
 CTCCCGGGGG TTTCTGATG CATAGAAATC TCAAACAACC GCAAAGTCTT TCTGACCAAT 540
 25 CAATTAGGGG TTGTAAACAT CACTGACGGG ATGGAACCTC CGATTATTGC CGGAGTCTCT 600
 GCTTCTATG GATCTTCCGT CCGGGTGTAT GGTGATGTCT CACAGCGGTG GGCATCATA 660
 GGCCATTGCT ATTTGGATAT CTACCCAACC AATTGCTATC CGCTCAGCAC GAAACCCGTT 720
 GCAGGAGACG ATGAGGTTTT TGTCAAACAA CAAGGCAGGC AAATAGAGAT CGATAGCAAC 780
 AGCCCATAG TCCAAGTGGT CGTATACCAT CTTGAGGGGA AAAGTGTTT TCGCAAAAGA 840
 30 ATGACCGAAA ACGCTTATAC CCTATCCTTT AGAGCACCCA TGCTCGGCTT TATGACCATC 900
 ATGATCGAAA CACAAAATTC GATTATCAAT AAAAACTTA ATGTTACACA GCTA 954
 (2) INFORMATION FOR SEQ ID NO:121
 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 45 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 50 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1383
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121
 AGACGGGCAG TTAATAATCCG ATCACCTCCC CATATCCACT CATTATTTGT ACGTAAATGT 60
 CTTTTTTCAG ACTTTAAATA CTTATATTTA TCCCGAAAAA TTACCCAGA GAGATTGGGT 120
 CGATTGTCGA TCCGTCTTAA GTCATACAAT CCAATAATCA TTATTGAAT GAAAAAACA 180
 60 ACCATTATTT CTTTGATTGT CTTGGGTGCT TTCTTTGCAG CCGTGGGCCA AACCAAGGAC 240
 AATCTCTCTT ACAAACCTTT TTCGAAAGAA GATATTGCCG GAGGAGTTTA CTCTCTCCCG 300
 ACTCAAATC GTGCGCAGAA GGACAATGCC GAGTGGCTTC TTACAGCGAC CGTCTCCACA 360
 AACCAGTCTG CAGATACTCA CTTTATCTTC GATGAGAACA ACCGCTATAT CGCTCGTGAC 420
 ATAAAGCCCA ATGGGGTAAG AAAATCCACG GACTCCATTT ACTACGATGC CAACGGGCCA 480
 65 ATATCGCATG TGGATCTTTA TATCTCGTTC AGTGGCGGAG AGCCTGCACT CGACCCCGA 540
 TTCAAGTACA CCTATGATGA CGAGGGAAAG ATGACCGTGA GSGAAGTATT CATGCTGGTA 600
 ATGGATCCGA ATACACCTAT CTCACGCTTG GAATATCATT ATGATGCACA GGGCAGACTG 660
 ACCCAGTGGG TTTCTTTTGC TTTGGGGGCA GAATCCCAAA AGAATACGTA TCATATAAT 720
 70 GAAAAAGGTC TGTGTTGTCG CGAAGTGCTG AGCAATGCAA TGGGGACAAC CTATTGAGAC 780
 ACCGGGCAAAA CGGAATACAG CTATGACGAT GCAGATAATA TGGTGAAGGC CGAGTACTTC 840
 GTCGTCCAGC AAGGAAAGGC ATGGCAAGTA CTCAAAAGAG AGGAATACAC CTATGAGGAC 900
 AATATCTGCA TACAATATTT GGCTATTAC GGTACCGACA CAAAGGTGTA CAAGCGAGAC 960
 ATCGAGAGCG ATAGATCCAT CTCGCCAAT GTCATTGACA TTCCTGCAAT GCCGGACAGC 1020
 ACCTGGCCTA ATATGTACGG ATTCAACGCA AAGCGACTGA AAGAGACTTA TTCCTCTAC 1080
 75 GAAGGAGATG TGGCTACTCC TATATTCGAC TATATCTATA CGTACAAGGC TCTTACCTCA 1140

WO 99/29870

PCT/AU98/01023

84 / 490

5 ATGGCAACAC CTTGACAGA AGCTCAGGTA GCAGTCTATC TCAATCCGTC AACGGACGG 1200
TTAGTGATTG TGGCCAAACG CATCACACAT CTGAGCATGT ACGACTTGCA GGGTAAGCTT 1260
ATCCGTGATT GTGCTTTGAG CGGCGATAAG GTGGAATATG GTGTCGGATC TTGACCAAA 1320
GGGACATACC TGCTTAAAGT GAATACGGAT CAGGGAGCCT TTGTGAGAAA AGTCGTGATT 1380
CGA 1383

(2) INFORMATION FOR SEQ ID NO:122

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

30 ATGGCAAAAG TTATAAAAC AAAAAAGGC TTGCACTTA ATCTGAAAGG AAAACCGCTG 60
CCCGAGATGC TGGCCGAACG GGGCCAAAGT CCTACTTACG CGGTGCTGCC CGACGATTTT 120
GAAGGTGTTA TCCCCAAGGT GACGGCTCGT CCGGGGGATA AGGTGCGTGC CGGCTCAGCA 180
CTGATGCACC ACAAGGCATA TCCGGAGATG AAGTTTACAA GTCCGGTTAG CGGCGAAGTG 240
ATCGCGGTGA ATCGCGGTGC CAAGCGCAAG GTGTTGAGCA TCGAGGTGAA ACCGGACGGA 300
CTGAACGAAT ACGAGTCATT CCCTGTCCGG GATCCGTCCT CCCTCTCTGC CGAACAGATC 360
AAGGAGCTTT TACTGTGAG CGGTATGTGG GGTITTATTA AGCAACGTCC TTACGACATA 420
GTGGCTACAC CGGATATAGC TCCACGGGAC ATTTATATTA CTGCCAACTT TACTGCACCA 480
TTGGCTCCGG ACTTCGATT CATGTTTCCA GGAGAAGAAC GCGCCCTGCA GACTGCCATC 540
GATGCCCTGG CCAAACTUAC GACAGGAAAG GTGTATGTGG GCCTGAAGCC GGGTTCATCT 600
CTGGGCTTGC ACAATGCAGA AATCGTAGAA GTACACGGAC CTCATCCGGC AGGTAACGTG 660
GGCGTGCTGA TCAATCATAC GAAGCCAAATC AATCGGGGCG AAACGGGTGT GACGCTCAAG 720
GCTACCGACC TGATCGTGAT CGGACGTTTC CTGCTTACGG GCAAAGCCGA TTTTACCAGA 780
ATGATTGCCA TGACCGGCTC AGACGCTGCA GCTCACGGAT ACGTCCGTAT TATGCCGGGT 840
45 TGCAATGTCT TTGCTTCCTT CCCCGGCCGA CTGACAATAA AGGAATCTCA CGAGCGTGTG 900
ATCGATGGCA ATGTGCTGAC CGGTAAGAAAG CTCTGCGAGA AGGAGCCTTT CTTGTCAGCC 960
CGGTGTGACC AGATCACGGT GATCCCCGAA GGCACGATG TGGACGAATC CTTCCGGTGG 1020
GCTGCACCCC GTCTCGATCA GTACAGCATG AGCAGAGCTT ATTTCTCTTG GTTGCAAGGG 1080
AAAAACAAGG AGTACGTACT CGATGCCCGG ATCAAGGGTG GCGAACGTGC TATGATCATG 1140
50 AGCAACAGAT ATGACCGCGT TTTCCCGATG GACATCTATC CGGAGTATTT GCTCAAGGCT 1200
ATTATAGCAT TCGACATCGA CAAGATGGAG GACTTAGGCA TATATGAAGT GGCTCCGGAG 1260
GACTTTGCCA CTTGCGAATT TGTGGATACA TCCAAGATCG AGCTGCAGCG TATCGTTCGG 1320
GAGGGCTTGG ATATGCTCTA TAAGGAAATG AAT 1353

(2) INFORMATION FOR SEQ ID NO:123

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...585
- 75

WO 99/29870

PCT/AU98/01023

85 / 490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

5 ATGGATAAAG TGAGCTATGC TCTGGGATG AGCATCGGTA ATAATTTCAA GTCTTCGGGC 60
ATCGACAGCG TCGTTATGGA TGATTTCATG CAAGGTCTGT CTGATGTACT GSAAGAAAAA 120
GCCCCCTCAGC TCTCGTATGA CGAGGCCAAG CGCGAAATAG AGGCGTATTT CATGGATTTG 180
CAGCAGAAGG CTGTCAAACCT GAACAAAGAG GCCGGAGAGS AATTCCTCAA GATAAATGCA 240
CACAAAGGAG GTGTGACGAC CTTACCSAGC GGCTTGCAAT ACGAAGTCAT TAAGATGGGA 300
GAGGGCCCGA AACCCACCTT TTCGGACACG GTAACCTGTC ATTATCACGG TACGCTCATC 360
10 AACGGTATCG TTTTGGATAG CTCTATGGAC AGGGGAGAAC CGGCCAGTTT CCCTCTAAGA 420
GGAGTTATAG CCGGCTGGAC GGAGATTCTT CAATTAATGC CTGTAGGATC CAAGTGGAAA 480
GTAACATAC CGAGCGATCT GGCGTATGGA GATCGTGTG CCGGCGAACA TATCAAACCG 540
GGTAGTACCG TCATTTTAT AATCGAATTA TTGAGTATCA ACAA 585

(2) INFORMATION FOR SEQ ID NO:124

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

40 ATGAAAAAAG CATTACTTAT TGGTGCTGCT CTTTGGGAG CAGTCAGTTT TGCAAGTGCT 60
CAGTCTTTGA GCACAATCAA AGTACAGAAC AATTCAGTAC AGCAACCTCG TGAGGAAGCC 120
ACTATTACAG TTTGTGGAGA ATTGGCAGAG CAAGTTGACT GCATTGGGAC AGGTAATTCT 180
GCAATCATAG CCGCTGCAGC GAAATTTGAA AGCGATGATC TCGAAAGCTA TGTGGCTGG 240
GAGATCATGA GTGTTGATTT CTTCCTGGA TATAAAGCGT GCAAGTACAC ATCTGCAGTC 300
TGGGCTGATG ATATGACCAT TTTGGGCCAA TCAGAAGATA GTGATCCCGA AATGCAGACT 360
45 ATCAACAATC TTGCTCTCAA GACTAGTGTG AAGATTGAAG CCGGCAAGAA TTACATAGTT 420
GGTATATATG CTAATACCGC AGGTGGACAT CCTATCGGAT GTGATCAGGG CCCTGCCGTT 480
GATGTTATG GAGATTGGT TTCTATATCA GAAGATGGTG GTGCTACTTT CCCTCCGTTT 540
GAATCTCTTC ATCAAGCAGT TCCTACCTTA AATTACRACA TCTATGTCGT TGTTCATTTG 600
AAGAAGGGTG AAGGTGTTGA GGCTGTTCTT ACCAACGACA AGGCTAATGC TTATGTTTCA 660
50 AATGGCGTTA TCTATGTAGC CGGAGCTAAT GGTGTCAGG TATCTCTGTT CGACATGAAC 720
GGTAAGGTTG TTTATACCGG CGTTAGCGAA ACGATTGCAG CTCCTCAGAA GGGCAATGAT 780
ATCCTCCGTG TAGGTGCTAA GAGCATCAAG CTGGCTATC 819

(2) INFORMATION FOR SEQ ID NO:125

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1662 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1662

WO 99/29870

PCT/AU98/01023

87 / 490

5 TGGCCATATG TATATGCAAA AGAAGCTAAA GATAAAAAAG GGGCGCGTCC GCAAGTAGCA 1260
CTCAATCCTA CCAATGGAAA GGCTTGTGG GTATGGCATA CTCGCAAGAG CCCATATGAT 1320
GAAACCAAA CACATCCTAC TCCTGTAAAT ATTAACATT TCCTATGGTC CGATACGGAG 1380
TGGGTACATG CTCTGGACGT GGGGGACGTA TTGCAGAAAG AGGGTAGCAT GAACTCTAC 1440
CCCAATCCTG CCAAAGAATA TGTTCGTATC AACCTACCCA AAGAAGGGGG GCACGAGGCA 1500
GTCGTATACG ACATGCAGGG CCGAATCGTG GAGAAAGTTT CATTTCAGG GAAAGAATAT 1560
AAGCTGAATG TGCAGTATCT GTCCAAAGGT ACGTACATGC TGAAGTTGT AGCGGATACG 1620
GAGTATTTCC TGGAAAAAT CATTGTAGAG 1650

10

(2) INFORMATION FOR SEQ ID NO:127

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
20 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
(ix) FEATURE:
30 (A) NAME/KEY: misc_feature
(B) LOCATION: 1...1170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

35 ATGAAACGAT TACTCCCTT TCTCCTTTA GCAGGACTCG TAGCCGTAGG AAACGTGTCT 60
GCTCAGTCAC CCGGAATCCC TCAAGTGGAT GTACACACTC GCATCGCAAG AAATGCCCGT 120
TATCGACTGG ACAAGATCAG TGTCCCGGAT TCTCGTCAGA TATTCGATTA GTTCTATAAA 180
GAAAGAAACGA TACCCACTAA AATACAAACG ACCACAGGAG GTGCAATTAC AAGCATCGAT 240
TCGCTTTTCT ATGAAGACGA CAGGTGGTT CAGGTGCGCT ATTTTGACAA TAACCTTGAA 300
40 TTAACAACAG CGGAGAAGTA TGTATACGAC GGTTCIAAGC TGGTCCTTCG AGAAATTCGC 360
AAGTCGCCGA CAGACGAAAC GCCAATAAAG AAAGTTAGCT ATCACTATCT CTGTGGCAGC 420
GATATGCCTT TTGAGATTAC GACAGAGATG AGCGATGGCT ATTTTGAAAG CCATACGCTT 480
AACTATCTGA ATGGAAAGAT TGCCCGAATA GATATCATGA CTCACAGAA CCCATCGGCC 540
GAATTGATCG AAACGGGTAG AATGGTATAT GAGTTTGATG CCAATAATGA TGCTGTACTG 600
45 CTTCTGTGAC GTGTATTCT TCCTCTTCAA AACAAAGTGGG TAGAAATGTT TACTCACCGT 660
TATACATAGG ACAATAAGCA TAATTGTATT CGTTGGGAAC AAGACGAATT CGGCACCTTC 720
ACCTTGCCA ACAACTTCSA ATACGACACC ACTATCCCTC TGTCGTCTGT ATTGTTCCCC 780
ACGCAATGAG AGTTCTTCCG TCCTCTTCTT CCCAATTTTA TGAAGCATAT GCGTACGAAG 840
CAAACGTATT TCAATAACTC CGCAGAGGCG TTGTACAGAG TATGCGATTA CAACTACTTC 900
50 TATACCGATA TGCAGGGTAA TGCACGTACC GATGTTGCCG TGAACGAATC GATCAAGATT 960
TATCCTCGTC CTGCCACGGA TTTCTGCGT ATAGAAGGTT CGCAACTGCT TCGCCTTTGG 1020
CTATTGACA TGAACGGGAA GCTCATCAGA GCTACCGAAT TGACAGGCGA TTTGGCCATT 1080
ATCGGAGTTG CATCTCTCC GAGAGGCACT TACATCGCAG AAATAACTGC TGCAACAGC 1140
55 AAAACCATAC GTGCAAAAGT ATCGCTCAGA 1170

(2) INFORMATION FOR SEQ ID NO:128

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
65 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
(ix) FEATURE:
75 (A) NAME/KEY: misc_feature

WO 99/29870

PCT/AU98/01023

88 / 490

(B) LOCATION 1...1233

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:128

5	ATGAGACAGC	ATTATCTCT	ATTTCTTTT	ATCTTGTTC	TGCTTCTTG	CTTCTTTAT	60
	GTGCGTTGCA	GAACAGTCCG	ACAAACACCT	AAGCAGTCGG	AACGGTACGT	CGTAGTCCCTG	120
	TCTTTGGACG	GCTTCCGACC	GGACTATACC	GATCGGGCAC	GTACACCGGC	GTTGGATCGG	180
	ATGSCACAGG	AGGGATTGAG	CGGGTCGCTC	CAACCATGCT	TCCCTCGCT	TACATTTCCC	240
	AATCATTACA	GCATGGCTAC	GGGGCTTTAC	CCCGATCATC	ACGGTATCGT	AGCCAATGAG	300
10	TTTGTGGATT	CGCTACTGGG	CATCTTTCT	ATATCCGACC	GAAGAGCCGT	GGAGACCCGC	360
	GGATTTTGGG	GCGGCGAGCC	GGTTTGGGAT	ACGGCCGCAC	GCCAAGGCAT	CCGTACCCGT	420
	GTCTACTTTT	GGGTAGGATC	CGAAACGGCT	GTGAACGGAA	ATCGGCCGTG	GCGGTGGAAA	480
	AAATTCTCCT	CCACCGTTCC	GTTTCGTGAC	CGTGCCGACT	CCGTATCGC	GTGGCTCGSA	540
	CTGCCCCAAA	AGGAGCGACC	GCGCTTGCTC	ATGTGGTACA	TGAGGAGCC	GGATATGATC	600
15	GGACACAGCC	AAACGCCCGA	AAGCCCGCTG	ACACTGGCAA	TGGTAGAGCG	GTTGGACAGT	660
	GTGGTCGGCT	ATTTCCGCAA	GCGTTTGCAC	TCTCTGCCCA	TAGCCGCACA	GACCGACTTC	720
	ATCATAGTAT	CCGATCACCG	TATGCCCCAG	TACGAATATG	AGAAATGTGT	CAATCTGTCT	780
	CATTATCTGC	CTGCGGACAG	TTCCTCTTAC	ATGGCCACCG	GGGCCCTTAC	CCACTTGTAC	840
	CCGAAGCCCT	CCTATACCGA	GCGAGCCTAT	GAGATCCTGC	GGGCCATTCC	ACATATATCG	900
20	GTTTACCGCA	AGGGGGAGGT	GCCCCAAGCGT	TTGCGCTGTG	GCACCAATCC	TCGTTTGGGC	960
	GAATCGTCTG	TGATTCCCGA	CATAGGCTCC	ACCGTCTTTT	TCGCAATAAA	TGAAGACGTT	1020
	CGTCCGGGAG	CGGCACATGG	CTATGACAAC	CAAGCACCGG	AAATGCGGGC	TTTACTCCGG	1080
	GCTGTCCGAC	CCGATTTCGG	TCGGGGCAGT	AGGGTGGAAA	ACCTGCCCAA	TATCACCATC	1140
	TATCCGCTCA	TATGCAGGCT	GTTGGGTATA	GAGCCTGCAC	CCAACGATSC	GGACGAAACG	1200
25	TTGCTGAACG	GCCTGATCCG	AGACAAACGA	CCA			1233

(2) INFORMATION FOR SEQ ID NO:129

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 738 base pairs
	(B) TYPE: nucleic acid
	(C) STRAIDEDNESS: double
	(D) TOPOLOGY: circular
35	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
40	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORPHYROMONAS GINGIVALIS
45	(ix) FEATURE:
	(A) NAME/KEY: misc feature
	(B) LOCATION: 1...738

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:129

50	ATGAAAGTAG	GTTTGTTCAT	CCCCTGTTAT	GTCAATGCAG	TGTATCCGGA	AGTGGGTATC	60
	GCCACGTACA	AACTGCTGAA	GAGTTTGGAC	ATAGATGTCT	ACTACCCGAT	GGATCAGACA	120
	TGTTGGCGCC	AGCCTATGGC	CAATGCCGGA	TTCGAACAGA	AAGCTCAAAA	GCTGGCTTTG	180
	CGATTCCGAG	AGCTGTTCGA	GTCTATGAT	GTAGTCGTAG	GGCCATCGGC	CAGTTGCGTT	240
55	GCTTTCTGTA	AAGAAACTA	TSATCATATC	CTCAGACCGA	CAGGACATGT	CTGCAAGTCS	300
	GCAGCCAAAG	TTCCGGGATAT	ATGCCAGTTC	TTGCAGGATG	ACCTGAAGAT	CACCAAGCCTC	360
	CCCTCCCGAT	TCGCCCATAA	GSTGAGCCTG	CACAACAGTT	GCCACGGTGT	GCGCGAAGTC	420
	CATCTGTCCA	CCCCCATGTA	AGTGCAACGA	CCGTACCACA	ACAAGGTGCG	CCGGCTATTG	480
	GAGATGGTGC	AGGGCATAGA	GGTATTCCGAG	CCGAAGCGAA	TAGACGAATG	CTGCGGTTTC	540
60	GGCGGTATGT	ACTCGGTGGA	GGAGCCGGAG	GTATCCACCT	GTATCGGGCA	TGACAAGGTG	600
	CTGGATCACA	TATCCACAGG	TGCGGAGTAC	ATCAGAGGSC	CGGACAGCTC	GTGCTCATG	660
	CATATGCAGG	GAGTGATAGA	CAGAGAGAAA	TTGCCGATCA	AGACARTTCA	TGCAGTAGAA	720
	ATTTTAGCAG	CAAACTTA					738

(2) INFORMATION FOR SEQ ID NO:130

70	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 738 base pairs
	(B) TYPE: nucleic acid
	(C) STRAIDEDNESS: double
	(D) TOPOLOGY: circular
75	(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
10 (B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

15 ATGGATATTG TAAGTATGGC CGATAAAGCT CTTGTAGTGG AGATGAGAGA TGTGACGCTC 60
TGTCAGGAGG AAAACGTCAT TTTTCAAAT TTGAATCTGA CCCTTTCCGC CGGAGACTTC 120
GTCTATCTGA TAGGCTCAGT GGGATCGGGG AAGAGCACTT TGCTGAAGGC TTTGTATGCT 180
GAGGTGCTTA TCTCTGCCGG TTATGCCCGC GTGATAGATT ATGATCTGGC AAAGTTGAAA 240
CGGAAGCAGT TGCCCTATCT CGGCAGGAAT TTGGGCAITG TGTTCAGGA TTTCAGTTG 300
CTGAACGGAC GTACTGTTGC GGAGAATTG GATTTCSTT TGCGAGCTAC GGAAGTGA 360
20 AACCGAGCG ATCGCGAGCA GCGATCGAG GAGGTTTGA CCCGTGTGGG AATGTCTCGG 420
AAGGCTTATA AGAGACCGCA CGAACTGTCC GGAGGGGAGC AACCAAGTGT GGGTATAGCC 480
AGAGCTTTCG TGGCGAAGCC TGCCTTGATC CTGGCCGACG AACCCACAGG CAACCTCGAT 540
TCGGTGACCG GATTGCAGAT CGCTTCTCTG CTCTACGAAA TCAGTAAGCA GGGCACTGCA 600
GTACTTATGA GCACGCACAA CAGCAGCCTG CTGTCGCATC TGCCGGCAGG GACATGGCC 660
25 GTTCGTAAGA ATGGCGATGC CTCCTCTTG GTGAGCTGA GTGCAGATGC TGTTCGAAGA 720
AAAAATACGG AAATAGAT 738

(2) INFORMATION FOR SEQ ID NO:131

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...723

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

ATGGCCGATA AAGCTCTGT AGTGGAGATG AGAGATGTGA CGCTCTGTCA GGAGGAAAAC 60
GTCATTTTTC AAAATTTGAA TCTGACCCIT TCCGCCGAG ACTTCGTCTA TCTGATAGGC 120
TCAGTGGGAT CGGGGAAGAG CACTTTGCTG AAGGCTTTGT ATGCTGAGGT GCTATCTCT 180
55 GCCGCTTATG CCCGCGTGAT AGATTATGAT CTGGCAAAGT TGAACCGGAA GCAGTTGCC 240
TATCTGCCGA GGAATTTGGG CATTGTGTTT CAGGATTTC AGTTGCTGAA CGGACGTACT 300
GTTGCGGAGA ATTTGGAATT CGTTTTCGGA GCTACGGACT GGAATAACCG AGCCGATCGC 360
GAGCAGCGTA TCGAGGAGGT TTTGACCCGT GTGGGAATGT CTCGGAAGGC TTATAAGAGA 420
CGGCACGAAC TGTCCGAGG GGAGCAACAA CGTGTGGGTA TAGCCAGAGC TTTGCTGGCG 480
60 AAGCCTCGCT TGATCCTGGC CGACGAACCC ACAGGCAACC TCGATTGCTT GACCGGATTG 540
CAGATCGCTT CTCTGCTCTA CGAAATCAGT AAGCAGGGCA CTGCAGTACT TATGAGCAGG 600
CACACAGCA GCCTGCTGTC GCATCTGCCG GCACGGACAT TGGCCGTTG TAAGAAATGGC 660
GATGCCCTCT CTTTGGTCTG GCTGAGTGCA GATGCTGTT CAAGAAAAAA TACGGAAATA 720
65 GAT 723

(2) INFORMATION FOR SEQ ID NO:132

70 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

75 (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...696
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132
- | | | |
|----|---|-----|
| 15 | ATGAGAGATG TGACGCTCTG TCAGGAGGAA AACGTCATT TTCAAAATTT GAATCTGACC | 60 |
| | CTTTCCGCGS GAGACTTCGT CTATCTGATA GGCTCAGTGG GATCGGGGAA GAGCACTTTG | 120 |
| | CTGAAGGCTT TGTATGCTGA GGTGCTATC TCTGCCGGTT ATGCCCGCGT GATAGATTAT | 180 |
| | GATCTGGCAA AGTTGAAACG GAAGCAGTTG CCCTATCTGC GCAGGAATTT GGGCATTGTG | 240 |
| 20 | TTTCAGGATT TCCAGTTGCT GAACGGACGT ACTGTTGCCG AGAATTTTGA TTTCGTTTGT | 300 |
| | CGAGCTACGG ACTGGAAAAA CCGAGCCGAT CCGAGCAGC GTATCGAGGA GGTITTGACC | 360 |
| | CAAGTGTTGG GTATAGCCAG AGCTTTGCTG GCGAAGCCTG CGTTGATCCT GCGCGACGAA | 420 |
| | CCCACAGGCA ACCTCGATTC GGTGACCGGA TTGCAGATCG CTCTCTGCT CTACGAAATC | 480 |
| | AGTAAGCAGG GCACTGCACT ACTTATGAGC ACGCACAAAC GCAGCCTGCT GTCGCATCTG | 540 |
| 25 | CCGGCACGGA CATGGCCGT TCGTAAGAAT GGCGATGCCT CCTCTTGTGT CGAGCTGAGT | 600 |
| | GCAGATGCTG TTTCAAGAAA AAATACGGAA ATAGAT | 660 |
| | | 696 |
- (2) INFORMATION FOR SEQ ID NO:133
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 657 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (iii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133
- | | | |
|----|--|-----|
| 50 | ATGATTGAAA TCAGCAACCT CACCAAGGTT TTCAGAACAG AAGAAATAGA GACGGTAGCC | 60 |
| | CTCGATGGCG TATCGCTCAA AGTGGACAAA GGCGAATTTA TCGCCATAAT GGGGCTTCG | 120 |
| 55 | GGATGCGGTA AGTCCACTCT GCTCAATATC CTCGGCCTTC TCGACAATCC CACTTCCGGT | 180 |
| | ATCTACAAAG TCGATGGGGC AGAAGTGGGC AACCTCCGGG AAAAAAGACG GACTGCCGTC | 240 |
| | CGTAAGGGCA ATATCGGCTT CGTATTCCAG AGCTTCAACC TCATCGAAGA GATGACGGTA | 300 |
| | AGCGAGAACG TGGAGTTGCC GCTCGTCTAT CTGGGTGTGA AGGCCTCCGA GCGGAAAGAG | 360 |
| | CGAGTGGAGG AGGCACTGCG CAAGATGAGC ATCAGCCACC GGGCCGCCCA CTCCCCAAT | 420 |
| 60 | CAGCTCTCCG GAGGACAACA GCAGCGGTG GCTATCGCCC GTGCCGTGGT GCGCAATCCG | 480 |
| | AAGCTCATCC TCGCCGATGA ACCCAGGGGT AACCTCGACT CCAAAAAACG AGCCGATGTC | 540 |
| | ATGGA/ACTGC TCAGAGGTCT CAATCGCGAA GGTGCAACCA TCGTCATGGT GACGCACTCC | 600 |
| | GAGCACGATG CAGTAGTGC CGGCCGATC ATCAATCTGT TCGACGGTAA GATTCCG | 657 |
- (2) INFORMATION FOR SEQ ID NO:134
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (iii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

ATGAAGAAT	TTTTAAAAT	GTTCCTCGCC	TCGATCCTCG	GGGTATAAC	GGCAGGAATC	60
ATCTTGTCT	GTATCTTCT	ATTIATCTTT	TTCGGCATCG	TAGCCGGTAT	TGCTCCAAG	120
GCAACGGGAG	GAACCATTC	GAAGATCGAA	GCAAACTCCA	TCCTACATAT	ANACAATTCT	180
TCTTTCCCTG	AGATCGTATC	GGCCAATCCC	TGGAGCATGC	TCACAGGCAA	AGACGAGTCC	240
GTATCGTCT	CACAGGCATC	CGAAGCCATC	GGCCAAGCCA	AAAATAATCC	CAACATAACC	300
GGTATCTTCC	TCGATCTGGA	CAACCTTTCC	GTCCGTATGG	CATCGGCAGA	GGATTGCGT	360
CGCGCGTTGC	AGGATTTCAA	GATGTCCGGC	AAGTTCGTGC	TATCCTATGC	CGACAGATAC	420
ACCCAAAAGG	GTTACTACCT	CTCCAGTATT	GCAGACAAAC	TCTACCTCAA	TCCGAAAGGA	480
ATGTTGGGGC	TTATCGGGAT	TGCGACCCAA	ACAATGTTCT	ACAAAGATGC	CCTCGACAAA	540
TTCGCGGTGA	AGATGGAGAT	CTTCAAGSTA	GGCACCTACA	AGGCAGCCGT	AGAGCCATTTC	600
ATGCTCAACA	GGATGAGCGA	TGCCAATCGC	GAACAAATCA	CCACATACAT	AAACGGGCCT	660
TGGGACAAGA	TCACATCCGA	TATTGCAGAG	TCGCGCAAGA	CGGCAATGGA	TTCCGTGAAA	720
ATGTTTGGCG	ACAAAGGCGA	AATGTTCCGT	CTTGCCGAGA	AAGCGGTGGA	GATGAAGCTC	780
TGGGATGAGC	TGGCTTACCG	TACCGATGTG	GAGAAAGAAC	TCAAAAGAT	GTCCCAACGC	840
GGAGAGAAAG	ATGAACTTCG	GTTCTATCG	CTTCTCAGG	TTCTGCCCAG	TGCCCCGATG	900
AACAAAACGA	AAGGCAGTCG	GATCGCCGTT	CTCTTTGCCG	AAGGTGAAAT	AACGGAAGAA	960
ATAATAAAGA	AGCCGTTCGA	CACGTACCGT	AGCTCCATCA	CACAAGAACT	CGCCAAAGAA	1020
ATCAAGGCGC	CAGCCGATGA	CGATGATATC	AAAGCCGTAG	TACTTCGTGT	CAATTCTCCG	1080
GGAGGTAGTG	CTTTCATTC	CGAACAGATA	TGGAAGCAGG	TAGCCGATCT	CAAGGCCAAA	1140
AAGCCTATCG	TGGTCTCCAT	GGGCGACGTA	GCAGCCTCGG	GCGGATACTA	CATAGCCTGC	1200
GCAGCCAACA	GTATCGTGGC	AGAGCATACG	ACTCTGACCG	GCTCCATCGG	CATATTCGGC	1260
ATGTTCCCGA	ACTTCGCGGG	CGTAGCCAAG	AAGATAGGAG	TGAATATGGA	CGTCGTACAG	1320
ACATCCCAAGT	ATGCAGACTT	GGGCAACACC	TTCGCTCCGA	TGACGGTCCA	AGATCGTGCC	1380
CTCATCCAAC	GCTACATAGA	GCAGCGCTAC	GACCTCTTCC	TCACTCGCGT	ATCGGAAGGC	1440
CGCAACCGCA	CCAGGCACA	GATCGACAGC	ATCGCTCAAG	GCCGTGTATG	GCTCGGCGAC	1500
AAAGCTCTTG	CACCTCGGTT	GGTGGATGAG	CTTGGAGGTT	TGGACACAGC	TATCAACCGG	1560
GCCGCGAAGC	TGGCTCAGCT	CGGTGGCAAC	TACAGCATAG	AGTATGGCAA	GACCAAGCGC	1620
AACTTCTTCC	AAGAGTTGCT	CTCCTCATCA	GCAGCGGATA	TGAAGTCTGC	CATCCTGAGT	1680
ACCATCTCT	CCGATCCGGA	AATAGAAGTT	CTGCGCGAAC	TCCGCTCCAT	GCCGCCCCGT	1740
CCTTCGGGCA	TACAGGCACG	TCTCCCTAT	TACTTCATGC	CGTAC		1785

(2) INFORMATION FOR SEQ ID NO:135

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1767 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

ATGTTTTTCG	CCTCGATCCT	CGGGGTTATA	ACGGCAGGAA	TCATCTTGT	CTGTATCTTT	60
CTATTTATCT	TTTTCGGCAT	CGTAGCCGGT	ATTGCCCTCA	AGGCAACGGG	AGGAACCAAT	120
CCGAAGATCG	AAGCAAATC	CATCCTACAT	ATAHACAATT	CTTCTTTCC	TGAGATCGTA	180
TCCGCCAATC	CCTGGAGCAT	GCTCACAGGC	AAAGACGAGT	CGGTATCGCT	CTCACAGGCA	240
GTGGAAGCCA	TCCGCCAAGC	CAAAAATAAT	CCCAACATAA	CCGGTATCTT	CCTCGATCTG	300
GACAACTTT	CGTCCGGTAT	GGCATCGSCA	GAGGAATTGC	GTCCGCGGTT	GCAGGATTTC	360
AAGATGTCCG	GCAAGTTCTG	CGTATCCTAT	GCCGACAGAT	ACACCCAAAA	GGGTACTACT	420
CTCTCCAGTA	TTGCAGACAA	ACTCTACCTC	AATCCGAAAG	GAATGTTGGG	GCTTATCGGG	480

WO 99/29870

PCT/AU98/01023

92 / 490

	ATTGCGACCC	AAACAATGTT	CTACAAAGAT	GCCTCGACA	AATTGCGCGT	GAAGATGGAG	540
	ATCTTCAAGG	TAGGCACCTA	CAAGGCAGCC	GTAGAGCCAT	TCATGCTCAA	CAGGATGAGC	600
	GATGCCAATC	GCGAACAAAT	CACCACATAC	ATAACCGGGC	TTTGGGACAA	GATCACATCC	660
5	GATATTGCAS	ASTCGCGCAA	GACGGCAATG	GATTCCGTGA	AAATGTTTGC	CGACAAAGGC	720
	GAAATGTTCC	GTCTTGCCGA	GAAAGCGGTG	GAGATGAAGC	TCGTGGATGA	GCTGGCTTAC	780
	CGTACCGATG	TGGAGAAAGA	ACTCAAAAG	ATGTCCTAAC	GCGGAGAGAA	AGATGAACTT	840
	CGGTTCTGAT	CGCTTTCTCA	GGTTCTGGCC	AATGSCCGA	TGAACAAAC	GAAAGGCAGT	900
	CGGATCGCCG	TTCTCTTTGC	CGAAGGTGAA	ATAACGGAAG	AAATAATAAA	GAAGCCGTTT	960
10	GACACTGAGC	GTAGCTCCAT	CACACAAGAA	CTCGCCAAAG	AAATCAAGGC	AGCAGCCGAT	1020
	GACGATGATA	TCAAAGCCGT	AGTACTTCGT	GTCAATTCTC	CGGGAGGTAG	TGCTTTCACT	1080
	TCCGACAGAA	TATGGAAGCA	GGTAGCCGAT	CTCAAGGCCA	AAAAGCCTAT	CGTGGTCTCC	1140
	ATGGGCGGAG	TAGCAGCCTC	GGGCGGATAC	TACATAGCCT	GCGCAGCCAA	CAGTATCGTG	1200
	GCAGAGCATA	CGACTCTGAC	CGGCTCCATC	GGCATATTCC	GCATGTTCCG	GAACTTCGCG	1260
	GGCGTAGCCA	AGAAGATAGG	AGTGAATATG	GACGTCGTAC	AGACATCCAA	GTATGCAGAC	1320
15	TTGGGCAACA	CCTTCGCTCC	GATGACGGTC	GAAGATCGTG	CCCTCATCCA	ACGCTACATA	1380
	GAGCAGGGCT	ACGACCTCTT	CCTCACTCGC	GTATCGGAAG	GCGGCAACCG	CACCAAGGCA	1440
	CAGATGAGCA	GCATCGCTCA	AGGCGGTGTA	TGGCTCGGCG	ACAAAGCTCT	TGCCTCGGT	1500
	TTGGTGGATG	AGCTTGGAGG	TTTGACACACA	GCTATCAAAC	GGGCGCGGAA	GCTGGCTCAG	1560
	CTCGGTGGCA	ACTACAGCAT	AGAGTATGGC	AAGACCAAGC	GCAACTTCTT	CGAAGAGTTG	1620
20	CTCTCTCAT	CAGCAGCGGA	TATGAAGTCT	GCCATCCTGA	GTACCATTTCT	CTCCGATCCG	1680
	GAAATAGAAAG	TTCTGCGCGA	ACTCCGCTCC	ATGCCGCCCC	GTCCTTCGGG	CATACAGGUA	1740
	CGTCTCCCTT	ATTACTTCAT	GCGGTAC				1767

25 (2) INFORMATION FOR SEQ ID NO:136

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) LOCATION 1...939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

	ATGAGAGCAA	ACATTGGGCA	GATACTTTCC	GTTCGGTTC	TCTTTTCTT	CGGGACAGCG	60
	ATCGGACAGG	CTCAGAGTCG	AAACCGTACA	TACGAGGCTT	ATGTGAAACA	GTACGCCGAC	120
50	GAAGCTATCC	GACAGATGAG	CCGCTACAA	ATACCGGCAA	GCATCACCAT	AGCACAGGCT	180
	TTGGTGGAGA	CAGGAGCCGG	AGCCAGTACA	CTGGCCAGCG	TACACAACAA	TCACTTCGGG	240
	ATCAATGCC	ACAAATCGTG	GACGGGCAAG	CGCACCTATC	GTACCGACGA	TGCGCCGAAC	300
	GAATGCTTCC	GCAGCTATTC	GGCGCTCGC	GAATCGTATG	AAGATCATTC	CCGATTCTG	360
	CTCCAACCAC	GCTATCGTCC	CCTGTTCAAA	CTCGACAGAG	AAGACTATCG	GGGCTGGGCT	420
55	ACGGGGTTGC	AACGCTGTGG	CTATGCCACC	AATCGGGGCT	ATGCCAATCT	GCTGATCAAG	480
	ATGGTGGAGC	TGTATGAGCT	ATATGCTTTG	GATCGCGAGA	AGTACCCCTC	ATGGTTCCAC	540
	AAGTCTTACC	CCGGGTCCAA	CAAAAATCC	CATCAACGA	CCAAGCAGAA	GCAGAGCGGA	600
	CTCAAGCAGC	AAGCTTACTT	CAGCTACGGA	CTGCTCTACA	TCATAGCCAA	GCAAGGCGAT	660
	ACCTTCGATT	CTTTGGCCGA	AGAGTTGAC	ATGAGAGCCT	CCAAACTGGC	CAAAATCAAC	720
60	GATGCTCCCG	TGGATTTCCC	GATCGAAAAG	GGCGATGTGA	TCTATCTGGA	GAAAAAGCAC	780
	GCATGCTCCA	TCTCCAAACA	CACACAGCAC	GTAGTGCSTG	TGGGCGATTC	GATGCACAGT	840
	ATCTCCCAAC	GCTATGGCAT	CCGGATGAAG	AACCTCTACA	AGCTCAACGA	CAAGGATGGC	900
	GAATATATAC	CCCAAGAGGG	CGATATACTG	CGCTTGCGC			939

65 (2) INFORMATION FOR SEQ ID NO:137

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1569 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
10 (B) LOCATION 1...1569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

15	ATGGACGGAC	GTGATATTC	GGATGGCCTC	CATCAGGCTA	TGGAAGCCAA	AGAGCATGTG	60
	AAAGTAGAGG	CTGCCGACACA	GACATTGCA	ACTATCACTT	TGCAGAACTA	TTTCCGCATG	120
	TATCATAAGC	TGGCAGGGAT	GACCGGTACT	GCTGAAACTG	AAGCGGGAGA	GCTTTGGGAC	180
	ATCTACAAAC	TGGACGTTGT	AGTTATTCGG	ACAAACAAGC	CTATCGCCCG	TAAGGATATG	240
	AATGATCGTA	TCTATAAGAC	GGCACGTGAA	AAATATGCAG	CAGTTATCGA	AGAGATTGTA	300
20	CGTCTTGTGG	AAGAGGGCAG	ACCTGTACTT	GTCGGTACTA	CTTCGGTGGG	AATATCCGAA	360
	TTGTTGAGCC	GTATGTTACG	CTTGGGTGGC	ATCCAACACA	ATGTAICTCA	TGCCAAATTG	420
	CATCAGAAGG	AGGCCGAGAT	TGTAGCTCAG	GCCGCTCAGA	AAGGAACITG	TACCATCGCA	480
	ACGAACATGG	CCGGTCGTGG	TACCGACATC	AAGCTCTCTG	CCGAGGTTAA	GAAAGCCGGG	540
	GGTTTGGCTA	TCATTGGTAC	GGAAAGGCAC	GAATCCAGAC	GAGTGGACAG	ACAGCTTCGT	600
25	GGTCGTTCCG	GCCGTCAGGG	TGATCCCGGT	TCGTCCATAT	TCTATGTTTC	CCTTGAAGAT	660
	CATCTGATGC	GCCTCTTTGC	CACAGAAAAG	ATTGCATCAT	TGATGGATCG	TTTAGGTTTC	720
	AAGGAAGGAG	AAGTGCTCGA	AAACAACATG	CTGAGTAAGT	CCGTGGAGCG	TGCTCAAAAG	780
	AAGGTGGAAG	AGAACAACCT	CGGTATCCGT	AAACATCTGC	TTGAGTACGA	TGATGTAATG	840
	AATTCGCAGC	GTGAAGTCAT	TTATACCCGT	CGCCGTCTATG	CTTGTATGGG	AGAGCGTATC	900
30	GGTATGGATG	TACTCAATAC	CATATACGAC	GTATGTAAGG	CTCTGATTGA	CAATTATGCA	960
	GAAGCCAAAT	ATTTCGSAAG	CTTCAAGGAA	GATCTGATGC	GTGCACTCGC	GATAGAATCT	1020
	CCTATCACGC	AAGAAATATT	CAGAGGTAA	AAAGCAGAA	AGCTGACCGA	TATGCTTTTC	1080
	GATGAAGCTT	ACAAGTCTTT	CCAACGTAAG	ATGGATCTGA	TGCGAGAAGT	GGCCCAACCT	1140
	GTGGTTTCATC	AGGTATTTCGA	GACCCAAGCC	GCCGTGTACG	AGCGCATCT	AATCCGCATT	1200
35	ACGGATGGTA	AACGTGTCTA	TAACATAGGA	TGCAATTGTC	GTGAAGCGGA	TGAAACTCAA	1260
	GGGAAAGCA	TCATCAAAGA	ATTTGAGAAA	GCTATCGTAC	TGCATACTAT	CGATGAGTCT	1320
	TGGAAAGAAC	ATCTGCTGTA	GATGGACGAG	CTTCGTAATT	CCGTTTCAAA	TGCCAGCTAC	1380
	GAAACAAAG	ATCCACTACT	TATCTATAAA	CTCGAATCTT	ACGAACTGTT	CCGCAAGATG	1440
	GTAGAAGCCA	TGAACCGTAA	GACCGTAGCG	ATCCTAATGC	GTGCTCGGAT	ACCGGTACCG	1500
40	GAGGCTCCTT	CCCAAGAAGA	GCTGGAACAC	AGGCGGCAAA	TAGAAATCCG	ACATGCAACC	1560
	CAACAACGT						1569

(2) INFORMATION FOR SEQ ID NO:138

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

60 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

65	ATGAATTTCT	TAAAAAAGA	ACCGTTTAAA	ATATTCTCTA	TGATTATCT	GCTGTTAGAT	60
	ACAATAACAA	ACCGTGCCGG	TACAGAACGC	GCCGTGATCA	ACTTGGCTAA	CAACCTGCAT	120
	GCCATGGTTC	ATCGCGTATC	ATTAGTCAGC	GTTTGTACAA	AAGAAGGAGA	GCCTTCCTTC	180
	CAAGTAGAAA	AAGGAATAGA	ACTACACCAT	CTCGGAATTA	GGCTTTATGG	CAATGCATTA	240
70	GCCCGCAAAA	CAGTATATT	CAAGGCTTAT	CGAAGGATAA	AAGCCCTATA	CAAGAAGCGT	300
	GAACCGGTTT	TATTGATAGG	GACTAATATT	TTTATCAATA	CAATTTTGTC	TCAGATCAGT	360
	AACAGAGGCA	GAATATTTAC	GATCGGATGC	GAACATATCT	CTTATGATAT	TGCCCGCCCT	420
	ATTACAAAAC	GCATAAGGGG	GTTTCTGTAT	TCAGGGCTTG	ATGCCGTTGT	AGCACTGACA	480
	AAAAGAGATC	AGCAATCGTT	CGAGGCAATC	TTACGTGGAC	GCTCTAAGC	ATATGTCATA	540
75	CCCAATCAAG	TTTCATTTAC	TACAGTCCAA	AGAGATGCTA	CTACTCACA	ACAAATGTTG	600

5 GCGATTGGCA GGCTTACCTA CCAGAAGGGT TTTGAATTCA TGATAGAAGA TGCATCACGA 660
GTGCTGGGAG AAAGGCCTGA TTGGAAGCTT ATCATAGTCG GAGATGGCGA AAATGAATCG 720
ATGCTACGTA AAGAAATTGC ATCTCGCAAT ATGGAGTCGC AAATAGAAAT ACATCCATCT 780
ACACCGGAAA TTCGCAATA CTACGAATCA TCTGCTATTT ATCTAATGAC GTCCCGTTTC 840
GAAGGACTAC CAATGGTACT TCTCGAAGCA GAAGCATATG CACTACCTAT AATCTCATAC 900
GATTGTCCGA CCGGCCCGAG GGAAGTGATC GAAAACGGTC GCAATGGTTT CCTTGTGCCA 960
ATGGAAGCAC ATGAAGACTT CCGGGATAAG TTACGCTTAT TGATGGATGA TGAAGCTCTT 1020
CGTAAGAAAA TGGGACAAGA ATCAGAGTTG ATGGTCAAAT CCTACTCTCC GGGAAATATC 1080
10 TATGAATGTT GGAAGAAACT ATTGCTCGAA ATGGGCTACA TGAAT 1125

(2) INFORMATION FOR SEQ ID NO:139

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 25 (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...1086
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

35 ATGATTATTC TGCTGTTAGA TACAATAACA AACCCTGCCG GTACAGAACG CGCCGTGATC 60
AACTTGGCTA ACAACCTGCA TGCCARTGGT CATCGCGTAT CATTAGTCAG CGTTTGTACA 120
AAAGAAGGAG AGCCTTCCTT CCAAGTAGAA AAAGGAATAG AAGTACACCA TCTCGGAATT 180
AGGCTTTATG GCAATGCATT AGCCCGCAAA ACAGTATATT TCAAGGCTTA TCGAAGGATA 240
AAAGCCCTAT ACAAGAAGCG TGAACCGGTT TTATTGATAG GSACTAATAT TTTTATCAAT 300
40 ACAATTTTGT CTCAGATCAG TAACAGAGGC AGAATATTTA CGATCGGATG CGAACATATC 360
TCTTATGATA TTGCCCGCCC TATTACAAAA CGCATAAGGG GGTTCCTGTA TTCAGGGCTT 420
GATGCCGTTG TAGCACTGAC AAAAAGAGAT CAGCAATCGT TCGAGGCAAT CTACGTGGA 480
CGCTCTAAG CATATGTCAT ACCCAATCAA GTTTCATTTA CTACAGTCCA AAGAGATGCT 540
ACTACTCACA AACAAATGTT GCGGATTGGC AGGCTTACCT ACCAGAAGGG TTTTGAATTC 600
45 ATGATAGAAG ATGCATCACG AGTGCTGCCG GAAAGGCCTG ATTGGAAGCT TATCATAGTC 660
GGAGATCGCG AAAATGAATC GATGCTACGT AAAGAAATG CATCTCGCAA TATGGAGTCG 720
CAAAATAGAAA TACATCCATC TACACCGGAA ATTCCGAAAT ACTACGAATC ATCTGCTATT 780
TATCTAATGA CGTCCCGTTT CGAAGGACTA CCAATGGTAC TTCTCGAAGC AGAAGCATAT 840
GCACTACCTA TAATCTCATA CGATTGTCCG ACCGGCCGSA GGGAACTGAT CGAAAACGGT 900
50 CGCAATGGTT TCCTTGTGCC AATGGAAGCA CATGAAGACT TCGCGGATAA GTTACGCTTA 960
TTGATGGATG ATGAAACTCT TCGTAAGAAA ATGGGACAAG AATCAGAGTT GATGGTCAAA 1020
TCCTACTCTC CGGCAAAATAT CTATGAATGT TGGAAAGAAC TATTCGTCGA ATTCGGCTAC 1080
ATGAAT 1086

(2) INFORMATION FOR SEQ ID NO:140

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...1920

WO 99/29870

PCT/AU98/01023

95 / 490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:140

5	ATGGGAAAAA TCATTGGAAT TGA	CTTAGGC ACAACGAACT CTTGTGTC	TGTATTGGAA	60
	GGTAACGAAC CTATCGTTAT TACA	ACAGT GAGGGCAAGC GCACAACGCC	CTCGGTAGTG	120
	GCTTTTGTGG ATGGTGGCGA GCG	TAAAGGTG GCGATCCCG CCAAGCGTCA	GGCCATCACC	180
	AATCCGACCA AGACGATATA CTCT	ATCAAA CGCTTCATGG CCGAACTTA	CGATCAGGTT	240
	TCCAGAGAAG TGGAGAGAGT GCC	ATTCAAG GTAGTACGTG GGGACAATAA	TACTCCGCGC	300
	GTAGATATAG ACGGTCGTCT CTAT	ACGCGG CAGGAAATTT CGGCCATGAT	CCTTCAGAA	360
10	ATGAGAAGA CGGCCGAAGA CTAC	CTCGGT CAGGAAATTA CGGAGGCGGT	GATCACTGTG	420
	CCCCATACT TCAACGACGC TCAAC	GTGAG GCAACGAAAG AAGCAGGAGA	GATCGCCGGC	480
	CTGAAAGTTC GCGGTATTGT GAAC	GAGCCT ACGGCAGCTT CTCTGGCCTA	CGGTCTGGAC	540
	AAGTCCAATA AGGATATGAA GATC	CGCTGT TCCGACTTGG GTGGCGGTAC	CTTCGATATC	600
	TCTATCTTGG AATTGGGCGA CGGC	GTTCCT GAAAGTGAAT CGACCAACGG	TGATACGCAC	660
15	CTCGGAGGAG ACGACTTCGA CCAC	GTGATC ATTGACTGSC TGGCAGAAGA	GTTCAGTCT	720
	CAGGAAGGTG TGGATCTTCG CCAG	GATCCCT ATGGCTATGC AGCGTCTGAA	AGAAGCTGCC	780
	GAAAAAGCCA AGATAGAGCT CTC	CAAGCACT TCATCTACGG AGATCAACCT	CCCCATATC	840
	ATGCCCGTGA ACGGCATCCC CAAG	CACCTTG GTGATGACGC TTACAAGGGC	TAAATTGAG	900
	CAGTTGGCCG ATCGTCTGAT TCAG	GCATGT GTGGCACCCCT GCGAAACGGC	CTTGAAAGAT	960
20	CGCGGTATGT CAGGTGGCGA TAT	CGATGAA GTGATTCTCG TAGGTGGTTC	CACACGTATT	1020
	CCTGCTATTC AGGAGATTGT GGAG	AAGATC TTCGTAAGG CTCGGTCCAA	GGGTGTGAAT	1080
	CCCGACGAAG TGGTAGCTGT GGG	TGCGCT ATTCAGGCG GTGTTCTGAC	CGGTGAGGTA	1140
	AAGGATGTCT TGCTGTGGGA CGTT	ACCCCC TTGTCTGTCG GTATCGAGAC	TATGGGAGGC	1200
	GTGATGACTC GCTTGATCGA TGCC	AATACC ACTATCCCGA CGAAGAAGAG	CGAAATCTTT	1260
25	ACCACACGAG TGGACAATCA ACC	TTCCGTA GAGATTCTATG TACTTCAGGG	TGAGCGTTCT	1320
	TTGGCTAAGG ACAATAAGAG CAT	CGGCCGT TTCAACTTGG ACGGTATTGC	TCCGGCGCCC	1380
	CGTCAGACAC CGCAGATCGA AGTA	ACGTTT GACATCGATG CCAACGGTAT	CCTGAATGTA	1440
	ACGGCTCATG ACAAGCTAC CGCA	AAGAGC CAGAAATATCC GCATCGAAGC	CTCCAGCGGT	1500
30	TTGTCCGATG ATGAGATCAA GCG	CATGAAG GAAGAGGCGC AGGCCAATGC	CGAAGCAGAT	1560
	AAGAAAGAGA AAGAAGCTAT CGA	CAAGATC AATCAGGCCG ACAGCATGAT	CTTCCAGACG	1620
	GAAAAGCAGT TGAAGGAGTT GGG	AGACAAA TTCCCGGCCG ACAAGAAGGC	TCCGATCGAT	1680
	ACCGCTCTCG ACAAACTGAA AGA	AGCACAC AAAGCACAGG ATGTAGCTGC	TATCGATACA	1740
	GCCATGGCCG AACTGCAAAAC CGC	CTTTCC GCAGCGGGCG AAGAGCTTTA	CAAGAATGCC	1800
	GGAGCAGCCC AAGGTGGCGC ACA	ACCCGGT CCGGACTTCG GCGGTGCTCA	AGGTCCCTCT	1860
35	GCCGGTGATC AGCCCTCTGA CGA	CAAGAAC GTCACAGACG TAGACTTCGA	GGAAGTGAAG	1920

(2) INFORMATION FOR SEQ ID NO:141

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1347 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: circular
45	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
50	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORPHYROMONAS GINGIVALIS
55	(ix) FEATURE:
	(A) NAME/KEY: misc feature
	(B) LOCATION 1...1347

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:141

60	ATGCGCTACG ACTTAGCTAT CATCGGTGGA	GGGCGGGCGG GTTATACGGC TGCCGAACGT	60
	GCTGCCAAGG GTGGCCTGAA AACCTCCTTA	ATTGAGAGA ATGCTCTCGG TGGTGTATGC	120
	CTCAACGAAG GATGTATACC GACCAAGACG	CTACTCTACT CGGCCAAAGT GCTACATCAA	180
	ATTGCTACCG CATCTAAATA TGCAGTAAGT	GGAAACGGCG ATGGAATTGA CCTCGGCAAG	240
65	GTGATTGCCA GAAAAGGTAA AATCATTGCG	AAGCTGACTG CAGGCATCCG TTCACGCCCTG	300
	ACAGAGGCCG GAGTAGAGAT GGTGACGGCA	GAAGCTACCG TAACGGGATG CGATGCAGAC	360
	GGCATCATCG GCATTACTGC GGGCGAAGCA	CAGTACAAAG CTGCCAACCT GCTACTATGT	420
	ACCGGTTCCG AGACGTTTAT TCCACCCATC	CCCGGAGTGG AGCAGACAGA GTATTGGACA	480
	AACCGTGAAG CTCTACAGAA CAAAGAGATT	CCGACCTCTC TCGTCATCAT CGGTGGTGGG	540
70	GTGATCGGAA TGGAGTTCCG TTCTTCTTC	TAACGGTATG GTACGCAAGT GCAAGTGGTG	600
	GAGATGCTGC CGGAAATACT CAACGGTATC	GATCCCGAAC ATGCAGCTAT GCTACGCGCT	660
	CACATATGAA AAGAAGGAAT CAAATTCTAC	CTCGGGCACA AAGTAACATC GGTTCGCAAC	720
	GGAGCTGTTA CGGTAGAATA CGAAGGAGAA	AGCAAGAGA TCGAAGGAGA ACGTATCCTG	780
	ATGAGTGTGG GACGTCGCCC CGTGCTGCAA	GGATTGAGT CGCTCGGATT GGTGCTTGGC	840
75	GGCAAGGTS TAAAGACTAA TGAGAGGATG	CAAACTTCCC TGCCCAATGT CTATGCTGCA	900

WO 99/29870

PCT/AU98/01023

96 / 490

5
GGTGATATTA CAGGCTTCTC GCTTTTGCCA CATACGGCTG TACGGGAAGC AGAGGTAGCA 960
GTAGATCAGA TTTTGGGCAA AACAGACGAA ACGATGAGCT ACCGTGCCGT ACCAGGTGTG 1020
GTGTACACCA ATCCUGAGGT CGCCGGTGTG GGAGAGACGG AAGAATCGCT TCGCAAAGCA 1080
GGACGTGCGT ACATGTTTCG TCGCCTTCTT ATGGCCTTCT CCGGTGCGAT TGTAGCAGAA 1140
AACGAACAA GCAATGGAGA GTGCAAACTA CTACTTGATG AAGAGAACCG CTTGATCGGA 1200
GCACACCTCA TTGGCAATCC GGCCGGCGAA CTCATCGTAA CCGCTGCCAT GGCCATCGAG 1260
ACCGGCATGA CGGATCGACA AATCGAACGA ATCATATTCC CTCATCCGAC TGTAGGCGAA 1320
ATCTAAAG AAACCTCTCC CGGAGGT 1347

10

(2) INFORMATION FOR SEQ ID NO:142

15

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2823 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

20

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

25

(v1) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

30

(1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2823

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:142

35
ATGGAATTGA AAAGATTTT ATCACTTGGT CTTCTGCTTG TGGGATTCAT TCCGATGAAG 60
CTTCTGCCCC AACAGGCTCA GCCACTCCCT ACAGATCCGG CTGTTCTGCT CGGTAAGTTG 120
GACAACGGAT TGACTTATTT CATCCGTCAC AACGAGAACC CGAAAGATCG TCGCGATTTC 180
TTTATCCGAC AAAAGGTAGG TTCTATTCTT GAAGAAGATA GCCAGTCCGG TTTGGCTCAC 240
TTCTTGGAAC ACATGGCTTT CAACGGTACG AAGAAGTTCC CCGTAAGAA CTTGATCAAC 300
TATCTCGAAA CGATCGGTGT ACGTTTCGGT CAGAAGCTGA ACGCTTCTAC CGGATTCGAC 360
AAGACGGAAT ATACGATAAT GGAATGTCCG ACTACACGTC AGGGAATCAT GACTCCCTGC 420
TTGCTTATCC TGCATGATTG GAGTAACAAT ATTACCTCG AGGGCATGA GATCGACGAG 480
GAGGCGGGTG TGATCCAGGA AGACTGGCGT GCTCGTCCGG ATGCCAACCT TCGTATGTTT 540
GAGGCTATAC TTGCCAAGGC TATGCCGGGT AATAAATATG CAGAAGCAT GCCCATCGGT 600
CTGATGGACG TCGTGTCAA CTTCAAGCAT GATGAGCTGC GCAACTATTA TAAGAAATGG 660
TATCGTCCCG ACCTGCAAGG TCTGGTGATC GTGGGAGATA TCGATGTGGA CTATGTGGAG 720
AACAAGATCA AAGAACTCTT CAAGGACGTT CCTGCTCCCG TGAATCCAGC AGAGCGTATC 780
TATACGCCGG TAGAGGACAA CGATGAGCCT ATCCTAGCCA TTGCTACCGA TGCTGAGGCT 840
ACTACCACGC AGCTCTCCAT CAGCTTCAAG AGCGACCCCA CTCCTCAAGA AGTCCGAGGA 900
TCGATATTCC GACTTGTGGA AGACTATATG AAACAGGTGA TCACTACAGC CGTGAATGAG 960
CGTCTGTCGG AGATTACTCA CAAGCCTAAC GCTCCTTTCC TCAGTGCAGG AGCTTCTTTC 1020
TCTAACTTCA TGTACATCAC CCAGACTAAG GACGCATTCA ATTTTGTTC CACGGTTCTG 1080
GAGGGTGAA GCGAGAAAGC GATGAACGCA TTGGTGGCAG AGATAGAAAG CCTCCGTCAG 1140
TTCCGTTATCA CCAAGGCGGA ATACGTCGCT GCACGCACGA ATGTGCTCAA GCGATACGAG 1200
AATCAATACA ACGAAAGAGA CAAGCGTAAG AACAAATGCT ATGCCAATGA ATACTCCACC 1260
TACTTCACCG ATGGCGGCTA TATCCCGGGT ATTGAGGTGG AATATCAGAC GGTGAATGCT 1320
TTTGTCTCTC AGGTTCCTCT GGAAGCATTC AATCAGGCTA TTGCCCAAT GATCGATCCG 1380
GTGAAGAATG CTGTCTGTAC CCTCACCGGT CCTTCAAAGG CTGAAGCCAA GATTCCGAGC 1440
GAAGCAGACT TCCTCGCTGC TTTCAAAGCT GCTCGTCAGC AGAAAGTAGA AGCCAAGAAA 1500
GACGAAGTCT CCGACCAAAA ATTGATGGAG AAAGCTCCTA AGGCCGAAA GATCGTTTCC 1560
GAGAAGAAAG ATCAGAAGTT CGGTACCACG GAACCTACCC TTAGCAATGG CATCAAAGTA 1620
TACCTCAAGA AGACCGATT CAAATCAAAC GAAATCTGA TGAGTGCTCT CAGCCCGGCT 1680
GGTATCTCT CCGGAAAGCA TGCTCCCAAC CAATCTGTA TGAATTCGTT CATGAACGTG 1740
GGTGGCTTGG GCAACTTCGA TGCTATCCAG CTGGATAAGG TGCTGACAGG TCGTCTGCT 1800
TCGTATCTC OCTCTTTGTC TCTGCTCAGT GAAGGTCTTT CCGGCAAAAC GACTGTAGAA 1860
65
GATATGGAAG CTTTCTTCCA GTTGATCTAT CTCCAATGA CTGCTAACCG CAAGGATCCC 1920
GAAAGCTTCA AGGCCACACA GGAAGAGTTG TACAATACT TGAATAATCA GGAAGCCAAC 1980
CCGATGGCTG CGCTTATGGA CTCTATCCGT CATACCATGT ACGGCGATAA TCCGATGATG 2040
AAACCCATGA AAGCTGCTGA CGTGGAGAAA GTAAATACG ATCAGGTAAT GGCCTTCTAC 2100
AATGAGCGAT TCGCTGATGC CGGCGACTTT ATGTTCTTCT TTATCGGTAA TCTGGATGAA 2160
70
GCCAAGATGA AGCCATTGAT CGAAACTTAT CTGCTTCAT TGCCCAACCT CAAGCGTGCC 2220
GATAAGATGA ATAAGGCTCA GCTACCGGCT GCCCGTTCGG GAAAGATCGA TTGCAAGTTC 2280
GAGAAGGAAA TGGATACTCC TTGCACTACT ATATTGATG TCGTGTCCGG AAATGTGGAA 2340
TATACGCTCA AGAACAGTCT CCGTCTGGAA GTCTTCTCAG CCGTAATGGA TCAGGTGTAC 2400
ACGGGTACCG TTCCGAGGAA GGAAGGCGGT GCATACAGT TGGCTGCATT CGGCGTCTC 2460
75
GAGCAATATC CTCAGCCCAA GGCTCTGATG CAGATCTATT TCCCCACGGA TCCTGCTCGT 2520

5	CCCCAGGAAA TGAATGCTAT CGTTTTGCT GAGTTGGAGA AGCTTGCCAA GGAGGGCCCC 2580 AATGTGGAAT ACTTTAAGAA GACTATCGAA AACCTGAATA AGCAGCAGAA AGAAAAGTCTG 2640 CGTGAGAATC GTTTCCTGGCT CGAAGCCATG AAGGCGTCTT TCTTCGAAGG AATGACTTC 2700 ATCAGAGACT ACGAATCCGT ACTGAACGGT CTTACTCCTG CTGAATTGCA AAAGTTTGG 2760 GCAGACCTCT TGAAGCAGCA GAATCGGGT GTTGTATGA TGGCTCCTGT TCAAAAGGCT 2820 CAA 2823
10	(2) INFORMATION FOR SEQ ID NO:143
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2052 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular
20	(ii) MOLECULE TYPE: DNA (genomic)
25	(iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) ORIGINAL SOURCE: (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
30	(ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION 1...2052
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143
40	ATGAGTAAGA AAGGAACAAT CGGGGTAACG AGCGACAATA TATTCCCGGT CATCAAAAAA 60 TTCCTGTACA GCGACCATGA GATATTCCCTG CGTGAGATCG TCTCCATGC CGTGGATGCT 120 ACGCAGAGAG TGAAAACGCT TACATCCGTC GCGGAATTCA AAGGCGAGAC GGGTGACCTC 180 CGCGTAACGG TCAGCGTGGG TGAAGTGGCA CGCAGCATCA CGGTCAAGCA CCGCGGCGTA 240 GGGATGACCG AAGAGGAGGT GGAGAAGTAC ATCAATCAGA TTGCTTTCTC CACTGCGGAA 300 GAGTTTCTTG AAAAGTACAA AGACGACAAG GCCGCCAATA TCGGCCACTT CGGACTCGGA 360 TTTTACTCGG CTTTCATGGT GTCCGAGCGA GTGGACCTGA TCAGCGGCTC TTTCCGAGAA 420 GATGCTACGG CGGTGAAATG GAGCTGCGAC GGATCGCCCG AATACAGGCT CGAAGCTGGG 480 GACAAAGGCTG ACCGTGGCAC CGACATCGTG ATGCACATCG ATGAGGAGAA TAGCCAGTTC 540 CTCAAAAAAG AAAAGATAGA GGGGCTCCTC GCGAAATACT GTAAGTTCCCT TACCGTGCCG 600 ATCATTTCG GCAAGAAGCA GGAATGGAAA GACGGCAAGA TGCAAGATAC GGACGAGGAC 660 AATCAGATCA ACGACACACA TCCTGCCTGG ACCAAAAGC CTGCCGACCT CAAGGACGAA 720 GACTATAAGG AATTTTACCG TTCGCTCTAT CCCATGTCCG AAGAGCCTCT CTTCTGGATC 780 CACCTCAATG TGGACTATCC GTTCAATCTG ACAGGTATCC TCTATTTCCC GAAGTCAAA 840 AACAACTTGG ATCTGCAGCG CAACAAGATT CAGCTCTACT GCATCAGGT TTACGTCACC 900 GATGAAGTAC AGGGTATCGT GCCGGACTTC CTCACCTCC TGCACGGGGT CATCGATTCC 960 CCGGATATTC CCTCAACGT ATCGCGCTCC TATCTGCAGA GCGATGCCAA TGTGAAGAAG 1020 ATCTCGTCTC ATATCACCAA GAAGGTGGCA GACGCTCTGG AAGAAAATTT CAAAAACGAC 1080 CGCCCCACAT TCGAGGAGAA ATGGGATAGT CTGAAGCTCT TCGTCGAATA CGGTATGCTG 1140 ACGGATGAGA AGTTCTATGA GCGTGCAGCC AAATTCTTCC TTTTCACCGA TATGGACGGA 1200 CACAAGTACA CGTTCGACGA ATACCGAAGC CTGTCGAAG GTGTACAGAC GGATAAGGAC 1260 GGACAGGTAG TGTATCTCTA TGCTACGGAC AAGCATGGAC AGTACAGCCA CGTGAACGCT 1320 GCATCCGACA AAGGCTACAG CGTGATGCTG TTGGATGCTC AGTTGGATCC GCATATCGTG 1380 AGCCTGCTGG AGCAAAAGTT GGAGAAGACA CACTTTGTCC GTGTGATAG CGATACGATC 1440 AACAACTTGA TCCGCAAGGA GGAAGAGACC GAAGTGAAC TGTCCGATAC GGAGCGCGCC 1500 ACTCTCGTGA AGCTGTTTGA AGCAGCGCTG CCACGGGACG AGAAGAAGCA CTTCAATGTA 1560 GCTTTCGAAT CGCTCGGAGC CGAAGGTGAA GCCATCCTTA TCACACAAGC CGAATTCATG 1620 CGCCGATATG GCGATATGGC ACAGCTGCAG CCGCGAATGA GCTTCTACGG CGAAGTCCCG 1680 GATTCGTACA ATCTGGTACT TAATACCGAT CATCCGCTCA TCGACAGGGT ACTCTCCGGT 1740 GAGAAAGAAAT CCGTAGAGCC TTCGCTCACA GAGCTTAGAG CGAAAATCGC CGAGCTGAAA 1800 GCCACGAAGG AAGCCAAAGG GAACAAAGCC GTCGAACAGG CCAAAACCGA AGGCAGTATC 1860 AACGATCAAC TGACCAATA TGCTCAGGAC AACGAGCTGA TAGGTGAGCT CATCGACTTG 1920 GCTCTGCTCG GAAGCGGATT GCTGACGGGA GAGGCTTTGG CGGAATTCAT TCGTCCGAGC 1980 CAGCGTCTTC TC 2040 2052
70	(2) INFORMATION FOR SEQ ID NO:144
75	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ATGGAAGAAC	TGATCGATAT	TTTGGTCGTA	GACGATGATG	TGGCAGTCTG	TGCCGCACTG	60
CGTCTGGTGC	TCAAGCGAGC	GGGCTATAAT	CCCGTTATAG	CCAACAGTCC	CGACGAAGCT	120
TTGTCCATAA	TGCGGAATCC	TGATGGCGGC	TGTAAGCCGG	CTGTGATTCT	GATGGATATG	180
AAATTTCTCC	TTTCGACCTC	CGGCGAGGAA	GGATTGGAAC	TACTGGAGAA	GATGCAGATA	240
TTCACTTCCT	GCCCTGTCAT	ACTGATGACG	GCTTGGGCTT	CGATTCCACT	GGCACTGGAG	300
GGAAATGAGG	TTGGAGCTTT	CGACTTCATA	GGCAAGCCAT	GGGACAACGA	TCCGGTCCTT	360
CGTACCATAG	ATACGGCCTT	GCATCTGGCT	GCTCCCTCAG	CTGTGGCGAA	TCCATCGGAA	420
CAGTCTGACA	GAGATACAGC	CGTCAGCCCG	AAAGCTACAG	TCCAAGAGAA	TGACCCCTGT	480
GCCCATATCA	TAGGCCGGAG	CGATGCCATC	TGTAAGATCA	AGGAAACGGAT	ACGCCGCATA	540
GCTCCCAACC	ATGCCTCTGT	GCTGATCAGC	GGCGAGAGCG	GTACGGGCAA	AGAGTTGATA	600
GCGGAAGCTC	TGCACCGTGG	GAGCAAACGA	GCCTCAGCCC	CATTCTGTAA	GGTCAATTTG	660
GGTGGGATTC	CCGAAAGTTT	GTTGAAAGT	GAGCTGTTCC	GACATAAGAA	AGGAGCTTTT	720
ACCAATGCTT	TTTCCGACAG	GAAAGACCG	TTGAGCTGG	CTGATGGGGG	CACGATCTTT	780
CTGGACGAAA	TACGCGAACT	ACCGGTCGGC	AACCAAGTAA	AACTGCTCGC	AGTGCTACAG	840
GAACAGACAT	TCCAGCCGTT	GGGCGAGAGC	GTCTCCCAAC	GAGTGGACAT	CCGTGTGGTA	900
TCCGCTACGA	ATGCTTCCTT	GGAGCGAATG	GTAGCCGAAG	GACGTTTCAG	AGAGGACCTC	960
TACTATCGAA	TCAACCTGAT	ACATCTGCAT	CTGGCTCCGC	TGCGTGAGCG	TCAGGAGGAT	1020
ATACAGCTGC	TGGTGGAAAG	CTTCAGTGAA	GCCTTTGCCC	AATCGAACGG	ATTGCCCCAT	1080
GCCGTTTGGA	GTGCGGAAGC	TATGCGAGCT	ATCTGTGCCA	TGCCCCCTACC	GGGCAATGTA	1140
CGCGAACTGA	AAAACGTAGT	GGAGCGTAGC	CTATTGCTCT	CGGGATCGAG	AGAAATCAGT	1200
GCCCGGGATG	TGGCTGACTT	CGGTTCGCAG	GTGACGGCAG	CAGACCACTC	CGACGAACGG	1260
GCTTTGACCG	ACATGGAGGA	AGCTGCTATC	CGAGAGACGC	TGACTAAATA	CAACGGCAAC	1320
GTTAGTCGTG	CTGCACGAGC	CTTGGGATTG	AGCCGGGCAG	CTCTTTACCG	GCGAATGGAG	1380
AAATACGGAC	TG					1392

(2) INFORMATION FOR SEQ ID NO:145

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

ATGCTTAAGA	TAAAGAACCT	CCACGCCACA	GTACAGGGCA	AAGAGATATT	GAAAGGAATC	60
AATCTGGAGA	TCAATGCCCG	AGAGATTGAT	GCTATCATGG	GGCCGAACGG	ATCGGGGAAA	120
AGTACGCTCT	CTTCGTTTTT	GGTGGGACAT	CCCTCCTTTC	AAGTCACGGA	AGGAGAGGTG	180
ACATTCAATG	GAATCGACCT	GCTCGAATTC	GAACCGGAAG	AACGTGCACA	CCTCGGACTC	240
TTTCTCAGTT	TCCAATATCC	GGTCGAGATC	CGGGCGGTCA	GCATGGTGAA	TTTCATGAGG	300
GCAGCTGTCA	ATGAACATAG	GAAAGCGATC	GGAGCAGAAC	CGTATCGGC	AAGCGACTTC	360
CTCAAGATGA	TGCGAGAGAA	CGGTGCCATT	GTGGAGCTGG	ACAACAAATT	GGCCAGCCGT	420
TCTGTGAACG	AAGGCTTCTC	CGGTGGAGAA	AAAAAGAGCA	ACGAATCTTT	CCAAATGGCT	480
ATGCTCGAAC	CCAAGCTGGC	TATTTTGGAC	GAACCCGATA	GCGGGCTCGA	TATCGACGCT	540
CTCCGCATCG	TACGAGCGCG	GGTAAACCGA	CTCCGCTCTC	CGGAGAATGC	TGCTATTGTG	600

ATCACACACT ATCAGCGTTT GCTCGAGTAC ATCAAGCCGG ACTTCGTACA CGTCCTTTAC 660
AAGGGGCGCA TCGTCAAGTC GGGAGGAGCC GAGCTGGCTC TCACGCTCGA AGAAAAAGGC 720
TACGACTGGA TCAAGGAAGA GATAGGAGAA 750

5

(2) INFORMATION FOR SEQ ID NO:146

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1383
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

30 ATGGCTAAGG AGAAACGAT CTACGCTGTC CGTTCGTGCG GAACCAAATA CGCCAAATGG 60
CAAGGCAACT GCAATGCCGTG TGGAGAGTGG AACTGCATTG ATGAGGAGAA GGTGCCGGCA 120
CCGGCATCGG GCAAGCATGC AGCCAAGAGT TTTATGCCTC GGGAGCAGGA CAACCGGCCA 180
AGACTCTTAC AGGATGTGGA GTCCGGCGAT GAAGAGCGTA TTCGCCTCGG CGATGAAGAG 240
TTCCACCGCG TACTGGGTGG AGGAATTCTC AAAGAGCAT TTGCTCTGCT TGGCGGCGAG 300
CCGGGAATCG GTAAGTCCAC GCTTATCCTC CAGACGGTGC TGGCTCTGCC GCAGTTGCCG 360
35 ACGCTCTATG TGTCCGGC3A AGAAAGTGCC CGACAACCTGA AGATGCGCGC CGAACGACTG 420
GGGCAAGCCA TGAATGGGTG CTACGTATAC TGCAGAACGA ATATAGAGAG GATACTCTCC 480
CGTGCAGAAG AACTCACACC CGATCTCCTC GTGATAGACT CTATACAGAC GGTCTATACC 540
GAGGAAATGG AAGGCTCGGC CGGCAGCGTG GGGCAGATCC GCGAATGTGC CGCCTTACTG 600
40 CTCAAACTACT GCAAGACTAC GGGTATCCCC GTCATCGTCA TCGGACACAT CACCAAAGAA 660
GGTAGCATAG CCGGACCGAA GGTGCTGGAG CATATAGTGG ATACGGTGCT TCTCTTCGAC 720
GGGGATAAGC ATCATCTCTA CCGGATACTC CGAGGACAGA AGAACCCTGA TGGCAGTACT 780
TCCGAGCTGG GGATATACGA GATGCGGCAG GACGGTCTGC GTGGCGTGA GAATCCGAGC 840
GAACATCTCA TCACACGCAA TAGGGAAGAC CTCAGTGGCA TAGCCATAGC CGTAGCGATG 900
GAGGGCATTC GCGCGATACT CATCGAAGCG CAGGCTTTGG TCAGCTCGGC CATTATATGCC 960
45 AATCCGCAGC GTTCGGCCAC GGGCTTCGAT ATTCGGCGGA TGAACATGCT CTTAGCCGTA 1020
CTGGAGAAAC GTCCCGGCTT CAAGCTCATA CAGAAGGATG TGTTCCTGAA CATTGCCGGA 1080
GGTATCAAAA TAGCCGATCC GGCTACGGAT CTGGCCGTTA TCTCGGCACT GCTGGCGTCG 1140
AGTCTGGACA TCGTTATCCC GCCGGCCGTA TGCAATGACG GCGAGGTGCG ACTCTCCGGA 1200
GAGATACGTC CCGTGAGCCG CATCGAGCAG CGCATAACGG AAGCGCGTCG CATAGGGTTC 1260
50 AAAGAGATAT TGGTACCGGC CGATAATTTC CGGCAGGAGG ATGCCGGCCG CTTCCGGTATT 1320
CGGCTCGTGC CGGTGAGAA GGTGGAGGAA GCCTTCCCC ATCTGTTCTC GAAAGGAAGA 1380
GAA 1383

55

(2) INFORMATION FOR SEQ ID NO:147

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...813

75

100/ 490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:147

5 ATGAATAGCA GACATCTGAC AATCACAATC ATTGCCGGCC TCTCCCTCTT TGTACTGACA 60
TTGGGCGGCT GCTCCGTAGC CCAACAAGAT ACGCAGTGGG CTCTCGGCGG AAAGCTCTTT 120
ACTTGGCGGT GGATACACCG TTCGGCCGAA TATCAAGCGC TTTCATTCA GGCATACAC 180
ATCGCTACGG AAGAGTGGG CGCTCTACCG GCAGAACGTA AACCAAGGAGA TAGGCCTTAT 240
GCCATCGTAA CGGACATAGA CGAAACCATT TTGGACAATA CGCCTAACTC CGTGTATCAG 300
GCTCTCAGCG GCAAGGATTA TGATGAAGAG ACTTGGGGGA AATGGTGTGC ACAGGCCGAT 360
GCCGACACAC TGGCAGGAGC TTGTCTTTC TTCTCCATG CAGCGAACAA GGGGATCGAG 420
10 GTCTTTTACG TCACCAACCG CAGAGACAAT CTGCGCGAAG CAATCTTCA GAACCTTCAG 480
CGTTACGGAT TCCCCTTTGC CGATGAAGAA CATTTGCTTA CGACCCATGG GCCATCCGAC 540
AAAGAACCCC GTCGGCTCAA AATACAAGAA CAGTATGAAA TAGTATTGCT CATAGGAGAC 600
AACTTGGGCG ACTTCCACCA CTCTTCAAT ACGAAGAAG AGTCCGGACG CAACAGGGCT 660
CTGGGCGTGA CAGCCCGGGA GTTTGGCCGG CACTTCATCA TGCTGCCCAA TCCCACTAC 720
15 GCATCTTGGG AACCGGCATG GTACGGCGGG AAGTATCCGC CACTGCCCGA AAGAGACAAA 780
GCACCTTAAAC AACTGCACCT ACAGAACAGC AGA 813

(2) INFORMATION FOR SEQ ID NO:148

- 20 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1251 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
30 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
35 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1251

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:149

40 ATGAGCACCA ATATAGATGT ACAACAGATC AACAGCGTT TCGGCATCAT CGGTAGCAGT 60
CCCGTGATGG AACATGCCAT ACGAGTGGCA GCACAGGTGG CTCTACCGA CATGTCCGTC 120
CTCGTGACGG GGGAGAGCGG TTCGGGGAAA GAGTTCCTCC CACAGATAAT CCACTACTAC 180
45 AGCGCCCGGA AACATCATAG CTACATTGCA GTCAATTGGG GAGCCATCCC CGAAGGAACC 240
ATCGATTCCG AGCTGTTCGG ACACCGCAAA GGTTCCTTTA CCGGAGCCGT ATCGGATCGC 300
AAGGGGTACT TCGAAGAGC ATCCGGCGGC ACGATCTTTC TGGACGAAGT GGGCGAAGTG 360
CCTTTGCCCC CGCAGGCGAG GCTGCTGAGG GTGCTGGAGA CGGGCGAGTT CATCCCGTA 420
GGAGCCAGCC AGTCGCAGAA GACGGATGTC CGTATCGTAG CCGGCGAGAA TGTGAACCTC 480
50 AAGGAGCGGG TAGCGAACGG GAAGTTCGGG GAAGACCTCT TCTTCCGGCT CAATACGGTA 540
CUATCGAGG TGCTCGGCT GCGTATGCGA CCGGACGACG TGCCCTTGCT TTTTCGCCGA 600
TTCCGCCCGG ACAGCGCCGA GAAGTATCGG ATGCTTCCGG TGCCCTATC GGACGAAGCC 660
CGTACCATAT TAATGCGTTA CCGCTGGCCC GGCAATGTGC GAGAGCTGGG CAATATAACC 720
GACAGGCTGA GCATCTTGA GAGGAGCGG ACGGTATCGG CAGAGACCAT CACTCGCTAC 780
55 CTGAGCGCTG AGGGGATGCA AGACCTCCAC CCGTCTGTA TCCGACGAA CGAAACGACC 840
GAAGCGGACA AACAAATCCC CCATTACGAG CGCAATCA TCTACCGGT GCTATACGAT 900
ATGAAGAAAG AGATAGCCGA TTTGAAGGGG ATGATGAACC GCCTGGCGCA CCACGAACAG 960
CCCTCATGGC CTGTAGGGTC GGACGTCTGG GGCAACGACG ACAAGCGCAC CGCAGATCCG 1020
AAGTGGGGCG TCAGUACGCA CAAGGCCCCC ATCGCGAAGC CGGCAGAACG CGTGGAGCCG 1080
60 ATACAGGAAG CCAGCGAATA CACCGAGGAT CCGTTTCGCG TGGAGGAGGT AGAGAGAGAA 1140
ATGATTTCCT TTCAATTGCA ACGCCACGGC GGAAGGCGCA ACGACACAGC CAGGGAAGTG 1200
AAGATTTCGG AGCGGACACT ATACCGTAAA ATCAAGGAGT ATGACTGGA A 1251

(2) INFORMATION FOR SEQ ID NO:149

- 65 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1806 base pairs
70 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
75 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

ATGATCTAC	TCTTCGGCGG	TACTACGGAA	GGCGGTGCGG	CAGCTCGCGT	GCTGGATGAA	60
GCGGGAAGTC	CGTTTTCTA	CTCCACCAA	GGCAATCTGC	AAGAGATCCA	GAGTAGCCAC	120
GGCCATCGTC	TGACAGGAGC	CATGACGGTT	GCGACATG	TTTCGTTTG	TCGGAAAGAA	180
GAGATCCGAC	TGATCGTGG	CGCGGTCTAT	CCTTTCGCG	AAGAATTGCA	CGCTTCAGTG	240
GCAGAAGCCT	CTGAACAAAC	AGGTATCCCC	GTAGTAAGAT	ACGAGAGACA	ATACCTCCCA	300
CGCGAAGAAG	GTATCGTCTG	GTGTGCAAA	TACGATACGG	CTGCCGAGCG	GATGCTTGCG	360
GATGGCGTGC	AGCGTCTGCT	GATGCTCACA	GGAGTGANTA	CGATCCCCAA	GCTGGCTGCT	420
TTCTGGAAAG	AGCGCACAC	CTTTGCGCG	ATATTGAAGC	GAGACGAATC	GTTGCTTTG	480
GCAGAGAAGA	ACGGCTTTCC	TGCCGAGCGC	ATCGTTTCT	TCGAACCGCA	TGCCGACGAG	540
GAGCTGATGC	AAGCCGTTCC	CCCCGATGCC	ATTATCACAA	AAGAAAGCGG	AGAGAGCGGT	600
TACTTCCGAG	AAAAGATAGA	AGCTGCCCGA	CGGATGGGCA	TCCGTATATA	TGCCGTCGTA	660
CGTCCCCCTT	TGCTCCTTC	ATTCATTCCT	GTAGGCGGGC	CTGTGCGTTT	GAGACGCGCG	720
GTAGAACGCC	TCGTGCGGG	ATTCTTTTCA	CTCCGAAGCG	GATTCACTAC	CGGCACCAAC	780
GCTACCGCTG	CAGTAGTAGC	AGCCATGTAC	CGATTGATGG	GGCTTGSGTC	TCTCGCCGAA	840
GCTCCCGTAG	AATTGCCTTC	GGGCGAATA	GTCACTCTGC	CCATAGCGGA	AATTGAGAG	900
GAAGAAGATC	CTGTCGTATC	CGCAGTCTGC	AAAGATGCCG	GTGATGATCC	GGATGTGACC	960
AATGGCATGG	CGGTATGCGC	TACGATCAGG	CTCAATCCCC	AACATGAGGA	AGTCCGCTTC	1020
CTGCAGGGTG	AAGGGGTGGG	GGTAGTGACG	CTCCCCGCG	TCGGTCTGGA	GGTCGGAGGT	1080
CCGGCTATCA	ACCTCGTACC	TGCAGCAATG	ATGACAGCAG	AGGTAGCGCG	ACTCTATGCG	1140
CAGGSAAGTG	TGGATATTAC	GATTAGCGTA	CCGGAAGGCC	GAGAGGCTGC	TACCCAGACA	1200
TTCAATCCCC	GACTCGGCAT	ACGGGACGGC	ATCTCTATTA	TCGGAACATC	GGGAGTCGTG	1260
AAACCTTTT	CGGCCGAAGC	GTTCGTTGGT	GCCATCCGTA	AGCAAGTGGG	TATTGCCACC	1320
GCCTTGGGAG	CCAATCATAT	CGTCTCAAT	TCGGGAGCCA	AGAGTGAGCG	TTATGTAAAA	1380
GGAGCCTATC	CGGCACCTAT	TCCACAGGCC	TTGTGTCAGT	ATGGCAATTT	CGTCGGCGAA	1440
TCACCTAGTT	GTGTAGCTTC	CTTCCCTTCT	GTCCGTTCCG	TAACGGTAGG	AATCATGCTC	1500
GGCAAAGCAG	TGAAACTCGC	CGAAGGCTAT	CTGGATACGC	ACAGTAAAAA	GGTAGTGATG	1560
AATCGGGATT	TCCTGCACGA	ACTGGCTCGT	CAGGCAGGTT	GTTCGGAAGA	CATCCATGCC	1620
ATATATAGACA	GCCTGAATTT	GGCTCGTSG	CTATGGAATA	TGCCGAGTGC	GGAGGACAGC	1680
GATCGACTGC	TACGAAGAT	TGCCGAACGA	TCTTGGGAAA	CTTGGCGCCC	ATCGGTACCA	1740
TCGGCCGAAT	TAGAACTCCT	GCTGATCGAT	GAGTCCGAG	CGATTGCTTT	TCGTATCGGT	1800
GGAGAA						1806

(2) INFORMATION FOR SEQ ID NO:150

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ATGTTGAGGA	CTTCCGAAT	CGGTGGTATT	CACCCCCCG	AAAACAAGTT	GTCCGCAGGC	60
AAGCCCGTAG	AGGTGTTGCC	TATCCCTCA	CAGGTAGTCA	TCCCTCTGG	TCAGCACATC	120
GGTGACCCGG	CAACTGCCAC	GGTCAAGAAA	GGGGATGAAG	TTAAGGTCGG	GAATATCATT	180
GCTCAGGCCG	GAGGATTCGT	ATCAGCTAAT	ATCCACTCAT	CTGTGTGCGG	TAAGGTGCTG	240
AAGATCGATA	ACGTATACGA	CTCAAGCGGC	TATCCCAAGC	CGCGAGTCTT	CATTAGCGTA	300
GAAGGTGACG	AATGGGAAGA	GGGCATCGAT	CGTCCACCAG	CCATCGTCAA	AGAATGCAAT	360
CTGGATGCAA	AAGAAATCGT	AGCCAAAATT	TCTGCAGCCG	GTATTGTGGG	TCTTGGCGGT	420

102/ 490

5 GCTACCTTCC CTACCCATGT GAAGCTGTCC GCTCCTCCGG GCAACAAAGC TGAGATCCTG 480
ATCATCAACG CCGTAGAGTG CGAGCCTTAT CTGACGAGCG ACCATGTCCT TATGCTGGAG 540
CACGGCGAAG AGATCATGAT CGGCGTGAGT ATCCTGATGA AAGCCATTCA GGTAAACAAG 600
GCCGTCAATCG GAGTTGAGAA TAATAAGAAA GATGCTATTG CTCACCTCAC CAAACTGGCC 660
ACTGCATATC CGGCGATAGA GGTAAATGCC TTGAAGGTGC AATATCCTCA AGGCGGTGAG 720
AAGCAGCTGA TCGATGCAGT GATCCGCAAG CAGGTAAAAA GCGGTGCCTT GCCTATCAGC 780
ACAGGTGCCG TAGTACAAAA CGTGGGTACG GTATTCCGCG TGTACGAAGC AGTACAGAAG 840
AACCAAGCCTC TGGTCGAGCG CATCGTGACG GTTACAGGAA AAAAATCTGC TCGTCCGCTT 900
AACCTCCTCG TTGCTATAGG TACTCCTATT GCGGCTTTGA TCGAAGCAGC AGGTGGCTTG 960
10 CCGGAGAATA CCGGCAAGAT CATCGGCGGA GGTCCGATGA TGGGACGCGC TCTGCTGTCA 1020
CCGGA'TGTGC CTGTGACCAA AGGCAGCTCC GGAGTATTGA TTCTCGATAG AGAAGAGGCA 1080
GTTCCGAAGC CTATGCGCGA CTGTATCCGA TCGCCCAAGT GCGTCGAGT GTGTCCGATG 1140
GGACTCAATC CCGCTTTCTT TATGCGCGAC ACCITATATA AGAGCTGGGA AACAGCGGAA 1200
15 AAAGGCAACG TGGTTGACTG TATCGAATGC GGTTCGTGCA GCTTCACCTG TCCGGCCAAAC 1260
CGTCTCTGCG TGGATTATAT CCGCCAAGCC AAGAAGACTG TGATGGGTAT CCAAAGAGCA 1320
CGTAAGCAA 1329

(2) INFORMATION FOR SEQ ID NO:151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

ATGAAAAGAA TACAACAAAC TCTTATCGCT CTCTTCGCGG CTGTTGCCGG TTTGGTCGCT 60
CAAAATGCTT ACGAGGGAGT AATTTTCATAT AAAATTTGCT TGGACAAAAC CGGAACAAG 120
GTTGTACTGA ATGGTGCGGC AGATATGAGT AATTAAAGC TCAAGAGCAC TCAGATGATC 180
45 ATTGTTACGC CTATTCTTGG TTCAGAAGAT GGTACCAGCC GGTGGGAATT TCCTTCGGTA 240
GTCATTACAG GCGCAATAG AACAAAAGCT CTCAGGCTG AAATCGCATT TAGTTCGGCT 300
TTGCCCAAG CAAAACATGC AGCTCAATAC ATTCGCCGTC ATAATGGGAA GAGCGAGCAG 360
TTTGCTTTTA CAGGAGAACA TGCTTATGCA TCAATGGATGA TGGATGCCAA GTTTGTGGTT 420
CGTGAGGAGG TACGAGGTTG TGCTAAATGC CCTGTAGGTC TCTCGAGTAA TATTGTTCTT 480
50 TTTGATCCAC TCTTCAATCC GGCAGAGGCT CCTTATTGTT TGGCACACAT TACTCCGGCA 540
GAAGAAGTGG AAAAAACAGC AGAGTCCAGC TTCGATGCTT ATATCAACTT CAAAGTCAAT 600
AAGGCAGATG TCCTTCCTGA GTATCGCAAC AATAAGGCGG AGTTAGAGAA AATCAAAGAA 660
TTTGTAAGCA CCGTTAAGGC TAATCCAAAC TATTCCGTCA ATAAATGAT CATCGAAGGG 720
TTTGCTTCTC CCGAGGCTTC AATAGCCAC AATAAGGCTT TGTCGGAGCG CCGTGCTAAA 780
55 AGACTCGCGG AAGAAATGGT GCGTAAGTAT GGCAAAACAT TGCCGAATAT AACCACTGAA 840
TTCCGGCGGTG AAGATTGGAA GGGGCTGAAA CTGGCTATCG AAAAGAGTGA TATAGCCGAT 900
CGTGACCGCG TATTGGAGAT AATCAACTCC GATAAATATG CCGATGATGA TGCAGGTGAA 960
CAGGCTCTGA AGCAACTTTC GTCTTATCGT TATATCTTGG ATCAGATCTA TCCGAATTGG 1020
CGTCGCAATA CGATAACCAT GGGGTATATC GTTCGTGATT ATACCCTCGA AGAAGCTCGT 1080
60 GAAATCATTG AGACTGCTCC GAAAGAACTT AGTGAGGCCG AAATGTACCG TGTGGCAATG 1140
TCTTATCCTG AGGGGACCA AGAGCGTTTG TTTGCTCTGA ATACGACCCT TAAGTATTTC 1200
CCTGAAAGTG TAACGGGCGG AATCAATTG GCTGTAGCCG CTTTAAATGG TGGAGACGTT 1260
CAACAGGCAA TTGCTCTGTT GAGTCCGATT CAGACAGAAA AGGGGTGAAG CAATATCCTT 1320
GGAGCTGCTT ATGCTCGTAC GGGAGATTTT GCTCGTGCCG AAACCTTCTT CCGTAAGGCC 1380
65 GTTCAGAAAG GAGATGCAAA TGCGCAGGCG AACCTCGATA TGCTGCTTGG CAAAVAG 1437

(2) INFORMATION FOR SEQ ID NO:152

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

103/ 490

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
5 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
10 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1149
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152
15
ATGGCAGAAA AAAGAGACTA TTACGAAGTC CTCGGTGTAT CGAAGAATGC CACCGACGAT 60
GAACTGAAAA AAGCATATCG CAAGAAGGCT ATCCAATACC ATCCTGATAA GAACCCCGGT 120
GACAAGGAGG CCGAAGAGCA CTTCAAAGAG GTAGCTGAAG CCTACGACGT ATTGAGCGAT 180
CCGCAGAAAGC GCAGTCAATA TGACCAAGTC GGCATGCGG GATTGGGCGG AGCTGCCGGT 240
20 GGAGGTTTCA GCGGAGGCGG TATGTCCATG GAGGATATTT TCAGTCCGCTT CGGTGATCTA 300
TTCGGTGGGT TCGGCGGTTT CCGCGGATTC TCCGATATGG GCGGTGGCAG TCGCAGACGT 360
GTTCCGAGAG GGTCTGACCT GCGAGTACGA GTGAAGCTTT CTTGGCCGA TATAGTAA 420
GGTGTGGAGA AGAAAGTGAA GGTAAAAAAG CAGGTAGTGT GCAGCAATG TCGTGGCGAT 480
GGCAGCGAAG AAGCCAATGG CAAGACTACC TGCCAGACCT GCCATGCAAC CGGCGTGGTT 540
25 ACACGTGTGA GCAACACTTT CCTTGGGGCC ATGCAGACCC AGAGCACTTG TCCCACTTGC 600
CACGGAGAGJ GTGAGATCAT CACGAAGCCA TGCTCCAAAT GTAAGGGCGA AGGTGTGGAG 660
ATCGGCGAAG AGGTGATCTC ATTCCACATC CCTGCCGCTG TAGCCGAAGG AATGCAAAATG 720
TCCGTGAACG GCAAGGGGAA TGCCGCGCCC CGAGGAGGCG TGAAATGGCGA CTTGATAGTC 780
30 GTGATCGCG AGGAACCGGA TCCGAATCTG ATCCGCAATG GCAACGATCT GATATACAAT 840
CTGCTTATAT CCGTTCGGTT GGCTATAAAA GGAGGTAGTG TGGAAATGCC GACGATAGAC 900
GGACGAGCCA AGATCCGCAT CGAGGCGGGG ACACAACCCG GCAAGATGCT GCGTTTGGCG 960
AATAAGGGGT TGCCAGCGT AAACGGCTAT GGCATGGGAG ACCAACTGGT GAATGTCAAT 1020
GTCTATATCC CCGAATCGAT CGATGCCAAA GATGAGCAGG CTATCGCAGC GATGGAAAAC 1080
35 TCGGACAGCT TCAAACCTAC CGATGCTGCT CGTAAGGATA TAGACAAGAA ATACAGAGAG 1140
ATGCTGGAT 1149
(2) INFORMATION FOR SEQ ID NO:153
40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
50 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...879
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153
60
ATGAAAAAAC TGATTTTAGC GACTTTGGGA CTTATGGCCA TTGCCATGCT CTCATGTTCA 60
AGCAACAACA AGGATTGGA GAACAAAGGG GAGGCTACTC TTTTGGTAAC GTTTGGTAGC 120
TCCTATAAAG CTCCACGCGA AACCTATGCG AAGATTGAGA AGACTTTTGC CGCACCTTAT 180
CCCGATCAAA GGATAAGCTG GACATACACG TCTTCTATTA TCCGAAAGAA ACTGGCTCAG 240
65 CAGGGTATTT ATATCGATGC TCCGGATGAG GCTTTGGAGA AATTGGCTCG TCTGGGTAT 300
AAGAAGATCA ATGTACAGAG TCTTCATGTG ATTCGCCGCC GAGAATATGA TGAGATGATC 360
GACTTTGTCA ATAAGTTTAA GGCAGCACAT AGTGATATTA CTGTGAAGGT AGGGGCTCCG 420
CTTTTCGATA CCGATGAAGA TATGCGCGAG GTGGCAGAGA TCTTGACAA GCGTTTTCAG 480
CAAAAGATAG AGAAAGGTGA AGCTATTGTA TTCATGGGAC ACGGCACCGA GCATGCTGCC 540
70 AATGACAGGT ATGCCCGTAT CAATAAGATC ATGAAGAACT ATAGCAAGTT CATGATCGTC 600
GGAACCGTCG AGTCCGATCC CTCTATCAAT GATGTTATTG CCGAACTGAA AGAAACCGGT 660
GCCACGGCCG TAACAATGAT GCCCGTGATG AGTGTGGCAG GCGACCATGC TACGAATGAT 720
ATGCGCGGAG ATGAGGACGA TAGCTGGAAG ACGTTGCTGA CCAATGCCGG CTACACAGTT 780
TCTATAGACA AGCTGGACAA TGGCAATTTC TCAGTCTTGG GAGATATAGA AGAGATCCGG 840
75 AATATCTGGC TCAAGCATAT GAAGGCCACC TCTGCTCGC 879

(2) INFORMATION FOR SEQ ID NO:154

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1068 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1068
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

ATGACATCCG TCAGCCACTT ACGTACAATT TCTGTCGCAG GTATCCTGGC TGGCTGGGA 60
GGGGCTGTAC TCATTCTCTT CGGGGTTAAI CTCTTCCTCG GCTCGGTGGC TATTCCGATG 120
AGCGAGATCT TCGGACATCT TTTTTCAGAT CGTCCCGAAG GAGGAGAAGC ACTCGTGAC 180
TACAAATATCC TATGGAAATC CCGCCTGCCC GAAGCCCTCA CGGCTGCTTT TGGCGGGCA 240
GGTTTATCCG TTAGTGGCTT GCAGATGCAG ACCGTCTTTC GCAATCCITT GGCGGTCCG 300
TCCGTCTCG GCATCAGCTC CGGTGCCAGT TTGGGTGTG CTTTGGTCGT TCTGCTGAGC 360
GGCTCGCTGG GAGGAGTGGC ATTGAGTAGC CTGGGTATA TGGGCGAGGT GGCCATGAAT 420
ATAGCCGCTG CCGTAGGCTC GCTGGCAGTA ATGGGGCTGA TCGGATATGT AGCCACTGCC 480
GTGCGCAGCC ACGTTACGCT GCTCATTATC GCGGTATGA TCGTTTGTGT CAGCACCAAG 540
GTGATCGGGG TATTCAAGTT TTTCAGTATC TCGCAACTGA GTTCTTTGC CATCTGTATG 600
GGTTTGGGCA GCTTTTCCCG TGCCACGGAT TCGCAACTGA GTTCTTTGC CATCTGTATG 660
TTGATCTTTA TTCCGGCCGG TATGCTCCTT GTCAAGCAGT TGAATCTCTT ATTGCTGGGA 720
GAAAGCTACG CACGTAATCT GGGACTGAAT ACTCGTCGGG CACGGCTGCT CGTGATCTCT 780
TCCGCGGTTT TGCTCATCGC TACCGTCACG GCCTATTGCG GTCCCATCGG CTTTTGGGG 840
ATGGCTGTGC CACACTTGGC ACGGGTTATC TTTACACAT CCGATCATCG GATCCTGATG 900
CCTGCTACCT GTTTGATTGG AAGTCTCTG GCTCTTTCT GCAATATCAT TGCTCGTATG 960
CCGGGCTTTG AGGGGGCTTT GCCCGTCAAT TCCGTAACGG CTTTGGTGGG AGCACCTATT 1020
ATCGTCACCG TTTTGTTCGG GCGCAGACGC TTCAAGGAAG AAACCGAC 1068

(2) INFORMATION FOR SEQ ID NO:155

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 60 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2271
- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

ATGCGGACAA AAACATCTTT TTTTGGGATT ATCTCTTTTA TTGCTCTATT GTCGTCTTCT 60
CTGTGCGCTC AGAGCAAAAGC CGTTTAAACC GGTAGTGTGT CCGATGCCGA AACCGGAGAG 120
CCTCTTGCGG GTGCTCGAAT CGAAGTCAAA CACACCAACA TAGTAGCCCG TGCCGATGCC 180
GGCGGACATT TCGAGATCAA GAACCTGCCG GCAGGGCAGC ATAATTATAT ATGTTCTGTT 240
GGGGGGTATG GACAGAAAGA GGAGGTGGTT GCCATCGAAG CCGGACAGAC CAAAACGATC 300
TCTTTTGATG TGCGACTGCG AACGAACAC TTGGAGGAAG TCCTCGTTAC CGGTACCGGT 360
75 ACACGTTACC GCTTGGTCTGA TGCTCCTGTG GCAACGGAAG TCCTACCGC TAAGGACATA 420

	GCCTCTTCT	CGGCTCCTAC	TTCCGAGGCC	TTATTGCAGG	GGCTGAGTCC	GTCTTTTGAC	480
	TTCCGCCCCA	ATCTGATGGG	CTCTTTTCATG	CAGCTGAACG	GCCTTAGCAG	TAAGTATATC	540
	CTCATCCTTA	TCGATGGTAA	GGGTGTGTAC	GGCGATGTAG	GCGGTCAGGC	CGATTTGAGT	600
5	CGTATTCTTC	CTGATCAGAT	CGAACGGATC	GAACGGGTGA	AAGGTGCTTC	GAGTTCGCTC	660
	TACGGATCCG	ATGCCATCGC	CGGGGTAATC	AATGTGATCA	CAAAAAAGAA	TACGAATCGA	720
	CTGAGTGCA	ATACGTCACA	TCGCATATCG	AAGTACAACG	ATCGGCAAC	CAATACTTCG	780
	CTCGATATAA	ACATCGGTAA	GTTCACTAGC	AATACCAACT	ATTTCTTCTA	CCATACGGAT	840
	GGCTGGCAGA	ATAGTCCGTT	CGAAATAAAA	AAGAAAAAAG	GATCCGGCGA	ACCGGTCTTG	900
10	GAGGAAACGT	ATAAGAAAAC	TTTTCGTGCA	CAGGAAAAATC	AGGGTGTAA	CCATCGCTT	960
	TCCTATTATG	CAACTAACAA	TCTTAGCTTC	AGCGGAAATG	TGCAGTACAA	TAAACGTCAG	1020
	ATCTTCACTC	CGACTTTTTC	CGAAAGAAG	GCCTATGACA	TGGATTATCG	TGCTTTGACG	1080
	GCTTCACTCG	GTACGAACTA	TCTTTTCCCC	AATGGTCTGC	ATACGCTTTC	TTTCGATGCC	1140
	GTCTACGATC	GCTTCCGTTT	CGGATATTTC	TATCATGACA	AGGACAGCAG	TGAGAGCCTG	1200
15	ATCAACAACC	AAGGTCAGAC	CGAGCAACCC	ACATTCTTTC	CGGGTCAGCT	ACGCAATAAA	1260
	AACGATCAGA	TCCGATACAC	GGCAGAGGCT	CGCGGTGTAT	TTACTCTGCC	TTATGCGCAG	1320
	AACTGACCG	GCGGTTTGG	GTATTTCCTG	GAGGAATGA	TCTCTCCCTA	TAATTTGATT	1380
	ACCGACAAGG	CAGATGCTTC	CACGCTCTCT	GCTTATGTAC	AAGATGATG	GAAACCGCTC	1440
	GATTGGTTCA	ATATGACAGC	CGGTTTCCGT	CTGGTACACC	ATCAGGAGTT	CGGTACACGA	1500
20	ATGAGGCTCA	AGGTATCCAT	ACTCGCCCAAG	TATGGGCGCG	TGAACCTCCG	CGCTACGTTAT	1560
	GCTAACGGCT	ATAAGACTCC	CACGCTGAAA	GAGCTTTTTC	CACGGAACGA	ACTCACCCTC	1620
	ATGGGTTCCG	ACAACTCTTA	TCTCGGCAAT	GCGGATCTTA	AGCCACAGAT	GTGGGATTAT	1680
	TATGCTTTGG	GCTTGGAGTA	CAATCAAGGC	CCTATCTCGT	TCAGTGCAAC	GTTTATGAC	1740
	AATGAATTC	GCAATCTGAT	CTCCTTTATG	GATATACCGA	CCTCACCCTA	GCACGAAGCT	1800
25	CAGGGAATCA	AGAAAACCAA	GCAGTATGCC	AACATAGGAA	AAGCTCGCAG	CCGCGGCCTT	1860
	GATGTCCTAT	GTGATGCTC	TATCGGTTGG	GGTATCAAGT	TAGGAGCGGG	ATACAGCCTC	1920
	GTGGAAGCTA	AGAATCTCCA	GACGGATGAG	TGGCTGGAAG	GAGCTGCACG	TCATCGTGCC	1980
	ATGTGACAG	CCGATTGGGT	TCACTACTGG	GGTCAGTATA	GACTTGGCGT	GAGCCTTTTC	2040
	GGCCGTTATC	AGAGCGAGCG	TTACTACAAA	GACGGCAATG	CTCGGAGTCA	TACCTTGTGG	2100
30	USACTCGCCA	CATCGCATCG	TTTCGCTCAT	TTCCGCCACA	TCATCCTGGA	TGGAACGCTC	2160
	GGTATAGACA	ACCTGTTTGA	CTACGTGGAT	GATCGTCTTA	TGGGTGTCAA	TTATGCTACC	2220
	GTAAACGCCG	GACGTACTTT	CTTGTCTCAA	ATAGCGATTC	GATTCAACAA	C	2271

(2) INFORMATION FOR SEQ ID NO:156

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- 40 (ii) MOLECULE TYPE: DNA (genomic)
- 45 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 50 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...993
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

	ATGACGGACA	ACAAACAACG	TAATATCGTA	TTCCCGGCGT	TTCTCTCTTT	GCTGGGAGTC	60
	ATCGCAGTGG	TGACGATCGT	TGGTTTTTTC	ATGCTCAGAC	CGGCCGAGGA	GATTATCCAA	120
	GGACAGATAG	AAGTGACCGA	ATACCGAGTG	TCCAGCAAAG	TGCCCCGGCG	CATCAAGGAA	180
60	CTTAGGGTAT	CCGAGGGACA	GCAGGTGCAG	GCCGGCGATA	CCCTCGCTGT	CATCGAAGCC	240
	CCCGACGTAG	CGGCTAAGAT	GGAGCAGGCA	AAGGCTGCCG	AAGCAGCTGC	ACAGGCTCAG	300
	AACGCCAAGG	CTCTCAAAGG	AGCACGCGAG	GAACAGATAC	AGGCAGCCTA	TGAGATGTGG	360
	CAGAAAGCTC	AGGCCGCGGT	AGCCATAGCG	ACCAAGACAC	ACCAGGCGGT	GCAGAACCTC	420
65	TATGACCAAG	GAGTGGTACC	GGCTCAGAG	TTGGACGAAG	CCACTGCCCA	GCGCGATGCG	480
	GCCATCGCTA	CGCAAAAGC	GGCCGAAGCC	CAGTACAATA	TGGCTCGCAA	CGGTGCCGAA	540
	CGCAAGACA	AGCTGGCAGC	TTCTGCCCCC	GTCCGATAGAG	CGAGAGGAGC	CGTCCGCGAG	600
	GTGGAGTCGT	ACATCAACGA	AACTTACCTC	ATCGCCCCAC	GGGCAGGCGA	AGTGTCCGAG	660
	ATATTTCCCA	AAGCCGGCGA	ACTCGTAGGT	ACCGGGGCAC	CTATCATGAA	TATCGCCGAG	720
	ATCGGCGATA	TGTGGGCGAG	CTTTGCCGTT	CGTGAGGATT	TCCTCAGCAG	CATGACCATG	780
70	GGAGCCGTTT	TGGAGACTGT	GGTGCCGGCT	CTGAATGAAG	AAAAAGTACG	CTTCAAGATC	840
	ACATTTCATC	AGACATGGG	TACCTATGCT	GCCTGGAAAG	CGACCAAGAC	AACAGGGCAG	900
	TACGACCTGA	AGACCTTCGA	GGTAAAGGCC	ACCTTGGCG	ATAAAGACAA	GGCAGAAAG	960
	CTACGCCCGG	GTATGTCCGT	GATCATAACG	AAG			993

(2) INFORMATION FOR SEQ ID NO:157

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
20 (B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

25 ATGCGTATTG TCAGTAATTT TTGTTTCGTC TCTTTTTCGG TTTTGCTTTT TGCATCATGC 60
CGTTCCACGC GAGAAAAGGT CGTTTACCTG CAAGATATCC AAACCTTTAA TCGGGAGATT 120
ATCGCTAAAC CATATGACGT AAAAATTGAG AAGGACGATG TGCTGAACAT CCTTGTCAGC 180
AGTAGAGACC CGGAGCTTTC AACGCCCTAC AACCAAGTGT TGACCACTCG TGCACCTGGC 240
CGCAACGGCT ATGGAACGAA CTCGAACGAA GGCTTCCTGG TCGATTGAA AGGGTACATC 300
AATTATCCTA TTTTAGGCCA GATCTATGTA GAGGGCCTTA CTCGTACCGA ACTGGAGAAG 360
GAGATACAGA AGAGGATTAT TTCCAGTGGG TTTATCAAGG ATCCTACGGT AACGGTGCAG 420
CTTCAAAATT TCAAGGTGTC GGTTTTGGGA GAGGTGAATC ATCGGGGTTT GATGTCGGTA 480
AAAGGAGAGC GAATAACTCT TTTGGAAGCG ATCGGAATGG CCGGAGACCT GACAATCTAT 540
GGTCCCGCGC ATCGGGTTT TGTGATTAGA GAAACCGATG GGCATCGCGA GGTTTTCCAG 600
ACGGATCTCA GAAAGGCCGA CTGCTCGCA AGCCCGGTGT ACTATCTGCA TCAGAACGAC 660
35 GTCATCTATG TGGAGCCGAA CGACAAGAAA ACACAGATGA GCGAGATCAA CCAGAATAAT 720
AACGTAAACG TATGGCTGAG TGTACCTCC ACTTTGGTAT CCATTTCCAC GCTGACGATT 780
ACGATAATAG ATAAGACCAA A 801

40 (2) INFORMATION FOR SEQ ID NO:158

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 50 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
55 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
60 (B) LOCATION 1...1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

65 ATGAAAAAGA CCAATCTGTT TTTATCTCTG CTGGTGATCT TTATCACCGG TAGTTTTATG 60
ACTGCCCTGT CACAGAAGTC CAAGACGAAC AAATCACCAG AAGAAGATCG GAGCCGCAAT 120
GAGTATGTAC AGTCGATGGA TGTGCTTAGC AATATTATCG GTAACGTGAG GCTGATTTTC 180
GTGATACCA TAAGTATCAA ACATATGACT CGGCGTGGA TAGATGCGAT GTTGGGCGGG 240
CTTGACCCCT ATACCGAATA CATTCTTAC GAGGAAATGG ATGAACTGAA ATTGATGACT 300
ACGGGAGAGT ATGCCGAGT CGGAGCTATC ATATCGCAGC GCCCGGATAG TGCTGTGATT 360
ATCCAGAGAC CTATGGAAGG TATGCCCGCA GACGAAGCAG GATTGATAGC AGGCGACCGC 420
ATCCTGACTA TCGATGGGAA AGACTTCCGC AAATCCACCA CACCGAAAGT AAGCCAAAGCA 480
CTGAAAGGGA TAGCCGGTAC TGTTCGAAAG GTGACAGTAA TGCGCTATGG CGAAACCAAA 540
CCTCGTACTT TTTCCGTGAA ACGTCAAAAA GTGATTATGA ATTCGCTCAC TTACAGCGGA 600
ATGCTCGATG GCTCGATAGG ATATATCCGC TTGAACAAC TTACGGACAA AAGTGCAGAA 660
GAGGTGCGCA CGGCCCTTGT GGTATCTCGT GACAAACRAG GAGCGAAAGG TCTCATTTTG 720
75 GATTTAAGAG GCAATGGTGG CGGACTGATG CAGGCTGCTA TCGAGATAGT CAATCTGTTT 780

WO 99/29870

PCT/AU98/01023

107/ 490

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GTCCCTAAGG	GCAAAGAGGT	GGTAACGACC	AAAGGTCGCA	TTGCAGAGTC	GGCGTCCGTA	840
TTTCGGACAT	TGACTGAACC	GATCGACACG	AAACTCCCGA	TAGTAGTCCT	GATCGATGGA	900
CAATCGGCAT	CTTCCTCGGA	GATTGTAGCC	GGAGCACTGC	AGGATATGGA	CAGGGCTGTA	960
CTGATGGGAC	AAAAGAGCTA	TGGCAAAGGG	CTTGTACAAA	CGACTCGTCA	GCTACCATAC	1020
AACCGCGTGA	TCAAATTGAC	TACGGCCAAG	TACTACATCC	CAAGCGGACG	TTGTATTTCAG	1080
CGTTTGGACT	ACAGCCGCAC	CAATCGGACA	GGTATGGCAA	CGGCCATTCC	TGACAGTCTG	1140
CACAAAATCT	TTTACTACTG	TGCCGGAAGA	CGTGTAGAAG	ATGCAGGAGG	AATCCTGCCT	1200
GACATCGAGG	TCAAACAAGA	TACAGCTGCG	ACATTACTTT	ATTATATGGC	CATCAATAT	1260
GACGTTTTCG	ATTTCGTAC	AGGTTATGTG	CTCAAGCATA	AAACGATTCC	CAAGCCGGAG	1320
GATTTTTCCT	TAAACGAACG	GGACTATGCA	GCTTCTGCA	AGATGATGGA	AGAAAAGAAA	1380
TTTGACTATG	ATCGCCAGAG	TGGCAAGATG	CTTGACAAAC	TGGAGGAACT	GGCTAAGATA	1440
GAAGGCTACC	TGCCGGAAGC	CAACTCGGAG	CTTAAAGCAC	TACGCGAAAA	GCTAAAACCC	1500
AACCTGTCGC	GTGATCTGCT	ACGATTCAAA	AAGGAGATAA	CAAACTATCT	CAACAATGAG	1560
ATTGTCACTC	GCTATTATTA	TGAGCGAGGC	AGTATCCGCC	AGAGTTTGCC	GGAGAGTAAG	1620
GTAGTCAAAG	AAGCTATTAA	GCTGCTGAAG	GACCATCCGG	AACAAATTCG	ACAGATCCTT	1680
GCAGCTCCGA	AAGCAGAGAA	TAAAGGG				1707

(2) INFORMATION FOR SEQ ID NO:159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

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ATGCAAAACA	AAGGATTGTG	GATTGTTATC	ACATCGGGTC	TGGCCATCAT	CTGTGGGTTT	60
TACCTGTGAT	TCTCTTTTCT	TACGAACCGT	TACGAAAAGA	AGGCTAAGGC	GATGGGCGAT	120
GTGGCCGGAA	TGGCCATATC	TGATTCCATG	TCGAATGAGA	AGGCTCGGTT	CGGCTACACG	180
CTGAAAGAAG	CTCAAGCCCA	GCAAAATTGGT	CTTGGCCCTTG	ACTTAAAGGG	GGGTATGAAC	240
GTATCTTTGA	AACTTAACGC	AAGCGATCTG	CTTCGTAAAC	TCTCTAACAA	AAGTTTGGAT	300
CCCAACTTCA	ACAAAGCTCT	GGAGATGCTG	GCCAAAGACA	CGGAGCAATC	CGACTTCATC	360
GATATTTTCG	TGAAGGAATA	TCGCAAGCTC	GATCCCAACG	GTCCGTTGGC	CGTTATCTTC	420
GGTTCGGGTG	ACCTTCGCGA	CCAGATTACC	GCAAAAGTCTA	CGGATGCAGA	CGTAGTGCCT	480
CTGCTCAAAAG	AAAAATATAA	TAGTGCTGTA	GAAAGCTTCG	TCAATGTGCT	CCGTGCTCGT	540
ATCGATGCTT	TGGGTGTGGT	TGCACCTAAT	TTGCAGCGAT	TGGAAGGGCA	AGGGCGTATC	600
CTTGTGCAAC	TCGCCGAGT	GAAAGACCGT	GAGCCTGTTC	GTACCCCTTT	GCAACCGCAT	660
GCCAACTAC	AGTTCTGGCG	TACATACAAA	TTGGAAGAGG	TCAGCGGAGA	CTTGATCGCT	720
GCCAAATGAT	GTCTGAGCGA	ATTGGCTATG	AACAAACGGG	ATGCTACCCC	GGAACAGAG	780
CCTGCAACTA	CTGACTCTGT	AGCTGCAACA	GCCGATTCTG	CTGCTGTACA	AGCTGTAGCT	840
GATTCTGCTA	CTGTAGCACA	AAAAGAGGCC	AAGGATGCTA	CTCGTAAAGA	CGCACTCTTC	900
TCTCTGCTTA	CTCCCGTGAA	TGTTGGCGGT	GCAGTAGTGG	GTGTGGCTCG	TGCTGTCAAT	960
ATGGCTCAGA	TATCTGAAAT	GCTCCAGCAA	GCTCACGATC	TGAAGGTTAC	ACGTGAAGAT	1020
GTGCTTTTCC	TCTGGGGTGC	TAAAGCAATC	GAAGACCCCG	AAACCAAAAA	GGAGACCGAC	1080
CTCTACGAAC	TCTATGCTAT	TGTAACCAAT	CGTACGGGAG	ATCCTGATTT	GGGAGGTGAT	1140
GTAGTGACTT	CCGCCAAGAG	TGATATCCAA	AATGACTTCG	GTGCTTCCGA	ACCGATCGTT	1200
TCGATGACGA	TGAATGAAGA	AGGTGCTCGT	AAATGGGCGC	GTATCACAAA	GGATAACGTG	1260
GGACGGGCAA	TCGCTATCGT	TTTGGATGGT	GTGGTTTATT	CTGCTCCGAA	CGTGAATGAT	1320
GAGATCACGG	GCGGTGCGTC	TCAGATCTCC	GGGCACITCA	CCGTGGAGGA	GGCCGGTGAC	1380
CTTGCCCAAC	TACTCAACTC	CGGTAAAATG	GATGCTACGG	TAAGCATCGA	ACAGGAAATC	1440
GTGATTGGTC	CTACGCTGGG	TGCCGAGTCC	ATTAAAGCCG	GATTCTTGTC	GTTCCTGCTC	1500
GCTTTGGTTA	TCCTGATGTG	TTACATGTGT	CTGGCTTAOS	GTTCCTTGCC	GGGTCTTATC	1560
GCAACGGGGC	CATTGATTGT	AAACAGCTTC	TTACATTGGG	CGGTATTGGC	TTCTTTCCAT	1620
CCCGTGCTGA	CCCTCTCGGG	TATCGCAGGT	TTGGTGTCTG	CGCTGGGTAT	GGCTGTGGAT	1680
GCCAAAGTAC	TTATCTTCGA	GGGTATCAAA	GAAGAGCTTC	GTGCGGTAA	GACTCCGATT	1740
CGTGGCGTTA	CGGATGGTTA	TGGCAACGCT	TTCTTGCCA	TCTTCGACTC	GAACGTTAGC	1800
ACTATTATTA	CCGATATCAT	CCTATTCTTC	TACGGGACGG	GGCCGATTCC	CGGTTTGCC	1860
ACTACGTTGA	TTATCGGTCT	TATCGCTTCT	TTCAATACGG	CTGTCTTCTT	GACTCGTATC	1920
GTCTTCGAGA	AACCTGGCAA	AAAAGTCTGT	TTGGATAAGA	TTACATTCAC	TACGAGCATT	1980
ACTCGCAATC	TCCTTGTCAA	TCCCTCATAC	ATCATCTTGG	GTAAGCGCAA	GACCGGCTTT	2040

5 ATCATTCGGG TGATTATCAT CGTTTTGGGA CTTATAGCTT CATTTACAAT CGGTCTCAAT 2100
AGGGGTATTG AATTCTCCGG AGGACGTAAC TACGTAGTAA AATTCGACCA GCCTGTATCT 2160
TCCGAAGCCG TTCGTTCCGC CTTGTCTTCT CCCCTGCAGG AAAAGGTATT GGTACCTCC 2220
ATCGSTACTG AAGGGACAGA GGTGCGTATA TCTACGAACT ATAAGATCCA GAGGAAAGC 2280
GAAGAACTG AAGCAGAGAT TACTGACAAA TTGTATCAGA GCCTGAAAGG TTTCTACACC 2340
CAGCAGCCTA CTGCTGATCA GTTCTTGGAC AATATCATTG GCTCTCAGAA AGTAAGTCCC 2400
AGTATGTCGA GTGACATCAC GAGAGGTGCT ATTTGGGCTG TGCTGTTATC GATGATCTTC 2460
ATGGCCATTT ATATTCTGAT TCGCTTCCGT GACATTTCTT TCTCTGCCGG GGTATTCGTA 2520
TCTGTGGCCG CTACTACATT CTGCATTATT GCTCTGTATG CGTGTCTGTG GAAGATTCTG 2580
10 CCGTTCACCA TGGAGATCGA TCAGAACTTC ATCGCTGCTA TTCTGGCTAT CATCGTTTAC 2640
TCGCTCAATG ACACCGTGGT TGTATTTGAC CGTATCCGAG AGACGATGAA ATTGTACCCC 2700
AACAGAGATC GCTATCAGGT GATCAACGAT GCCCTTAATT CAACATTGGG TCGAACATTA 2760
AATACGCTTT TGACTACGTT TATCGTTATG TTGGTAATCT TCATCTTTGG AGGTGCTACG 2820
ATGCGTAGTT TCACGTTCTC GATCCTGCTC GGTATCGTTA TCGGTACATA CTCTACGCTC 2880
15 TTTGTTGCTA CACCCCTTGC CTACGAGATC CAAAAGCGCA AGCTCAACAA AGCAGCTAAG 2940
AAA 2943

(2) INFORMATION FOR SEQ ID NO:160

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3051 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
30 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3051
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

ATGAAAAGAA TGACGCTATT CTTCTTTGCG TTGCTGACGA GCATTGGGTG GGCTATGGCC 60
CAGAATAGAA CCGTGAAGGG TACAGTTATC TCCTCCGAGG ATAATGAGCC CCTGATCGGC 120
45 GCGAATGTCG TGGTTGTCCG AAACACCACT ATCGGTGCTG CAACCGACTT GGTATGGCAAC 180
TTACCGCTTA CGGTGCTTGC CAATGCCAAA ATGTTGAGAG TGCTCTATTG CGGTATGACT 240
ACCAAGAGAG TCGCCATCGC TAATGTGATG AAGATCGTAC TCGATCCGGA CTCTAAGGTT 300
CTGGAGCAGG TAGTTGTATT GGGTTACGGT ACGGGACAGA AACTCAGCAC TGTTCGGGT 360
TCTGTGGCCA AAGTGTCCAG CGAAAAGCTC GCGGAAAGC CGTTGCCAA TATCATGGAT 420
GCCCTCCAAG GTCAAGTAGC CGGTATGCGA GTTATGACTA CATCCGGTGA CCCTACTGCC 480
50 GTCCCTCTCG TGGAGATCCA TGGTACAGGG TCGTTGGGSC CAAGCTCTGC ACCATTGTAT 540
ATCGTGGATG GTATGCAAAC TTCTTTGGAT GTTGTGGCTA CGATGAATCC GAATGATTTT 600
GAATCTATGT CCGTTTGAAG AGATGCTTCT GCAACATCTA TTTATGGAGC TCGTGCTGCA 660
AACGGAGTCG TTTTCATTCA AACGAAGAAA GGTAAAATGA GCGAGAGAGG TCGTATTACC 720
TTTAATGCCA GTTACGGGAT TTCTCAAATC CTGAANTACTA AGCCCTTGA TAATATGATG 780
55 ACTGGAGATG AATTGCTGGA TTTTCAGGTG AAGGCAGGTT TTTGGGGGAA CAATCAAACC 840
GTTCAGAAGG TTAAGATATG GATCCTTGCC GGAGCTGAAG ATTTGTATGG CAATTATGAT 900
TCTTTGAAGG ATGAGTATGG TAAGACATGG TTCCAGTGG ATTTTAATCA TGATGCAGAC 960
TGGCTCAAGG CTTTGTTTAA AACAGCACCC ACCAGTCAAG GTGATATTTT TTTCTCCGGA 1020
GGGTCTCAGG GAACCTCATA TTATGCCTCT ATAGGCTACT TCGATCAGGA AGGTATGGCT 1080
60 CGTGAACCCG CAAATTTTAA GCGCTATAGT GGCCGGCTCA ACTTCGAAAG TCGTATCAAT 1140
GAATGGCTGA AAGTTGGTGC AAATTTGTCT GGTGCGATAG CGAATAGACG ATCTGCCGAC 1200
TATTTTGGAA AGTATTATAT GGGGTGAGGT ACTTTCGCTG TGTTAAGCAT GCCTCGTTAT 1260
TATAACCCCT TTGATGTGAA TGGGGATTTA GCAGATGTCT ATTACATGTA TGGAGCTACC 1320
AGACCTTCTA TGACAGAACC GTACTTCGCA AAAATGAGAC CGTTCAGTTC CGAATCACAT 1380
65 CAGGCCAATG TAAATGGTTT CGCCAGATT ACTCCGATCA AAGGCCCTTAC TTTAAAGGCA 1440
CAGGCTGGTG TTGATATTAC TAATCTGCG ACTTCTTCTA AGAGAATGCC CAATAATCCG 1500
TATGATTCTA CTCCTCTTGG GGAAAGAAGA GAAAGAGCTT ATCGAGATGT TAGCAAGTCT 1560
TTTACAAATA CCGCTGAATA TAAGTTTCA ATTGATGAAA AACATGATCT TACAGCATGG 1620
ATGGGGCATG AATATATTGA ATATGAAGGG GATGTTATTG GGGCATCTTC TAAAGGATTT 1680
70 GAAAGTGATA AGTTGATGTT ACTGAGCCAG GGAAAACCG GAAATAGTTT GTCTTTGCTC 1740
GAACACAGAG TCGCTGAATA TGCTATTG TCTTTCTTTA GTCTTTTAA TTACGGTTTT 1800
GACAAATGGA TGTATATAGA TTCTCTGTT CGTAATGACC AATCCTCTCG ATTCGGATCC 1860
AATAATAGAA GCGCGTGGTT CTATTCTGTC GGTGGAATGT TTGACATATA TAATAAATTC 1920
ATTCAAGAAA STAATTGGCT CAGTGATCTT CGACTGAAA TGAGTTATGG TACAACGGGT 1980
75 AACTCGGAGA TTGGTAATTA CAACCACCAA GCATCTGTTA CTGTGAACAA TTATACTGAA 2040

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GATGCTATGG GGCTTAGCAT TTCTACAGCA GGCAATCCCG ACCTCTCGTG GGAAAAGCAG 2100
TCTCAGTTCA ACTTCGGTTT GGCTGCAGGG GCTTTCAATA ATCGCTTATC TGCAGAGGTA 2160
GATTTCTATG TCCGCACTAC GAATGATATG TTGATTGATG TCCGATGCC TTATATCAGT 2220
GGTTTCTTCT CACAGTATCA GAATGTAGGC TCTATGAAA ATACGGGTGT AGACCTTTCT 2280
CTTAAGGGGA CGATCTACCA AAATAAGGAC TCGAATGTAT ATGCTTCTGC GAATTTCAAC 2340
TACAATAGAC AGGAAATAAC AAAGCTTTTC TTGGTCTCA ATAAGTACAT GTTGCTTAAT 2400
ACCGGTAATA TATGGGAAAT TGGGTACCCC AATTCGTTCT ATATGGCTGA ATATGCTGGA 2460
ATCGACAAAA AAACCGGTAA GCAGTTGTGG TATGTTCTG GTCAAGTGA TCGGATGGT 2520
AAATAAGTTA CAACAAGCCA GACTCAGCT GACTTGGAGA CACGAATTGA TAAGTCTGTT 2580
ACTCCTCCTA TTACAGGTGG TTCTCCTTA GGTGCTTCTT GGAAAGGACT TTCTTTAGAT 2640
GCTGATTTTG CCTACATCGT TGGTAAATGG ATGATCAATA ATGACCGTTA CTTTACAGAG 2700
AATGCAGGTG GATTGATGCA ATTAAATAAA GATAAAATGC TATTGAATGC CTGGACAGAG 2760
GATAAATAAG AAACAGATGT TCCAAAATTG CGACAGTCTC CTCAGTTTGA TACGCATTG 2820
TTGGAGAATG CTTCTTTCT GCGTTTGAAG AATCTCAAAC TCACTATATG ACTCCCAAT 2880
AGTCTTTTGG CTGGGCAGAA TGTGATTGGT GGAGCTCGTG TCTATTGAT GGCAGCAAT 2940
CTGTAACTG TTACGAAGTA TAAAGGCTTT GACCTGAGG CAGGGGGGAA TGTGGGAAA 3000
AATCAATATC CTAATCTAA GCAGTACGTT GCGGGTATTC AGTTGTCTTT C 3051

- 20 (2) INFORMATION FOR SEQ ID NO:161
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3042 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- 30 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...3042
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

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ATGACGCTAT TCTTCCTTTG CTTGCTGACG AGCATTGCGT GGGCTATGGC CCAGAATAGA 60
ACCGTGAAGG GTACAGTTAT CTCTCCGAG GATAATGAGC CCCTGATCGG CGCGAATGTC 120
GTGGTTGTGG GAAACACCAC TATCGGTGCT GCAACCGACT TGGATGGCAA CTTACGCTT 180
AGCGTGGCTG CCAATGCCAA AATGTTGAGA GTGCTCTATT CCGGTATGAC TACCAAGAG 240
GTGCCCATCG CTAATGTGAT GAAGATCGTA CTGGATCCGG ACTCTAAGGT TCTGGAGCAG 300
GTAGTTGTAT TGGGTTACGG TACGGGACAG AACTCAGCA CTGTTCCGG TCTGTGGCC 360
AAAGTGTCCA GCGAAAAGCT CGCGGAAAAG CCGGTGCCA ATATCATGGA TGCCCTCCAA 420
GGTCAGGTAG CCGGTATGCA GGTATGACT ACATCCGCTG ACCCTACTGC CGTCGCTTCT 480
GTGGAGATCC ATGGTACAGG GTCGTTGGGG GCAAGCTCTG CACCATTTGA TATCGTGGAT 540
GGTATGCAAA CTCTTTTGA TGTGTGGCT TGCAACATCT ATTTATGGAG CTCGTGCTGC AAACGGAGTC 600
TCCGTTTGA AAGATGCTTC TGCAACATCT ATTTATGGAG CTCGTGCTGC AAACGGAGTC 660
GTTTTCAATC AAACGAAGAA AGGTAAAATG AGCGAGAGAG GTCGTATTAC CTTTAAATGCC 720
AGTTACGGGA TTTCTCAAAT CCTGAATACT AAGCCCTTG ATAATATGAT GACTGGAGAT 780
GAATTGCTGG ATTTTCAGGT GAAGGCAGGT TTTGGGGGA ACAATCAAC CGTTCAGAG 840
GTTAAAGATA TGATCCTTGC CGGAGCTGAA GATTTGTATG GCAATTATGA TTCTTTGAAA 900
GATGAGTATG GTAGACATT GTTCCAGTG GATTTAATC ATGATGCAGA CTGGCTCAAG 960
GCTTTGTTTA AAACAGCACC CACCATTCAA GGTGATATT CTTTCTCCGG AGGGTCTCAG 1020
GGAACTTCAT ATTATGCCCT TATAGCTAC TTCGATCAGG AAGGTATGGC TCGTGAACCG 1080
GCAAAATTTA AGCGCTATAG TGGCCGGCTC AACTTCGAAA GTCGTATCAA TGAATGGCTG 1140
AAAGTTGGTG CAAATTTGTC TGGTGGGATA GCGAATAGAC GATCTGCGCA CTATTTTGA 1200
AAGTATTATA TGGGGTCAGG TACTTTCGCT GTGTTAACA TGCCCTCGTTA TTATAACCTT 1260
TTTGAATGTA ATGGGGATT T AGCAGATGTC TATTACATGT ATGGAGCTAC CAGACCTTCT 1320
ATGACAGAAC CGTACTTCGC AAAAATGAGA CCGTTCAGTT CCGAATCACA TCAGGCCAAT 1380
GTAAATGGTT TCGCCAGAT TACTCCGATC AAGGCCCTTA CTTTAAAGGC ACAGGCTGGT 1440
GTGATATTA CTAATACTCG CACTTCTTCT AAGAGAATGC CCAATAATCC GTATGATTCT 1500
ACTCCTCTTG GGGAAAGAAG AGAAAGAGCT TATCGAGATG TTAGCAAGTC TTTTACAAAT 1560
ACGGCTGAAT ATAAGTTTTC AATTGATGAA AAACATGATC TTACAGCATT GATGGGGCAT 1620
GAATATATTG AATATGAAGG GGATGTTATT GGGGCATCTT CTAAGGATT TGAAGTGAT 1680
AAGTTGATGT TACTGAGCCA GGGAAAAACC GCAATAGTT TGTCTTTGCC TGAACACAGA 1740
GTGCGTGAAT ATGCCATTTT GTCTTTCTTT AGTCGTTTTA ATTACGGTTT TGACAAATGG 1800
ATGATATAG ATTTCTCTGT TCGTAATGAC CAATCCTCTC GATTCGGATC CAATAATAGA 1860
AGCGCGTGGT TCTATTCTGT CGGTGGAATG TTTGACATAT ATAATAAAT CATTCAAGAA 1920
AGTAATTGGC TCAGTGATCT TCGACTGAAA ATGAGTTATG GTACAACGGG TAACCTCGGAG 1980

110/490

5	ATTGGTAATT ACAACCACCA AGCACTCGTT ACTGTGAACA ATTATACTGA AGATGCTATG 2040
	GGGCTTAGCA TTCTACAGC AGGCAATCCC GACCTCTCGT GGGAAAAGCA GTCTCAGTTC 2100
	AACITCGGTT TGGCTGCAGG GGCTTTCAAT AATCGCTTAT CTGCAGAGGT AGATTTCTAT 2160
	GTCCGCACTA CBAATGATAT GTTGATIGAT GTCCGATGC CITATATCAG TGGTTTCTTC 2220
	TCACAGTATC AGAATGTAGG CTCTATGAAA AATACGGGTG TAGACCTTTC TCTTAAGGGG 2280
	ACGATCTACC AAAATAAGGA CTGGAATGTA TATGCTTCTG CGAATTTCAA CTACAATAGA 2340
	CAGGAATATA CAAAGCTTTT CTTCGGTCTC AATAAGTACA TGTTCCTTAA TACCGGTACT 2400
	ATATGGGAAA TTGGGTACCC CAATTCGTTT TATATGGCTG AATATGCTGG AATCGACAAA 2460
10	AAAACCGGTA AGCAGTTGTG GTATGTTCCCT GGTCAAGTCG ATGCGGATGG TAATAAAGTT 2520
	ACAACAAGCC AGTACPCAGC TGACTTGGAG ACACGAATTG ATAAGTCTGT TACTCCTCCT 2580
	ATTACAGGTG GTTCTCCTT AGGTGCTTCT TGGAAAGGAC TTTCTTTAGA TGCTGATTTT 2640
	GCCTACATCG TTGGTAAATG GATGATCAAT AATGACCGTT ACTTTACAGA GAATGCAGGT 2700
	CGATTGATGC AATTAAATAA AGATAAAATG CTATTGAATG CCTGGACAGA GGATAATAAA 2760
15	GAACACAGATG TTCCAAAATT GGGACAGTCT CCTCAGTTTG ATACGCATTT GTTGGAGAA 2820
	GCTTCTTTCC TGGCTTTGAA GAATCTCAA CTCACCTATG TACTCCCAA TAGTCITTTT 2880
	GCTGGGCAGA ATGTGATTGG TGGAGCTCGT GTCTATTGTA TGSOGCGCA TCTGTTAACT 2940
	GTTCAGAACT ATAAAGGCTT TGACCCTGAA GCAGGGGGGA ATGTGGGAAA AAATCAATAT 3000
	CCTAATTCTA AGCAGTACGT TGGGGGTATT CAGTTGTCTT TC 3042
20	
	(2) INFORMATION FOR SEQ ID NO:162
	(i) SEQUENCE CHARACTERISTICS:
25	(A) LENGTH: 2463 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: circular
30	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
	(iv) ANTI-SENSE: NO
35	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORPHYROMONAS GINGIVALIS
	(ix) FEATURE:
40	(A) NAME/KEY: misc feature
	(B) LOCATION 1...2463
	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:162
45	ATGAAGAAAA AGAATTTTTT GCTTCTTGCC ATTTTCGTTG CTTTGCTGAC TTTTCATCGGC 60
	AGCATGCAGS CACAACAGGC CAAAGATTAT TTCAACTTTG ACGAACGGGG CGAGGCGCTAC 120
	TTCTCACTCA AAGTGCCTGA TAGGGCCGTT CTACAAGAGC TGGCTCTGAT CATGTCCATC 180
	GACGAGTTTG ACCCCGTAA CAAATGAAGC ATTGCCTATG CCAGCGAAGA GGAGTTCGAG 240
	GCATTCTTGC GCTATGGGCT CAAGCCTACA TTCTTGACTC CTCCATCCAT GCAGCGCGCT 300
50	GTGAGATGT TCGACTACCG CTCAGAGAAA AAATACGAAT GGAATGCTTA CCCCACCTAT 360
	GAAGCCTATA TCAGCATGAT GGAAGAGTTC CAAACAAAGT ATCCATCACT TTGTACTACT 420
	TCCGTCATTG GCAAGTCCGT AAAGGATCGT AAATCTGATG TTTGCAAGCT GACGTCCTCT 480
	GCCAATACAG GGAAGAAAGCC TCGCGTCTC TATACTTCTA CGATGCACGG AGACGAAAGC 540
	ACCGGATATG TGSTACTGCT CCGACTCATA GACCATCTGC TGTGCAACTA CGAATCCGAT 600
55	CCGAGGATTA AGAATCTCT GGATAAAGC GAAGTATGGA TCTGCCCTTT GACCAATCCG 660
	GACGGAGCAT ACAGAGCCGG AAACCAACAC GTACAAGGAG CTACTCGCTA CAATGCCAAC 720
	AATGTCGATT TGAACCGTAA CTTCAGGAT GATGTAGCCG GTGATCACCC CGATGGAAAA 780
	CCTTGGCAGC CGGAGGCCAC TGCAATCATG GATTGGGAG GAACACCTC TTTCTGTCTC 840
	GGTGCCAATA TACATGGAGS AACAGAGGTG GTGAACATC CATGGGATAA TAAAAAGAA 900
60	AGACATGCAG ACGATGAGTG GTACAACTG ATCAGTCGCA ACTACGCAG CGCTTGTGAC 960
	AGTATTTCCG CCGACTACAT GACCTCCGAA ACCAATTCGG GAATCATCAA CGGTTTCAGAC 1020
	TGGTATGTAA TTCGCGGAAG TCGTCAGGAC AATGCAAAAT GTGCCGGCCT CTCAACTTCC AAAGTATTGG 1080
	ATTACCTTGG AAATCAGCAA CACGAAGTTG GTGCCGGCCT CTCAACTTCC AAAGTATTGG 1140
	AATCTGAACA AAGAATCTCT GCTTGCTCTG ATCGAAGAAT CCTTATACGG CATCCATGGT 1200
65	ACAGTGACTT CCGCTGCGAA CGGACAGCCT CTCAATGCC AGATCTTGAT AGAAACCAT 1260
	GACAAGCGCA ACTCCGATGT TTACTCGAT GCTACACAG GCTACTAGT ACGTCCATC 1320
	AAAGCCGGCA CTTATACGGT GAAATACAAA GCGAGGGT ATCCTGAGGC AACTCGTACC 1380
	ATTACGATCA AGSACAAAGA AACCGTCATC ATGGACATG CATTTGGGCA CTCGGTTCTT 1440
	CTCCGTGTAC CCGATTTCAC AGCTTCTCCT ATGACCAATC CAGTAGGCGA AAGCGTCCAA 1500
70	TTCCAAGATC AAACGACAAA TAACCCACAG AATTGGGAGT GAGCGTTTGA AGGCGGACAG 1560
	CCTGCCATGA GTACAGAGCA GAATCCGCTC GTATCCTATA GTCATCCCGG TCAGTACGAC 1620
	GTTACGCTCA AAGTGTGGA TGAAGTGGT TCCAACACGA TTACGAAAGA AAATTCATC 1680
	ACTGTCAATG CCGTTATGCC TGTAGCTGAA TCGTGGGTA CCCGACGGA AATAGAAAGAG 1740
	GGCCAGACGG TATCTTTCCA AAACCAATCC ACCAATGCCA CCAACTACGT ATGGATATTC 1800
75	GATGSCGSCA CTCCGCTAC CAGTGAAGAC GAAACCCGA CTGTGCTTTA CAGCAAGGCC 1860
	GGCCAATACG ATGTACAGCT CAAGGCGATC AGTGCTTCCG GTGAAACGGT GAAGACGAAA 1920

111/ 490

5 GAAAAATACA TCACTGTCAA GAAAGCTCCG GTCCCTGCTC CGGTAGCCGA CTTCGAAGGA 1980
 ACACCTCGAA AAGTAAAGAA AGGCGAGACA GTTACTTTCA AAGACTTGTC TACGAACAAT 2040
 CCGACTTCAT GGCTTTGGGT GTTCGAAGGC GGCTCTCCTG CCACCAGCAC GGAGCAAAAC 2100
 CCGGTGGTCA CCTACAATGA AACAGGCCAAG TACGATGTCC AGCTGACTGC CACCAACGAG 2160
 GGGCGAAGCA ATGTGAAGAA AGCAGAAGAC TACATTGAGG TTATCCTCGA TGACAGTGTC 2220
 GAGGACATAG TGGCACAGAC GGGTATCGTC ATTGCTCCGC AAAACGGGAA GAAGCAGATC 2280
 CTCATAGAAG CCAACGCTGC TATCAAAGCG ATCGTTCTCT ATGACATCAA TGGACGGGTC 2340
 GTACTCAAAA CTACTCGAA TCAGCTCCGC TCGACCGTAG ATCTTTCCAT CTGCCCCGAA 2400
 10 GGAATCTACA CCATCAATAT CAAAACGGAA AAATCCGCTC GCACGGAAAA GATCCATATC 2460
 GGG 2463

(2) INFORMATION FOR SEQ ID NO:163

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 20 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 25 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 30 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...228
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

35 ATGGGACTGA TCAAGGCTTT TCTCGTGCAA CTCTTACTGC TCCCCATTTT CTCTACAAAG 60
 CGGTTTATAT CGCCGCTTAC ACGGCTTCA TGCCGGTTTA CCCCCTCATG TTGTCCTTAT 120
 GCCATCGAAG CTTTACGTAA ATATGGCCCG GGCAAGGAC TATTGCTGAG CATCAAGCGT 180
 40 ATTCTCCGCT GTCAACCCGTG GGGTGGAAAT GGCTATGACC CCGTTCCG 228

(2) INFORMATION FOR SEQ ID NO:164

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2577 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 50 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 55 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 60 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2577
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

65 ATGGCATACG ACTTTACACA AACATTCCGC AACAGCCTGG AGTACAGCTA TCAGGAAGCA 60
 ACCCGTCTCG GCGTCGTAGC CGTGACGCAA GATATGCTCG TACTCGGTAT CATTCGCGAC 120
 GGAGACAATG GCGCATCGA CATCATGGGG CACTATGGGA TCAACTTGTA CGAACTCAAA 180
 CGGTTGATCG AGTTGGAAGC CATCGCCGAG AGTTTGCTCG CTTCGCTGA GGGATCGCCC 240
 ATCTTCACCC CTTCGGCTCG GGAGGCTATC GATGATGCLA CAGACATCTG TGCCGACATG 300
 70 GAGGACGAGG CCGTCAGCCC GGTCCATCTG TTGCTGAGTA TCCTCAACTC GACACAGGAG 360
 AGCTTAGTAC AAAAGATATT TATGAAACAA GGTATAAAAT ACGACACCAT CCTGTCCGAT 420
 TACTTCGGAC AGCGCAACCC CTCGAAGGG AAGTCTCCCT CCGAAATGGA GATCCTCGAC 480
 GGGTACCAAG ACAACGACTT CGACGACGAA GAGGACGAAT CCTCTCGGCC TTCCGGGAAT 540
 AGCGGACAG GCGGAGGCTC CGGCGACGCC CCCGAACAGA ATACCGGCGG AGGCGATACT 600
 75 ACCACCACGA CACGGAGTGG AGGCGACACG CCGCACTGG ACACCTTCGG CACCGACATC 660

TTGCCTGAST CTGACGACTA CTTACCGTG GCCGGATTTA TCCTGAATAG CCATCAAAAT 1140
ATCCACACAGG CCAATGAGGT CGTGAGATT GCTCCTTATA CTTTACCAT TCTCAGATCT 1200
TCTTCCACCA AGATCGAAGT GGTGAAAATG TCCATCGACG ACCAATCGAA C 1251

5

(2) INFORMATION FOR SEQ ID NO:166

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...879

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

30 ATGAAACAGA ACTACTTCAA AAGAGTCTGC TCACTGCTTT GGCTGGTTTT ACCCATGCTT 60
ATTATGCCAT TGAAGTAGC AGCTCAAGAG ATTATTCCGA ACGAAGAGGT GTTGGGAATCA 120
TTGACTTTTCG TTGCACCGGT TGAGGAGACA GACGCAATAG AGGCAGAGGT AGAAGCTCTG 180
CAGGAGATAG TCGCTACTGA GGAGATTGCG GAGCAGGCTG TTCGTTCTTA TACCTACAG 240
GTCTATCGTG ATGGCGTGAA GATTGCTTCA GGATTGACTG AGCCCACTTT TCTCGATGAA 300
GATGTTCCCTG CCGGCCGAACA TACCTACTGC GTAGAAGTAC AGTATCAGGG AGGCGTATCC 360
35 GACAAAGTAT GCGTGGACGT ACAGGTGAAG GACTTCAAAC CGGTTACCAA TCTCACCGGA 420
ACTGCTTCCA ATGACGAAGT TTCTTTGGAC TGGGACGGTG TGAAGAGAA AGCTGAAGAG 480
CCGGCAAGTG ATAAAGCAGT CAGCTACAAC GTCTACAAGA ATGGAACCTT GATCGGTAAT 540
ACAGCTGAAA CTGATTATGT GGAGACCGGT GTAGCCATG GTACATACAT CTACGAAGTG 600
GAAGTAAAGT ATCCTGACGG TGTATCTCCG AAGGTGGCTG TAACCGTGAC CGTGACCAAC 660
40 AGCTCATTTGA GCAATGTAGA TGGACAGGCT CCTTACACAT TGCGAGTAGA AGGCAAGAAG 720
ATTATTGCGG AAGCCCATGG TATGATCAGG CTCTACGACA TCAACGGAAG TACCGTGGCC 780
GTAGCCCGGA ATCGATTGGA ATACATGGCG CAACCGGTT TCTATGCAGT GCGCTTCGAT 840
GTGGGGAATA AACACCATGT ATCGAAAATA CRAAGTAAGA 879

45

(2) INFORMATION FOR SEQ ID NO:167

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...936

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

70 ATGATTCTCT TAAGCGAGAG TTTTGAATCA GGTATTCAG CTATATGGAA GACCATTGAC 60
GCAGATGCGG ATGGCTATAA TTGGATGCAT TTGACCAATT TCACGGGACA GAGTGGTCTC 120
TGTGTCTCTT CGGCTTCATA CATAGGCGGC GTCGGAGCTT TGACTCCGGA CAATTATCTG 180
ATAACACCGG AATTAAAACT ACCACAGAC GCGTTGGTGG AAATAATCTA TTGGGTATGT 240
ACTCAAGATC TCAGTGCTCC ATCGGAGCAC TATGCGGTTT ATTCTCTTTC TACAGGCAAT 300
AATGCTGCTG ACTTGTATA TCTCTTATAT GAAGAGACTT TGACTGCCAA ACGGATACAA 360
75 TCCCCCGAST TGATCCGCGG AAATCGGACA CAAGGTGTTT GGTATCAAAG AAAGGTGGTA 420

114/ 490

5 CTCCCTAAGC ATACTAAATA TGTTGCTTTC CGCCATTITA ATTCCACGGA TAATTTCTGG 480
CTCAATTTGG ATGAAGTATC TATCTGTAT ACCCCTCTTC CCCGAAGAGC TCCGTGTCCG 540
CATCCGGGTG GTTACACTTA TTCTGTATTC CGTGATGGAC AAAAGATAGC GAGTGGATTG 600
TCGGCATTGG CATATATCGA TACGGATGTA CCGTATGGGA CTCAGACTA TTGTGTCCAA 660
GTCAATTATC TGCAAGGAGA CTCGTATAAA GTCTGCAAAA ATATAGTGGT GGCAAAATCT 720
GCAACATCT ATGGGGCCGA TAAGCCTTTT GCGTTGACCG TGGTTGGCAA GACCAATTGT 780
GCGAGTGTCT TCAAAGGAGA GATCACTCTT TATGACATTC GTGGCCGGCT GATAGCTTCC 840
GGTTCGGATA CGCTTAGGTA CAAAGCGGAA AATGGTITTT ACCTCATTAA AATACAGGTA 900
10 AACGGAACCTG TCTATACTGA GAAATCCAA ATCCAA 936

(2) INFORMATION FOR SEQ ID NO:168

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

35 ATGAAAAA GTTTTCTTT AGCCATAGTA ATGCTCTTTG GCATTGCCAT GCAGGGACAT 60
TCTGCTCCGG TTACGAAAGA GCGAGCTTTG AGTCTGGCTC GGCTGGCTTT GCGACAGGTA 120
TCCTTGGCAA TGGGACAAAC AGCAGTATCT GACAAGATT CCATCGATTA CTTTATCCGG 180
CAAGGAGATG CTGAGAGGGG TATCAGATCA CAAGAGGAAG GCTCTCTGTC ATATTTTAT 240
GTAGCTAATC GTGGAATATA TGAGGGCTAT GCTCTGTAG CAGCAGATGA CAGAATACCG 300
40 ACAATTTTAG CCTATTCCAC CATTTGGCCGT TTCGACATGG ACAGTATGCC GGACAATCTT 360
CGCATGTGGC TACAAATTTA CGATCAGGAA ATAGGCCCTGA TACTTTCCGG AAAAGCTCAG 420
CTCAATGAAG AGATATTACG TACCGAGGGC GTACCGGCTG AAGTACATGC TCTGATGGAT 480
AAGCGTCAAT TTGCAACGTA TCCCATGCGA TCGAATCAAG GTTACCCATG GAACAATAAG 540
GAACCACTGC TTCTAATGG CAATCATGCC TATACCGGCT GTGTGTCTAC TGCTGCAGCA 600
45 CAAATCATGC GCTACCATAG CTGGCCGCTT CAAGGTGAAG GCTCTTTGGA TTATCATGCA 660
GGTTCTATTG TTGGCAACTG GTCGGCCACA TTTGGTGAAA TGTACGACTG GATCAATATG 720
CCCGGAATTC CCGACCTTGA TAATCTGACT CAATCTCAAG TGGATGCTTA CGCCACACTG 780
ATGCGTGATG TGAGTGCATC TGTTCGATG AGTTTTATG AAAATGGAAG TGGTACGTAC 840
50 AGCGTTTATG TAGTAGGAGC CTTGCGAAAC AACTTTCTGT ACAGCGCTTC ACTGCAGCTA 900
CATGTACGCG CCTTATATAC CTCACAGGAG TGGCACGATA TGATCCGCGG GGAACCTGCC 960
TCCGGAAGGC CGGTCTATTA TGCAGGGAAT AACCAGAGCA TAGGACATGC TTCTGTTTGC 1020
GATGTTATG CTTCGGATGG TACTTTCCAT TTCAACTGGG GTTGGGGAGG TGTTTCCAAC 1080
GGTTTACCA TTTATCAAGA GATCATCACC GGTATCGAAG CCGCTAAGAC TCCCGCTGAA 1140
55 GCCGGTACAG ATGCTTTGCC GATCTTGGCA CTGAAAGACA TAGAAGCCGA GTATAAAAGT 1200
GAATCCGGAT TGAACGTAGG GTATTGATA TATAATACAG GTGAAGAGCA ATCAAACTCT 1260
GACCTCGGAT ACAGATTGAA CAAGGCTGAC GGAGAAGTCA TAGAGGTGAA AACTCATCT 1320
ATCAATATCT CTTGGTACGG ATACGGAGAG CATCCCGAGA GTTCTTCATT GGCACCTAAT 1380
CAGTTGTCCAC AAGGAATCAA CACCATCACC CTACTTTATC GTCCGACAGG CACCGAACAG 1440
60 TGGGAGCCGG TACGGCATGC ACAGGGAGGA TATGTCAATA GCATTAAAGT AAATACGACA 1500
GACCCGAACA ATGTGCTAGT CACGGTAGAT AATAACGAAG GCAAGCTCAG TATCGTCCCC 1620
AACAGCTTGG TCGCAGATCT GAATTCCTAT GAACATAGTA CGATTACAGT ACAGTTCAT 1680
AGCGACAGCC CTGATGAGAT CCGTACACCC GTAGCCTTTG CTCTATCTAC AGGAGCTACT 1740
65 CCGCAGCATG TAATATCTTT GGGCTGGGTA ATGGCTGAAG TTCCGGGGCGG TAGCAGCAAC 1800
TATCCGGTGG TTTGGTCTAA AGACGTTCTC ACTCTCTCGG AAGGCGACTA TACATTGTGG 1860
TATAGATTTT CCATCAACAA CAAAAGGAT GAATGGAAAA AGATCGGAAG CGTGTCACTA 1920
TATACGCTGG ATATGGCACA CAACAGAGTA TTGCCCGACT TTACACTCAA AAATCTCGGA 1980
70 TTGCTTTTCA ATGGTGAGTT GGTGTGTGTT TTCCGCCAMA CACAATCTCT ATCGGGGTCT 2040
TTATGGGCGC CTCAAGAAAC AGTACATATC AAGCAAGGAG AAATTTCTGT ATATAAACCT 2100
GTTGTGCAAG GCCCTATACC TGATGGATCC TATCGTGCGA CCTCTCATGC ATTCGTAAC 2160
GGACAACAAC AGTTGTACCT CAAGGGGAAA AGGAATACA CCGTGAAGAT CGTCAATGGT 2220
ACAGCGGTAG AAGCAATAGA ATCGTCAGAA GAGATCAGAG TATTCCTTAA TCCGGCACGC 2280
75 GATTATGTGG AAATATCGGC ACCTTGCAAT CCCCAGAAA CATCTATCAT TCTTTCTGAT 2340
CTGTACGGCA AGATTGTCAT GAAGAATAGT TTATCAGCGG GGCATGGCAG AATGGATGTC 2400
2460

AGCCGACTTC CTAATGGGGC CTACATCCTT AAGGTGGATG GATATACGAC GAAAATAAAT 2520
ATAGTGAC 2529

5 (2) INFORMATION FOR SEQ ID NO:169

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 870 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

10

(ii) MOLECULE TYPE: DNA (genomic)

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...870

25

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:169

ATGAAAAAGC TATTTCTCTC GCTCAGAGT CTTGTAATGG TCTTCGCTGT TCCAAAGTTGC 60
GATATAATCG ACAAGGATCA AACCTCTCTG CCGGCTCCGA CCAATGTGAC ACCCGATAAT 120
30 CCGGATGACA ATCCTTCGGA GATCGACATT ACGCAGACGC ACACAGAAAA ATATGTTTTG 180
GCTGAAGAAT TTACCGGCCA AAAATGTCCTC AACTGTCCGA AAGGTCATCG CAAACTGGCG 240
GCTCTCAAGG AGCAATACGG TAAGAGATTG ACTGTTGTCTG GTATACATGC CGGCCCTGGA 300
TCTCTCGTGC CACCTCTTTT CCGTACAGAA GCCGGAGACG CATATTATAG CAACTTCGCC 360
AATAATACCC CTCTCCCTGC GCTGATGGTT TCGCGCAAAA AGTTGGGCTC TTCTACGTT 420
35 TATGATAAGA GCTACAAAAC GTGGGACGTG CCTATTGCCG AGCAGATGGA CCAAAAGGCG 480
AAGATCAATA TCTTTGCCGT GGCCGAATAC ACCGATACCC AAAAGATCAA GGTGACTGTA 540
AAGGGTAAAA TACTGGAGGG GAATACACTC CGGAAGTCCA TGGTTCAGGT GTATCTGTTG 600
GAGGATAAGC TGATCGCTCC GCAGGTGGAT GGCAATACGA CAGTCGAGAA TTACGAGCAC 660
AATCACTGTG TCGGTGGAGC CGTTAATGGT ATTTGGGCGC AAGAATTTGT GAATCTCAAA 720
40 GATTATTTGT ATACTTACGC CGTTGAACCG CTCCTGGGTA TGTCTTCGT AGCCGAGAAT 780
TATTCGATTG TGGCTTTTGT ATACGATGTG CAGACGTTG AAGTGATGA CGTTGTGCAT 840
GTAAAGATCA ATCCGCAATC CGATGGCAAA 870

45 (2) INFORMATION FOR SEQ ID NO:170

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

50

(ii) MOLECULE TYPE: DNA (genomic)

55

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

60

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...669

65

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGAAGAAAT CAAGTGTAGT AGCCTCAGTT TTGSCCGTGG CTCTCGTGT CGCCGTTTGC 60
GGACTGAACA ATATGGCAA AGCGGCGCTT ATCGGCGCCG GAGTAGGAGG TGCCATTGGT 120
70 GCCGGACTAG GTAAACGTAG CGGAATACG GCTGTCCGTT CCATCGTCGG TACTGCAGTC 180
GGTGGAGCAG CCGGTGCTCT CATCGGAAG AAGATGGACA AGCAGAAAAA AGAACTGGAG 240
GCCGCACTAC CCGATGCTAC GATTGAGACA GTAAATGACG GAGAGGCTAT TCTGGTTACT 300
TTCCGATACG GTATCCTCTT TGCGACGAAC TCCAGCACTC TGAGTCCCAA CTCACGCACT 360
GCGCTGACGA AGTTTGCTGC AAACATGAAC AAAAACCCCG ACACGGATAT TCGTATCGTA 420
75 GGCCATACCG ACAATACCGG CTCGACAAAG ATCAACGATC CTCTCTCTGA GAGACGTGCA 480

116/ 490

GCCAGCGTAT ATTCTTCTCT GAATTCTCAG GGTGTGASTA TGTGCGCAT GGCAGCCGAA 540
GGGCGTGGGA GCCATGAACC GGTGCGAGAC AATAGCACAG TTGCGGAGC TTCGGCCAAC 600
CGCCGTGTGG AGGTTTATAT CTTGCGAAT GCCAAGATGA TCGAACAAGC ACAGCAAGGT 660
ACGCTGAAG 669

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(2) INFORMATION FOR SEQ ID NO:171

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1011 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

15

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

20

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1...1011

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

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ATGTCGAAAA AATCGATCCT TCTGCTTTCG TGTTCGCTGT GCTTCATTTC TGCTACGAAG 60
GCTGTGACCC CCGTCAGAAA TGTGCGCAAT AGCCAAGTGA ACAGCAAAGC AAAGACCGAA 120
CGTACAAAGC CCTCGGACTC TGTACGGTAC ATTAGCAACA TGATTGCAGA TCCGCTGGAG 180
TTCCGCAACA AGATTCTCTC CGAAAAAGAG CTAGAAAAG CCGAATATGA AATCGGCTG 240
GCGATGGAAG CACTCAATTA CCCTGCCATA GATTATATG GTGAAGATTC TTGGAGCGAG 300
TATGTAAACC CTTTCGTGGG TGCAGGAACC GATGTCGAAA TTCCGAATC CTATGACATT 360
GATTGCTCTT CGTTCGTGAT GCCCGTCGAA GATAAGCAGG TCACCTCTCA ATTGGCTAC 420
CCTCGGCGTT TCGGACGGAT GCACTATGCT ATTGATCTTT CAGTGAATCG TGGCGATACG 480
ATACGAGCAG CCTTTGACGG GAAAGTTCGT GTACGCAGCT ATGAAGCGCG TGGCTATGGC 540
TACTACATAG TCTTGGCCCA TCCGAACGGA CTGGAGACTG TGTACGGACA CATGAGTCGG 600
CAATTGGTAG ACGAGATCA GATCGTTGGA GCAGGACAAC CGATCGGATT AGGAGGCAGC 660
ACGGGTGAAA GCACCGGTCC TCATCTTCAC TTCGAGACOC GGTTCATGGG TATTCCTATC 720
AATCCGAGTA CCATTATAGA CTTGATAAAC GGAGTGCCGC TCCGAGACAT TTACACATT 780
AAAGGAGGA GCAATTCTCG CTATGCAAAA GCCTCTAAGA CTTCTTCTCG CTATGCAAAA 840
AAAGGGAAGA AAGGCAGACA AGCTTCTTCT CCTATGACCT ATAGAATCAA AAAAGGCGAT 900
ACTTTGGAAA CAATAGCCAA AAGGCACGGC ACTTCTGTTC AGAAACTCTG TGCTACCAAT 960
GGCATTTGGA AGAGTAAAT TTTGACTCCG GGCAAAACCT TGAGGATCAA A 1011

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(2) INFORMATION FOR SEQ ID NO:172

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

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- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

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- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1...453

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

ATGSCAAAAA TCAATTCTA TGCTGAAGC CTCAGCCTTC CTCGGATCAG AAGACGGATC 60
GTCGTAAGT GGATAGCCGA AGTATGCAGC CGATATGGGA AAGCGGTGGG AGAAATCTCC 120
TATCTTTTCT GTGATGACGA ATATATCTTG AAAGCCAATC AGGAATTTCT CGATCATGAC 180
TACTACACCG ACATCATCAC CTTGATTCC TGCGAAGCGG ATACGGTGAA TGGCGACCTG 240

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117/ 490

5 CTTATCAGTC TCGATACCGT ACGCTCGAAT GCCCGTGCTC TTGATCTTCG ATACGAAGAC 300
GAACTGCATC GTGTCAATTAT CCACGGCATA CTGCATCTTT GCGGATTGAA AGACAAGAGC 360
AAAAAGGATG AAGCCCAAT GCGTGCAGCC GAAGAGAAAG CCCTTGTCAT GCTGCGAGAA 420
ACCATCGGAT CGGAGCTTTC CCTATTGCAT ACA 453

(2) INFORMATION FOR SEQ ID NO:173

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

30 ATGAAGGTAA AGTACTTAAT GCTCACATTG GTTGGAGCAA TTGCACTGAA CGCAAGTGCA 60
CAGGAGAATA CTGTACCGGC AACGGGTCAG TTACCCGCTA AGAATGTTGC TTTTGCTCGC 120
AATAAAGCAG GCAGCAATTG GTTTGTAACA CTGCAASGCG GTGTTGCAGC GCAGTTCCTC 180
AATGACAACA ACAACAAGA CCTCATGGAC CGCTTAGGAG CCATAGGTTT TCTTTCTGTC 240
GGAAAGTATC ACAGCCCTTT CTTTGCAACT CGTTTGCAA TTAACGGAGG TCAAGCCAC 300
35 ACTTTCCTCG GAAAAAATGG CGAACAAGAA ATCAACACCA ATTTTGGTGC AGCTCACTTC 360
GACTTTATGT TTGATGTGGT TAACTACTTT GCACCATATC GCGAAAATCG TTTCTTCCAT 420
TTAATTCCAT GGGTAGGTGT TGGCTACCAA CACAAATTCA TCGGTAGCGA ATGGAGCAAA 480
GACAATGTGG AATCACTGAC GCGCAATGTA GGAATATGA TGGCTTTCAG ATTAGGAAAG 540
CGAGTAGACT TTGTGATCGA AGCACAAGCA GCTCACTCCA ATCTCAATCT AAGTCGCGCA 600
40 TACAATGCCA AGAAAACTCC CGTATTCGAA GATCCGCGAG GACGTTATTA CAATGGATTTC 660
CAGGGGATGG CTACAGCAGG TCTTAATTC CGCCTGGGAG CCGTAGGCTT CAATGCCATT 720
GANCCATGAG ACTACGCACT TATCAATGAT CTGAATGGTC AGATTAACCG TTTGCGCAGC 780
GAGGTCSAAG AACTCTCAA ACGTCTCTGA TCATGCCCGG AATGTCCTGA AGTAACTCCT 840
55 GTTACTAAGA CAGAAAATAT ACTGACGGAA AAAGCTGTAC TGTTCGTTT CGACAGCCAC 900
GTGTGTGACA AAGATCAATT GATCAACCTG TATGACGTAG CTCAGTTTGT AAAAGAAACT 960
AACGAGCCGA TTACCGTTGT TGGTTATGCT GATCCTACGG GTAATACTCA ATACAACGAG 1020
AAATTTGCTG AGCGTCGGGC TAAAGCCGTT GTTGATGTTT TGACAGGTAA ATATGGTGTG 1080
CCTTCGGAAT TAATCTCTGT AGAATGGAAG GCGGACTCTA CGCAACCGTT CAGCAAGAAA 1140
50 GCTTGSAAAT GTGTTGTAAT CGTTGCTCC AAG 1173

(2) INFORMATION FOR SEQ ID NO:174

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 60 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 65 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 70 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

75 ATGACATACA GAATTATGAA AGCTAAATCT TTATTATTAG CACTTGCGGG TCTCGCATGC 60

118/ 490

5 ACATTTCAGTG CAACAGCCCA AGAAGCTACT ACACAGAAC AAGCAGGGAT GCACACCGCA 120
TTCCAAACGTG ATAAGGCCTC CGATCATTGG TTCATTGACA TTGCAGGTGG AGCAGGTATG 180
GCTCTCTCGG GATGGAATAA TGATGTAGAC TTTGTAGATC GTCTAAGTAT CGTTCCTACT 240
TTGGGTATCG GTAAATGGCA TGAGCCTTAT TTCGGTACTC GTCTCCAATT CACAGGATTC 300
GACATCTATG GATTCCCGCA AGGGAGCAAG GAGCGTAACC ACAATTACTT TGGAAACGCC 360
CACCTTGACT TCATGTTTGA TCTGACGAAC TATTTGGGTG TATACGTCC CAATCGTGTC 420
TTCCATATCA TCCCATGGGC AGGTATAGGA TTTGGTTATA AATTCCATAG CGAAACGCC 480
AATGGTGAAA AAGTAGGAAG TAAAGATGAT ATGACCGGAA CAGTIAATGT CGGTTTGATG 540
CTGAAATTCG GCCTATCAAG AGTCGTAGAC TTCAATATTG AAGGACAAGC TTTTGCCGGA 600
10 AAGATGAAC TTTATCGGGAC AAAGAGAGGA AAAGCAGACT TCCCTGTAAAT GGCTACAGCA 660
GGTCTAACGT TCAACCTTGG CAAGACAGAG TGGACAGAAA TTGTTCCCTAT GGAATATGCT 720
TTGGTCAATG ACCTGAACAA CCAATCAAC TCACCTCGCG GTCAAGTGGG AGAGTTGAGC 780
CGTCGTCCTG TTTATGCCC TGAATGCCCT GAGCCTACAC AGCCTACAGT TACTCGTGTGTA 840
15 GTCSTTGACA ATGTGGTTTA CTTCGGTATC AATAGTGCAA AGATTGATCG TAATCAAGAA 900
ATCAATGTTT ACAATACAGC TGAATATGCG AAGACCAACA ACGCACCGAT CAAGGTAGTA 960
GGTTACGCTG ACGAAAACCG CGGTACTGCG GCCTATAACA TGAAGCTTTC AGAGCGTCGT 1020
GCAAAAGCGG TAGCCAAGAT GCTTGAAAAG TATGGTGTTC CTGCGGATCG CATTACAATT 1080
GAATGCAAGG GCTCATCAGA GCAATCTAT GAAGAGAAGC CTTGGAATCG TATTGTAGTA 1140
20 ATGACTGCAG CGGAA 1155

(2) INFORMATION FOR SEQ ID NO:175

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 40 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...570
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

45 ATGGAATTTT TCATGTTTAT CATAGCGGCG GTTTTCGTTA ATAACGTCGT GCTGTGCGAG 60
TTCTCGGTA TATGCCCAT CTAGGCGTA TCGAAGAAGG TAGACACCTC AATCGGTATG 120
GGTGCAGCCG TGACATTGCT ATTGGCACTG GCTACCTTGG TTACCTTCCT GATTCAGAAG 180
TTCTGTTTGG ATCGTTTCGG ATTGGGCTTT ATGCAGACCA TTGCATTTAT TTTGGTCATT 240
GCCGCTTGG TGCAATGGT GGAGATCATA CTCAAGAAAG TATCTCTCC CCTGTATCAG 300
50 GCACTGGGTG TATCTTGCC CTTGATTACG ACGAAGTCTG GTGTGCTCGG TGTGGCTATT 360
TTGGTTATCC AGAAGGATTA TACCCTGCTC CAGAGCTTCG TCTATGCAAT ATCCACGGCT 420
ATCGGTTTCA CTTTGGCAAT GGTACTTTC GCAGGTATTC GAGAGCACT CGATATGACC 480
AATCTCCCA AAGCTATGAA GGAATACCT TCGGCACTCT TGGTGCCTGG TATATTGGCT 540
55 ATGGCTTCA TGGGCTTCAG CGGTATCGCC 570

(2) INFORMATION FOR SEQ ID NO:176

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...558

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:176

5	ATGTTATTCA TAGCGGCGGT TTTCGTTAAT AACGTCGTGC TGTGCGAGTT CCTCGGTATA	60
	TGCCCATTC TAGGCGTATC GAAGAAGGTA GACACCTCAA TCGGTATGGG TGCAGCCGTG	120
	ACATTCGTAT TGGCCTTGGT TACCTTGGTT ACCTTCTCTGA TTCAGAAGTT CGTTTGGAT	180
	CGTTTGGAT TGGGCTTTAT GCAGACCAAT GCATTATTT TGGTCATTGC CGCCTTGGTG	240
10	CAGATGGTGG AGATCATACT CAAGAAAGTA TCTCCTCCCC TCTATCAGGC ACTGGGTGTA	300
	TTCTTGCCCT TGATTACGAC GAACTGCTGT GTGCTCGGTG TGGCTATTTT GGTATCCAG	360
	AAGGATTATA CCTGCTCCA GAGCTTGTG TATGCAATAT CCACGGCTAT CGGTTTCACC	420
	TTGGCAATGG TTACTTTCCG AGGTATTCCA GAGCAACTCG ATATGACCAA TCTCCCAAA	480
	GCTATCAAGG GAATACCTTC GGCACCTCTG GCTGCCGTA TATTGGCTAT GGCTTCATG	540
15	GGCTTCAGCG GTATCGCC	558

(2) INFORMATION FOR SEQ ID NO:177

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(11) MOLECULE TYPE: DNA (genomic)

(111) HYPOTHETICAL: NO

(1v) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(1x) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2499

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:177

40	ATGAACAAC TAAACATTAT CAGCTTCATC ATTGCTTTCC TATTCTTAGG AACGAGCGCA	60
	TCGGCTCAGC AATCGGGCGG ATCCGTTACA GGTACCGTAG TGGACAAAAG CTCAAAAGAA	120
	CCTATCGCAT ACGTACAAGT ATTCTGTCAAA GGAACCACTC TCGGAACCTC CACGGATGCA	180
	AACGGAACCT ACTCGATCAA GGGAAATCCCT TCGGGTAATC AAATATCGT AGCCCGACTC	240
45	ATGGGTTACT CCACTTGCGA AGAAAAAGTA CATATAGAAA AGGGTGGTTC CCGCCACGTA	300
	GACCTCTATC TGACCGAAGA GATTCTCTCT CTCGATGGGG TAGTGGTATC TGCCAATAGA	360
	AACGAGACTT TCCGCGCTCA AGCACCCTCG TTGGTAACTG TACTGTCCGC GGAACCTTTC	420
	CTCAAAACCA ACTCTACCAA CCTGAGTCAG GGACTTAACT TCCAGCCCGG TCTGGCGGTG	480
	GAGGCAACT GTGAGAACTG CGGTTTCAAC CAAGTTCGTA TCAATGGACT CGAAGGAGCC	540
50	TATTGCAAAA TTCTTATCGA CAGCCATCCC ATCTTCAGIT CGCTTGCCGG TGTCTATGGC	600
	TTGGAGCAGA TGCTGCCAA TATGATCGAA CGTGTAGAAG TAATTCGCGG TGGAGGTTTG	660
	GCTCTGTTCC GCTCTAATGC TGTGGGAGGC GTTATCAACG TAATTAACGA AGAACCCGTT	720
	CGCAATTCGG CCGAGATCAG CCATTCTACG ATGACCTTCG ACCACGCGAA AGGGTGGGGG	780
	AGCTTCCAAA ATACGACCCA GTTCAACGGT TCTATGCTGA CGGAAGACCG CAAAGCCGGT	840
55	GTATGGTAT TCGGCCAACA CAACTACCGT CCGGACAGG ATATAGACGG CGACAACCTT	900
	ACCGAATAC CCAATCTGCG CAACCGCTCG CTCGGTTTCC GCTCATACTA TAAGACCGGT	960
	CTCTACAGCA AAGCAACCTT CGAATATCAC AGCATGCAAG AGTACCGTCG TGGTGGCGAC	1020
	AGACTGGACA ATCCTCCTTT CGAAGCCCGC ATAGCGGAAT ATCTCCAGCA CTATATCAAT	1080
	GGCGGAAGTT TCAAAATCGA TCAGGGCTTC AGCGGTGGCA AGGATTTCCT CAGTCTGTAT	1140
60	GCTTCAGCAC AAGACGTTCA GGTCTGTAGC TACTACGGGG GTGGCGACTA TACCGAAAAT	1200
	CTGCTGAACG GAGCAGTTCA GAGTGGAAAG ACCGAATCGG ACGAATACAA CGATGCTTTC	1260
	ACGGCTCTTA CTTCCTACGG GACTACCAAG GGAATCGATT TGCAAGGAGG AGGTATGTAC	1320
	CGTCATACCT TCGGAGAAAA CTGGGACTTT ACCGGCGGAC TCGAATATAT CTACGGCCAA	1380
	CTCGATGACA GAAGCGGCTA CAGACCGAGC AATATAGATC AGAATACCTC TACTTTTAGT	1440
65	CAGTACGACC AGCTCGAATA TAAGACGGAG AAGTTAAGTG CCTTATCGG AGCAGGTATC	1500
	GACTATGTTT TCCTCAATCA GGATGCCAAA CGCTATATCG ATCCGCTCTT CATTTTCAGT	1560
	CCTAGAGCCA ACGTACGATA CAATCCCAAT AAGAACTTCA GCTTCCGACT CTCATACAGC	1620
	GAAGGATTCC GCGCTCCTCA GTATTTCGAT GAAGATCTGC ACGTAGAGTT GGCCGGTGGT	1680
	ACTCCTATCA CCGGTGTCCT TTCCCAATCT CGAAAGAAAG AACGTTACAG AAGCATCAGT	1740
70	GCTTCTTTCG ATTATTACCA CAGAGCCGAC GAATGGCAAT TCAATATCAT GGGAGAAGCC	1800
	TTCTCCACCT TTATCAGCAA TCAGTTTCAA CCATCCGATA AGGTGCAAAAC CACGAGCGAT	1860
	GGCAAGAAT GGATCATTCT TACCATCTAC AACGACAAGG ATGGAGTATC GAAGGTATAT	1920
	GGTGTGAATC TGGAGGGAAG AATCGCCTAC AACAAATCGT TCGACCTCCA GCTCGGCGGT	1980
	ACATGGCAGA GAAGCCGCTA CGGAAGCATC TATACCGCTG TGGAAAGCGA CAAACAACG	2040
75	GGACAAGCCG AGATCTCTGT GAAAGACTAT GTACGCACTC CGAATCTGTA CGGCTATTTT	2100
	GTGCTACGG TACGTCCTAC CGAGCACTTC GCCATCAATC TCTCCGCTAC ATTCACGGCC	2160

5 AAAATGGATG TAGTACACGA AGCCTATGAA GGCGATATTC CCGCAGAAACA CATAGCTCCG 2220
GACGGATCGT TCGACTTTGA AATGAATGGT CAGCAATTC AAGGTTTGGC CGAAGGTCAT 2280
GCCAAGCTCG TCAAGACTCC GGCCTTCGCC GATATAGACC TCAAGCTGAG CCACGACTTC 2340
CACCTTGCTT CCACATATGAC CTTGGAATTG AATGCCGGAA TACAGAACAT ATTCACACGC 2400
TATCAGAAAG ACACGGACAA GGGACCGGGT AGAGCTTCTA CTTACGTATA CGGTCTCTATG 2460
CAGCCAGAA GGATTTTCGT CCGTACAAAG ATCAATTTC 2499

(2) INFORMATION FOR SEQ ID NO:178

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...2673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

ATGTACAAA AGATTATTGC CGTAGCAGCT CTCTCTGCG CAGCATAGG GATCCTGAAA 60
GGACAGTCTT CGGATCTGAC CCCTCAGGAT ACTATATATA GCCCTGAAAT ATCCTATGCC 120
AAGCCTATTC ATAAGACCAT AGCATCTATT GAGATCGAGG GAATGACGTC TTTCGATGAC 180
TTTGTCTTGC GCAATCTTTC AGGCTTGGCT GTAGGTGATG AAGTCTGAT TCCTGGAGAT 240
GCCATGCTCG CTCCTGTGAA TAGAATTATG CGTCAGGGCT ACTTCTCAA TGTGCGAATC 300
ATCGCGGATA AATATGTCGG CAATAAAGTC TATCTGAAAA TCATTGTGAC TGAACGTCCT 360
CGCATCAGTA AGGTTACTTT TAGCGGGGTA AAGAAGTCTG AGAGAGAAGA TCTTGAATG 420
AAATCGGTC TCGCGAGGG GATTACAGAT ACCAGAAATA ATGAAGACAA GGTCAAGCAA 480
ATCGTACAGA ACTATTTTAC TGAGAAAGGT TATCGCGATG CCAGCATACG GATAACGCAG 540
GAACCGGATC TTTCCAAAGA TGGCTTTGTC AATGTGCTTA TCTCGATTGA GAAGAAAAGC 600
AAAACCAAGG TGAATGAAAT TTATTTTTC GGCAACAAGG CCCTTAGCAA TCATAAGCTA 660
AGAATGGCGA TGAAGAACAC CAATGCCAAA TTCAGTCTTA GAAAGCATAT TCGCTCATCT 720
TTCTTGAATC TTTTATGATC TCATAAGTTT GTGGAAGAGA GCTACCGTGA AGATTTGGTC 780
CGATTGATAG AGAAGTATCA GGAATATGGA TATCGTGATG CTCAAACTACT GACCGACAGT 840
GTCGTGAAGG CTCCTGACGG CAAAAGAGTG GATATTTATC TCAACATCCA AGAGGGGCG 900
AAGTATTATA TTAAGGATGT CAATCTTGTG CGCAATTCAC AATATCCATC GGAGTATTTG 960
GAACGAGTGC TCGGAATAAA ATCCGGAGAT GTGTACATC AGAGACGATT GGCTAAGCGT 1020
CTCAATGAAG ATGAAGATGC TGTGGGGAAC CTGTACTATA ACAATGGCTA TATTTTGGC 1080
TGGGTCGATC CCGTGGAAAC AATGTAGTG GGGGATTCTG TTTCCGTTGA TATTCGTATA 1140
CGCGAGGGGA AGCAGGCCAA TATCAATAAG GTGATCATCA AAGCCCGGCC AGCTCTTTAG TCGCGAGGAT 1200
GAAGACGTAG TACGCGGAGA GCTTTACACA AAGCCCGGCC AGCTCTTTAG TCGCGAGGAT 1260
ATCATTAATC CTATTCGTCT CATCAATCAG CTTGGGCATT TCGATGCCGA AAAATCTATT 1320
CCCCGTCGGA TTCCCAATCC CGAAACAGGA ACAGTGGATA TAGAGTATGA TTTGGTGCCG 1380
CGTAGCAGTG ACCAATTGGA GCTTTCTGTC GGTGGAGTC AGTCCGGACT TCTGTTCGGA 1440
GGAGCCATTA AGTTACAGAA CTCTCTGTGC GGCAACTTGC TCCATCCCTC GATGTATAAG 1500
AAAGGGATCA TTCCGCAAGG GGATGGGCAA AACTATCAC TGAGTGCTCA GACCAATGGA 1560
AAGTACTATC AGCAGTATAG TGTCACATTT ATGGATCCAT GGTTTGGGGG CAAGCGGGCG 1620
GATATGTTCA GCTTCAGTGC ATTCTATTCC AAGACTACGG CGATTGACTC CAAGTTCTAC 1680
AATAGCAATC CCGGCAACTA CTATAATGCC TACTATAATA GCTACTACAA CAATATAAT 1740
AGTTATTACA ACGGTATGTC GAACTATACC GCGGACCTCT ATACTCAGGC CAGCGATCCG 1800
GATCGTTCGG TTTCAGATGT AGGTACTTCC ATCGGTTACG GTAAGCGTTC GACTTGGCCG 1860
GACAATTGGT TCCAGATTTA TACTTCTCTG AACTACACCT ACTATAGACT GCGAAATTGG 1920
AGCTACAATA CCTTCCAAAA TTCCATCAT GGCTCGGCTA ATGATCTCAA CTGGAGCTG 1980
CGTCTCTCTC GTACTTCCAT CGATAATCCT ATTTATAACA GAAGCGGATC GGATTTCTATG 2040
GTTTCTGTG GCTACTCTCT TCCTTATTCT TTGTGGGACA ATCAAGACTA TGCCAGCCAG 2100
AAGCTCAGCG TAAGCGATCG TTACAGATT ATCGAGTATC ACAAGTGGA GTTTAGAGGA 2160
CGAGTTTITA CTCCATTGCT CAATCCTGCT ACGCATAAAT ATACACCGGT GCTCATGAGT 2220
CGAGTGGAA GAGGTGATGG TATGTCCAGC TATTATGGTG GCTACATGAA TGAGACTATA 2280
GGTTTGGTG GTTATAAGAA CGGATCTATT GCCGGTAATA ACTACGACTA TGCAATGCT 2340
TATATGCGCG TTACGATGGA ACTACGTTTC CCGATTCTGT TTGAAAACCT ATTCATGCG 2400
TGGCTCTTAG CTTTGGCGGA AGCAGGCAAT GCGTGGCGCA GTATCGCAA TTATAATCCC 2460
TTAACTTGA ACCGATCGCG CGGTGTAGGA TTGCGGTAA CGTTACCGAT GGTGCGAATG 2520
CTCGTATCG ATTGGGGA TGGCTTTGAC CGTCCGGA ATTCTCTACA GCGAGGAGGA 2640

AGCAATGTCC ACTTTGTGCT CGGACAGGAG TTC

2673

(2) INFORMATION FOR SEQ ID NO:179

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

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(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...522

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

ATGAATGGCG	ATATGAAACG	GTITTTGATT	TTGATCGGCT	TTGCACTGGC	GGTAGCTTTC	60
TCCGGTTTTT	CCCAAAAGTT	CGCTTTGGTA	GATATGGAAT	ATATCCTCAG	GAATATTCCT	120
GACTATGAGA	TGATGAACGA	ACAGCTGGAA	CAGGTGTCCA	AGAAATGGCA	AAATGAAATC	180
GAAGCTCTCG	AAAATGAAGC	CCAATCTATG	TATAAGAAAGT	ATCAGAGCGA	TCTCGTATTC	240
TTGTCTGCTG	CACAGAAGAA	AACCCAAGAA	GAGGCTATCG	TAAAGAAAGA	GCAGCAAGCA	300
TCCGAGCTCA	AGCGGAAGTA	TTTCGGCCCG	GAGGGGGAGC	TGTATAAGAA	ACGCTCCGAT	360
CTGATGAAGC	CTATTCACGA	TGAGATTGG	AATGCTATCA	AAGAGATTGC	CAAGCGTAAC	420
AACTATCAGA	TGGTGCTTGA	TAGAGGTACG	TCCGGAATTA	TCTTTGCCAG	TCCGTCTATT	480
GACATTAGCG	ACCTTGTACT	GAGCAAGATG	GCCTTTAGCA	AG		522

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(2) INFORMATION FOR SEQ ID NO:180

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

45

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...510

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

ATGAACGGGT	TTTTGATT	TATCGGCTTT	GCACTGGCGG	TAGCTTTCTC	CGGTTTTTCC	60
CAAAAGTTGG	CTTTGGTAGA	TATGGAATAT	ATCCTCAGGA	ATATTCCTGA	CTATGAGATG	120
ATGAACGAAC	AGCTGGAACA	GGTGCCCAAG	AAATGGCAAA	ATGAAATCGA	AGCTCTCGAA	180
AATGAAGCCC	AATCTATGTA	TAAGAAGTAT	CAGAGCGATC	TCTGATTCTT	GTCTGCTGCA	240
CAGAAGAAAA	CCCAAGAAGA	GGCTATCGTA	AAGAAGAGC	AGCAAGCATC	CGAGCTCAAG	300
CGGAAGTATT	TCCGGCCCGA	GGGGGAGCTG	TATAAGAAAC	GCTCCGATCT	GATGAAGCCT	360
ATTCAGGATG	AGATTGGGAA	TGCTATCAAA	GAGATTGCCA	AGCGTAACAA	CTATCAGATG	420
GTGCTTGATA	GAGGTACGTC	CGGAATTATC	TTTGCCAGTC	CGTCTATTGA	CATTAGCGAC	480
CTTGTACTGA	GCAAGATGGG	CTTTAGCAAG				510

70

(2) INFORMATION FOR SEQ ID NO:181

75

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS

15 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

20 ATGAAGAAAT TTTTCTCAT GCTTCTGATG GCTCTTCTT TGAGCTCTT GGCACAAAAG 60
GTGGCAGTGG TAAACACTGA GGAGATCAAT TCCAAAATG CGGAACAAGT AGCTGCTACC 120
AAACAGCTCA ACGAATTGGC CGAAAAGTAT CGCCTTGATC TCAGAGATAT GGACGATGAG 180
TTTGCCAAAA AGACAGAAGA ATTTGTAAAG GAAAAAGACT CTCTACTGGA GAACATCCGC 240
AATCGTCTGC AGCAGGAACT TCAGGATATT CAAACTCGTT ATCAGCAGTC ATACCAAACG 300
25 ATGCAGGAGG ATTTGCAAAA GCGCCAACAA CAGCTTTTGG CTCCTATCCA ACAAAGGTG 360
GCTGATGCCA TCAAGAAAGT GGGTGACGAA GAAAACTGTG CCTACATCAT GGAGGCCGGT 420
ATGATGCTTT ACACCGGAGC TACTGCTATT GACTTGACCG CAAAGGTAAA AGCGAAACTC 480
GGAATCAAG 489

30 (2) INFORMATION FOR SEQ ID NO:182

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

35 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

40 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS

45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...2481

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

55 ATGAAGGAAG CTATTCCCGG AAAGAACAAG TATATAAAGC TCAACGGTAT ATACAGATTG 60
TCATTCATTC TGCTATGCTG CCTGCTATGC TCTCAGGCAG CTATGGCACA AGCGCTCAGG 120
GTATCGGGCT ATGTGCTCGA CCGTGGGGAA AAGCCGATCC CGTTCCGCGG AGTCAAAGTG 180
CGTGGTACGG GGACAGGCGC AACGACGAAT CTCAAAAGAT ACTACGAGTT TCGGATGAAG 240
GCCACGACGG ACAGCATCAC GATCGAGTTC AGCTCCATGG GGTACCAAGG GGTAAGTCGC 300
60 ASCTTTCCGT CTCTGACCAA GGACACTCGG CTGAATGTTT GTTTGGCAGA GGCCGAGATG 360
GAGCTTTGGA GCGTGACGGT ACAGGCCACA AAACGCAGAC TCAACACGAT GGAGCGCGTC 420
AATACCCGAG ACCTTCGTGT CAATGCAGGG CCTACGGGAG GGGTGGAAAT GCTCATCAGT 480
ACCTACGCAG GAGTAACGCA GAACAATGAA CTAAGCTCGC AATACTCGGT TCGCGGAGGA 540
AGCTACGATG AGAATATGGT CTATGTAAAC GGAGTGGAGG TTTATCGCCC GCTGCTGGTT 600
CGCTCTGCAC AGCAGGAAGG TCTGAGCTTC GTCAATCCGG ATCTGACACA ATCCGTACAG 660
65 TTCTCCGCGG GAGGGTTCAC GCGCGACTAT GCGGACAAGA TGCTCTCGGT ACTGGATATT 720
CGCTACRAG AACCGCAGGA GAAGGAAGGA GCGGTACTCC TCGGGATGCT ACAATCGAGT 780
GCCTACTACT GCAGCAGTGC CCGAGCCTTC AGCCAAATCA CCGGTGTACG CTACAGAGT 840
GCCAAATCGC TCTTGGGCAC TACGGACAAG AAAGCCGAAT ACGATCCGAT CTATGCGGAC 900
70 GGACAGACAT TCATGACGTA CCGTTTCAGC CCCAAGCTGT CCGTTAGTTT CCTCGGCAAT 960
ATTTTCGCAA CTCGTACAA GTTTGTCCCT CAGACCGGTG AGACGAGCTT CCGTACACTG 1020
AGCGATGCCA AAAAGTTCAA GATCTTTTTC GACGGTCAGG AACAGATGOS TTTCTGACC 1080
TACTTCGGTG CCTTCAGCAT GAACCTTCGTG CCGGACGACA AACAGCGGCA TACGTTTACG 1140
CTTTCGGCCT TCAACAGTAA CGAACGGGAG ACCTACGATA TTCAGGGAGA ATACTTTCTG 1200
AACGATGTGC AGCTGGGGGC GGACGGAACT GCTTCGATGG CTTCCGGGTC AGAGAACTCC 1260
75 AACGGCTTGG GCATCGGGCG CAATACGAG CATGCGCGCA ACAGGCTGAG CTACCGCGTG 1320

WO 99/29870

PCT/AU98/01023

123/490

5	CTGAACATGG GTTACAGAGG GGAGATGAAG CTGAACGAGA AGCATCGCCT GCAAGCCGGC 1380
	GTATCGGCAC AGATGGAGAA AATAGCCGAC CATATCAGCG AATGGGAACG GAGGGATTCTG 1440
	GTAGGATACA ACCTACCTCA CTCGGAGACC GTATTGCTGA TGTACAATAA CCTATATGCC 1500
	GATACGCAGA TGAGGGGAAC GCGCTTGTGG GCATTCTGAC AGGATCGATT CAACCTCAGC 1560
	ATGGGAGGAG GTACATTTC TCTCATTCGG GGTATCAGAG CTTCGTGGTG GAGCTTCAAC 1620
	AAGGAGTTGC TCGTCAGCCC ACGTATCAGC GTGGGTATT CTCCCGAAAG CAACCCGGCT 1680
	TTGGTACTCG GTGCAGCCGC CGGACTTTAT TATCAGGCAC CGTTTTACAA AGAGCTAAGG 1740
	CAGACGCATA AGGATGCCGA AGGCAATAAC GTGGTTGTCC TCAGAGAGAA GATCCGCTCT 1800
10	CAGGGAGCTT TTCACATTCT CGCAGGAGCA GACTATACCT TCGAAATGGG GGGGCGAAAA 1860
	TACAAGTTTA CGGCAGAGGC TTAATACAAG AGCCTGTTC ACATCAACCC GTATATAATA 1920
	GAGAAGCTGA AGATCCGCTA TCTGGGCGAA AACATCGGTT CGGGTTATGC TCGGGGTATC 1980
	GATCTCAAGC TCTTGGCGGA ACTGGTACCC GGAGTGGATT CGTGGCTGAC GGCTTCCATT 2040
	ATAAAGCCGC GTCAAGAACT GGATGGCTAC GGTCTTTTAC CACTGATGAA CGCAGCCACT 2100
15	TACAATTTCT CCTTCTTCCT TCAGGAGTAC GTGCCGGGCA ATAAACGCAT CACAGCCACC 2160
	CTGGCGGGCT CACTAAGCGG AGGATTGCCC CAGCTCAATC CGAGCAAGAG GCTTAGCTCG 2220
	CCGGCCTTTA CGGCACCGGC CTATAAGCGT GTCGATCTGG GGGTAATGTA CAAATGGCTC 2280
	CAGCCGGATG ACTCCTTTGC CGGCCGAAGC AAATGGCTAA TGGGAGTAAA AGGGGCGCTAC 2340
	ATAGGGGCTG ACCTCTTCAA TCTGTTCGAC ATGACCAACG TCAATTCCTA CTACTGGGTG 2400
20	TGGGATGCCT ACCACAGCA ATACGCCGTA CCCAACTACC TGACACGCCG CCAATTCAC 2460
	CTGCGTCTCC TCGTGAATT C 2481

(2) INFORMATION FOR SEQ ID NO:183

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2016 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

35 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORPHYROMONAS GINGIVALIS

40 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

45	ATGTACAGCG GACATCATAA AATCCATTAT CCTTTTCTTA TCCTGTGGT ATGCCTTGCT 60
	TTTGTGCTCT GCAAGAGCGT GAAGTTGAAA SATGCCGAGA AGGCACATGA TCGCCACAGAG 120
	TATACCAAGG CTGCCGATAT GTACAATACA TTATACAGGC GTACCCGACG AAAGCAGGTG 180
50	GAGATGAAAG CTTATACGGC TTTCGGATCC GGTGAAAAC ATCGTGCCGC CGGCAGACAA 240
	GCCAAAGCTT TGGCTGGCTA TCTGAATGCC AGACGCTACG GGTATCCGGA TTCTGTGGTA 300
	CTGCTCCGTT TGGCACAGAC TTATCAGCAA GGAGGTAAC ATAAAGGAAGC CGAGGTAATC 360
	TTCCGTGGAT ATCTGGAAGC TTATCCGAAA AGTTATTTTG CAGCTATCGG TTGGAGGGGG 420
	TGCTCTTTTG CCGGCCAGCA AAAGGAATAT CCTACAGTT ACCGGATAAG GCGAGCTGCC 480
55	GAGTGAATTT CCGCACGGGG CGACTTCGGC CCGGCTATG CACCCGATGC TTCGGCTCTC 540
	TATTTACAT CGAGCAGAAG CAAAGACGAC GGTTTGGATA ATAGCAGCAT AACGGGACTG 600
	AAACCCAACG ACATTTATAT CATCAACGA GATGCACAAG GACGATGGGG ACGTCCCGAT 660
	AGCGTGTCCG GAGGAATCAA CACTCCATGG GATGAAGCGG TGCCAACGAT CACGCCCGAT 720
	GGTAGTACCA TATATTATAC GTTGGCCGAG CAAGGAGCCG ATTACGACCG TACGGTACAG 780
60	ATCTATTCCG CCGCTCGGAG CCGGAGAGGC GGTGGAGCA ACGGTTCCGT CGTGACATT 840
	ATGCGGATTT CGCTCCGTAT GGCTGCTCAT CCTCTATGT CGGCATCGGG CGATTACCTG 900
	TATTTGCTCA GCAATATAGG CGGTAGCTAT GCGGCAAGG ATATTTATCG TGTCAAGGTG 960
	TCGGATCGTT CTTATGGTTC ACCGGAGAAAT TTGGGGCTTG ATATCAATAC GCGGGGGGAC 1020
	GAAATGTTTC CCTTCATAGA TGGGGATAGT ACCCTTTTCT TCGCTTCGGA CGGACACGCC 1080
65	GGTCTGGGAG GACTGGATAT TTCAAAAGCC ACGCTGGACT CTACCGGCCA ATGGCATGTA 1140
	GTCAATATGG GACAAACCGT CAATTCCTCT GCCGATGATT TCGGCTTGCC TGTGGAGCCT 1200
	AAAGGCAAAA ACAAGAAGA AGCTTTGCGG GACAACGGAG TCAAAAGGTG ATTTTGTTC 1260
	AACCGAGGGC ATGCACGCGG ATGGCCGACG CTCTTCATT TCGAACTGCC GGCTATCTAC 1320
	ACCGAGATTC AAGGTTATGT GATGGACAGA GAAGAAAATC CCATAGCCGG AGCCACTGTC 1380
70	AGGATCGTAG GCGAACCGGG CCGCGTAGGA CAGGGATTCT TGACTACTCG TGACGATGGC 1440
	TCTATAAGA TGAGCGTGCA GGGCGATACT CGTATGTAA TGCTTGCCGG AGCATCGGGT 1500
	TATTTGAATC AGTACGTAGA ACTCAAGACC GATACCGCCA AGCAGAGTGA GACCTACTAT 1560
	GTGGACTTTT TCCTTGCAAT GCGTGAGAAA GCGAGGGGCT TGCAAAATAT TTCTATGAT 1620
	TTCGATAAAG CTACTCTTCG CCGCGAAAGC ATGAAGAGCT TGGACGAAT GATTGTATC 1680
75	CTACCGGACA ATCCGATAT TCGGATCGAA TTGGGTTTCC ATGCCGACG GAAAGGCCCC 1740
	GATGCTTACA ACCTCGGACT ATCTGACCGC AGAGCCAAAT CCGTGGTGA TTACCTCAG 1800

124/ 490

AGTCGTGGCA TAGCGGCCGA CAGGCTTACG TGGAAAGGCT ACGGTAAGTC TGTCCCCAAG 1860
ACGGTGACAG CCAAAATTCG CGAACGGCAC GATTTCCTGA AGGAAGGCGA TGTGCTCACC 1920
GAGGAATTGG TAGCACCTTT GACCGAGGAG CAGCAGTCAG TCTGCGACCA ACTGAACCGT 1980
CGTACCGAGT TCCGTGTGAT CGAAGAAGAG TTGCGT 2016

5

(2) INFORMATION FOR SEQ ID NO:184

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

25

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

30

ATGAAAAAGT TTTTCTTCGC GCTACTATCG ATTGGTATTT CAGCGCAGGC TTTTGCCAAG 60
ACGGCAACAG TCCCGACAGA TTCGCTACGA GTACACAATC TTCAGACCGT CACGGTCTAT 120
TCTACACGCA CGCCCGTACC TCTGAAAAAG ATACCGGCCA AGATGGAAGT CATCTCATCG 180
CGCAACATCA AGCAGTCCGG CTTTAACAAC ATGACCGACA TCCTCAAGAC GCAAAAGTTCG 240
CTCGATGTCA TACAATACCC GGGCTTTAGT TCGAACATCG GTATCCGCGG TTTCAAGCCC 300
TCCGCGCAAGT ATGTAACCGT ATTGGTAAAC GGCATCCCTG CGGGAACGGA CAATATCTCT 360
ACGCTCAACA CGAGCAACAT CGAACAAATC GAGATCCCTA AAGGCCCGGT CTCTTCCATC 420
TAGCGCACCA ATGCCATGGG CGGTGTGGTG AACATCATCA CCCACAAATC CAAGGACAAG 480
ATCCATGGCA ACGTTTCTCT CTTCGGCGGT AGCTACCAGA CCATGGCCGG ATCATTCAAC 540
TTGGGTGGCC GCTTCGAGGA TATTTTCTCA TTCGATCTTA GTCTGGGCTT GGACAAGCAG 600
AACAAAGGACT ATAAGACCGG ATCAACAAT TTCCTATCCC TGAGCAAACT GGAAGAAGCT 660
ATAGTAGATG TAAATGCTAC CAAAAACRAG AAAATGAAGG GGAGCGACTA TACTGTAGCA 720
ACGGGACGCT TGCGTTTCGG TATCGACTTC ACGCCCGAAT GGTCCCTGAA TCTGTATCAA 780
AACGTATTCC TCGGAGATGC GATCCCGGTA GGAGGATCTA TATGGGGCGT TTACGGAGAA 840
TCCAAAAAAA ATCTGAATCG TTCTTCGACC TCTTTCGAGC TGCTCGGCAG ACATGGCTGC 900
CACACGCTTC AATTCTCCCC CTACTTCAAC ATAGAGAAAT CGGAGAACTA TAACAATGCC 960
GATCCACCCG GTTTCATCAA CTACAAAGC GACTACTACA CCTATGCTCC CTTACTCCAG 1020
GACAAGATTT CCTTGGAGG ACAAATATC GTACTCGGTG TCGACAGCCG AAACATGAGC 1080
ATGGAGTCAG AAGGATTGCA GCAGGCAGGA GTGAATACAA AGCCATACAA CCCCAGATAT 1140
GCCACGAACT ATATCGGTTT GTTCGGACAG GCCAATTCTT ACCTGCTGAA CGATGCTCTA 1200
TCGATATCTG CCGGTGCACG TGCCGACTTC ATGTTCTTTG ACCTGAAAGC GAACGAGTAT 1260
CTCAACAATG AAGCCAAACA GGAAGCTCAT AACGTAATCA ATCGGAATGT CGGAATCAAA 1320
TATGAGTTTG TGAAGGCCCT TACAGCTCAT GGTACATTCT GTAGTGCAIT CAGTCTCCC 1380
GATGCTTTCC AAAAAGCAGG CCAATACGTA GGCCCGTTCG SCACGACCAT AGGCAATCCT 1440
GACCTGAAAC CCGAAAGTC CATGACCTGG GACTTCGGTA TCGGATACAG CAATGCACGC 1500
TGCGGGATCC AAGCCGAGCT AACCTTAACC TATTTCCACA CCGACCAACA AGATCTGATC 1560
TTGTCCAGCC CTGACTATGC TAATAATATC ACCACATACA TCAATGCCGA CAAGGCTCGT 1620
ATGAGCGGTA TCGAGGCCCT TTTGTCTTAT GACTTCGGCA GCCTCTTTGC CAACAAGTTC 1680
TCTCTCCGCG CATTTGCGAA TGCCACGATC ATGTCTCAAT CCGAGATGAA GAAAGGCCAG 1740
ACCGATGCCG CTTGGAGCGA AATGTACTAC GTTCGCAAGC AGAACATCAC CTTCCGGTATC 1800
ATCGAGCAAA ACTGGTATGC TTACTACCCC GAAGTTCGCC CCGAACTCCA GCAACTGCTT 1860
GCAGCAGAAG AGCCTGAATT GGCTGCTCAG GGACTGCTCC GTCATCCGCA AGCAATGGTG 1920
TTCAATGCTT CTGCTTACTA CCACATGAAC AAGTATCTCA CCTTCGGTGT GAACCTGAAC 2040
AACATCTTGG ATGAGCTTTA TACGGAGAAA GACGGCTACC ACATGCCCGG ACGTAACATC 2100
ATGGGTAAGG TTATGGTCAA CTTC 2124

70

(2) INFORMATION FOR SEQ ID NO:185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

75

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
5 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
10 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1386
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185
15
ATGAACAGGT TTTCAAATCA TTGGCCCTGC ATCCTCGTGG GTTTGTACT CTGGTTTGTA 60
TCGGCGAGTC GGACTGTGGC ACAAACGCC TCCGAAACGA CGGTATCGTA CGATACGGAT 120
ACCGCCGTAC TCTCCGAAGC CGATGTGCTT CGGATCGCTC TTAGTGAGAA TGCCACAGTG 180
AAAGTGGCCG ATATGGATGT GCGCAACAG GAATATGCAC GTAGGGCAGC ACGTGCCGAT 240
CTCTTCCCGA AAGTAGACT CAATGGCGTT TACAGCCATA CCTAAAGAA GCAGGTCTTA 300
TATATAGATA TGCCCGGTTT CAGCAGTAGC GAAGGTATCG AAATGGGGCG TACACACAAT 360
ACGCAAGGAG GGGTGAACGT CTCCATGCCA TTGGTGTCCG CACAGCTTTG GAAAAGCATT 420
GCCATGACCG GAGAACAGCT CGATCTGGCT CTGGAGAAAG CTCGCAGCTC CCGAATCGAT 480
TTGGTGGCAG AGGTGAAGAA GGCTTACCTC AGTGTATTGT TGGCCGAGGA CTCTTATGSC 540
GTATTCAAGC GCAGTATGSA CAATGCTCTG GCCAATTATA AGAACATATC CGACAAGTTC 600
GATCGTGGAC TTGTGGCCGA GTATGATAAG ATTGAGGCCA ATGTACAGGT ACSCAACATC 660
GAGCCTAACC TCTTGCAAGC GCAGAACTCC GTAGCCCTTG CTCTCTGGCA GCTCAAGGTC 720
CTGATGAGCA TGGAASTGGA AACTCCGATC AGACTCTCCG GTTCATTGTC CGACTATAAA 780
GAACAAGTCT ATACCGGCTA TTTTGGCCGC GATACGGCTA TTTCCAAACA CTCCTCCCTG 840
30 CGTCAGCTCG ATATACAGCG TCGTCTGGCT GTCACTGCAG ACAAGCTGAA CAGTACAGC 900
TTCCTGCCA CACTCAATCT GGGAGGGCAG TACACCTATT CGCTCAACAG CAACGACATC 960
AAATCTG3G GCGAGGGACA ACGCTGGAGC CCTTCTCCA CCATATCGCT CAGCCTGTAC 1020
ATTCCTATAT TCAATGGAGG CAAACGTCTG TACAACGTGA AGCAAAGTGC TTTATCGATC 1080
CGTCAGATCG ATCTGCAACG ACGCCACATA GAGCAATCCA TCCGAATGGG AATCAAGAAC 1140
35 CAAATGACC GTCTGCGTAC CTGTATGAG AGATTTGTGG CCTCGGAAGA GGCTGTCCGA 1200
AGTGCAGAAA AGGGCTATCA GATAGCAGAG AAACGCTATC AGACAGGCGA AGGCACTCTC 1260
GTGAGTCA ACGATGCCGA TGTGGCTCTT TTGCAGSCTC GACTCAATTA TAATCAGGCC 1320
ATATTGCACT TTATGACCGC AAAGGCCGAA TTGGACAAGA TGAACGGCAT GGGGATTCCC 1380
40 CAACAA 1386
(2) INFORMATION FOR SEQ ID NO:186
45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
50 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1476
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186
65
ATGTGGGGGG ACAGCCATGG AGTGGGCGCG AACCAAGTGC GCCGAACGCT GGTGAAGGTA 60
GCCTTAAGTG AATCCCTTCC TCCGGGTGCA AAACAGATTC GTATCGGATT CTCTCTCCG 120
AAAGAAACCG AGGAAAAAGT CACCGCCCTA TATCTCCTTG TGAGTGATTG TTTAGCGGTG 180
UCGCACTTGC CGGACTACAA AGGGCGAGTC TCTTACGATA GCTTCCCGAT CTCAAAGGAA 240
GATCGTACCA CAGCCCTTTC TGCGGATTCC GTAGCGGGAC GCCGCTTCTT TTATTGGCT 300
70 GCGGATATAG GGCCTGTTGC TTCTTTTCC CGATCCGATA CGCTGACTGC CCGTGTGGAA 360
GAGGTGCTG TCGATGGCCG CCTTTGCCG TTGAAAGAGC TGTGCGCTGC CTCCCGTCGT 420
CTGTATAGGG GGTATGAGGC CCTCTTTGTA CCGGTGATG CGCGATCGCG GAACATTCGT 480
ATCCCGGCCA TTTTGAAGC GGCTAATGGA ACATCATAG CGATGGCCGA CAGACGAAAA 540
TATAATCAGA CGGATCTGCC GGAGGATATA GATATAGTCA TGCGGCGCAG TACGGACGGA 600
75 GGGAAATCGT GGAGCGATCC CAGGATTATC CTACAGGGAG AGGGGCGCAA TCATGGCTTT 660

126/ 490

5 GGCATGTAG CCCTGGTGCA AACCCAAGCA GGAAAGCTCC TGATGATCTT TGTCTGGTGA 720
GTAGGCTGT GGCAGTCTAC CCCGATCGT CCTCAGCGCA CTTATATATC GGAAAGTCGG 780
GACGAAGGAC TGACTTGGTC GCCTCTCGG GATATAACCC ATTTCACTCT CGGCAAGGAT 840
TGTGCGGATC GGGGACGCG TCGCTGGTTG GCCTCCTTTT GTGCTTCGGG ACAAGGGCTT 900
GTGCTGCCAT CCGGTCTGAT CACGTTTG TGCTGCCATCC GCGAATCAGG GCAGGAGTAC 960
GTCCTGAACA ACTATGTCCT CTATAGCGAC GATGAGGGCG ATACATGGCA GCTTTCGGAC 1020
TGTGCATACC GCCGTGGCGA TGAGGCAAAAG CTTTCATTGA TGCCCGATGG CAGGGTACTG 1080
ATGAGCATAAC GCAATCAGGG ACCGCGAGAG AGCCGACAGC GTTTCCTCGC TCTCTCTCC 1140
GACGATGGCC TTACTTGGGA GAGAGCCAAG CAGTTCGAGG GCATCCATGA CCCCCTGCT 1200
10 AATGAGGCTA TGCTTCAAGT GAAAGGAAC GGAAGGGGATC AAGTGCTGCA CTCCTGCT 1260
CTCGGCCCGG ATGGGCGTCG CGATGGAGCT GTCTATCTCT TCGATCATGT CTCGGCCCG 1320
TGGTCCGCTC CCGTTGTGT CAATTCAGGA TCGAGTCCCT ACTCGGATAT GACTCTGCTG 1380
CGGATGGAA CGATCGGTTA TTTCGTCGAA GAGGGCGATG AGATCTCATT GGTTCATT 1440
15 CGGTTCTGTC TTGACGATCT CTTCGATGTC CGCAA 1476

(2) INFORMATION FOR SEQ ID NO:187

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 735 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 30 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...735
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

40 ATGAAAAAAG AAAAATTG GATTGCGATC GTCGCCGTT TGGCTTTCGT ATTGGGCCTT 60
TATGCTCTTG GCCGAGTGT CGCTCAGCTA CGCCGCTCTC AGCCTTCGGT GACTGTGACC 120
GGTATGGCCG AGCGTAATTT CAAATCCGAT CTGATCGTTT GGACTGCTTC GTACCAGCTC 180
CAGATGATGG ATCTCGAATC GGCCTACAAG GCTTTGAAGG AAAACAGAT ATTGGTAGCA 240
GACTATTTGA AAAACAAGCA GCTGCCGAT TCGTCTTATA TCTTCTCAAG CGTAGCCATC 300
45 TCTAAGAAT ACAACTACTA TTACGATCCT CGGCAGGAAC AAAACGTCAG GACCTTTGCC 360
GGGTATCTGC TCAGCCAGAC AGTTACGCTG ACCTCAGAGG ACATCGAACA TGTGGAGAAA 420
ATATCTCGCG ATATAACGGA GCTGATCAAT CAGGGGGTAG AGATTACCTC CGACCGTCCG 480
GCCTATTACT ACACCAAGCT CAATGATCTG AAGGTGGAGA TGCTGGCAA TGCCTCCGAA 540
50 GACGCTTTCA ATCTGTGCTT GGTCAATTGCG GAGGGGAGCG GTTCTCCGT GGGTAAGATG 600
CTATCTTCTT CGATGGGCGT GTTCCAGATA GTGGGGCTCA ACTCGAACGA AGATTATAGC 660
TGGGGAGTTT CGTTCAATAC GTCTTCCAAG ATGAAGACGG CAAGCATAAC GGTAAAGGCT 720
TCTTTCGCTT TGAAG 735

55 (2) INFORMATION FOR SEQ ID NO:188

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- 65 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
75 (B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

5 ATGAAAAA CAATTGCAAT TATCGCCTCA GCCCTCTTGG CTTTAGGAGC CGTCGGCTGT 60
AAGAAAAATG CTGACACTAC CGCTGTCACT GAAAAGGATA GCATAGCCTT GTCCATGGGT 120
ATTTTGTACG GACAGGATT TGCATATCAG TTCGAAATGT CCGCTTGTCA AGGCCAGCCG 180
ATTGATTCGG TAGCTTTCTT GGACGGTTTC AAATATGGTA TCGATACGAC GCGCTTCTCG 240
TACAATCTCG GAGCCATCTA TGCTTCCAAT ATAGCTCGTC AGCTGGCTCA TGATTCCATC 300
GATATCGACA AGTTCTATGC AGCCATGCGT GCGGCTCTTC TTAAGAGACG CGTATCTATC 360
GCCATGAAGC CTGCAGATGC ACAGGCTTTC ATGCAACGAA TCCAAGCCAA AAAGCAGCGA 420
10 GAAAAAATA TGAAGCAGTT TGGCCAGAAC ATCGAAAAAG GTAATGAATA CATCGATACC 480
TTTAAAAAAG AAGATGGTGT AACTGTTACG ACAACTGGTC TGGCATACAA GACTCTTCAG 540
GAAGGTACGG GAGCTACTCC CTCTTGGGCC GATACTGTAC GTGTCAAGTA TGTGGGTACT 600
CTGGTCGATG GTAAAGAGTT CGACAAAAAC GAAGAAGGAA TCGAATTTCG CGTTACCGGT 660
GTGATTAAAG GCTGGACGGA GATGCTCCAA CTCATGAAGG TCGGTCAGAA AGTTGCGGTG 720
15 GTAATCCAC AGGAGCTGGC TTATGGGGAG ACCGGCAACT ATACCATCGA ACCGTTCTCT 780
ACCTGACGCT TCGAGATGGA ACTTATCGGG ATCAAGCCCG GAAAAAAG 828

(2) INFORMATION FOR SEQ ID NO:189

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2325 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
30 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
35 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...2325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

40 ATGAAGATAT TACGGCAAGT ATTCCTCCCC ATCCTTTTGG TCCTACTGAC AGGTGCCTGC 60
TCCACCACAA AGAATCTGCC GGAAGGCCGAA CAGCTGTATA TCGGAATGGG CAAGACACAG 120
ATACTCCGGC AGGACAAGAG CCACGCCGGC CAACAGGCTC TGACCGAAGT GGAGAGTACA 180
45 CTGAAAGTTA CACCAATGG AGCTATTTTC GGCAGTGCAA GTGCCTCCTT ACCCAAGATA 240
CCATTGCGGC TATGGCTATA CAACAGCTTC GTGGGGGATT CCCTGTCTAT TTGGAATGG 300
ATATTGACAA AGTTTGCAGC CAAGCCGGTT TTCATCAGTC AGGTCAAATC CGATAGCCGG 360
GCTAAGGTGG CGAGCAACAT CCTCCGGGAA CAGGGGTACT TCGATGTCAA AGTAAAAAGC 420
50 AGTGTGACCA CTCTGAAAAA GGAATCGCTC AAAGCCAAAT TCTCTATAC GGTGGATATG 480
GCCTCTCCTT ATCATTACGA CAGCATCATT CCTTACCGA TCAGCACTTT CCGGACAGC 540
ATTCTGGCTT ACAGGCGAGC TCCGTCTTTG ATCAGGAAAG GAGACCAATT CAATTTGGCA 600
AAGTGCACG AGAGCGTCA GACCATCAGT GCCCTGCTGA GAGACAATGG TTACTACTAC 660
TTCCGCCAC AGGATATTAT CTACGAAGCC GATACCTCC TCGTAAGAGG TGCCGTATGC 720
55 CTGCGAGCCA AGCTCTCGGA AGATACTCCA CCCCAGCCA TGGCCCGCTG GAGGATAGGG 780
AAACGGACAG CAGTCTTGCT CGGAATGAAC GGAGAAAGCC CGACAGACTC GCTCGAAGTG 840
GAGGATATGA AAGTCTTTA CTATCGTAAA ATGCCGGTTC GCGCCAGAT TTTGGCCAAA 900
CGCTTTCTGT TCTTCTCGG CAATCTGTAT CGGCAGAAAG ACCATGAGAC GACACGCAA 960
60 TCCTTGGCTC GTTTGGGAGC CTCTCCGTT ATCGATCTCA ATTTTTCGA ACGGATTCC 1020
ATTTCGGCC TTTTGGATGT GCGACTGCTA ACCACCTCG ACAACCTTG GATGCATCA 1080
TTAGAGACCT TGTTACAGAG CAAAGCAAT GACTTCATCG GTCCCGGACT GAATTTTGCT 1140
CTTGCTCGGC GCAATGTATT CGGCGGAGGA GAAAATCTTT CTGGAATAT CGGTGGATCG 1200
TATGAGTGGG AGACCGGCAA TCGTCCCGAA AATAGCAGCA ATCGGCTGAT CGATATAAAT 1260
TCGTACAAAC TGAATACGGC CGTGAACCTC TCGTTTCCCT CGATTGTATT TCCCGTCTG 1320
65 CTGGATAAAT ACTATTACTA CCCCACGACT ACGACTTTTC AGGCTTCTGC CACCGCGCTG 1380
AACAGGGCAC ACTACTTTAG CATGTACTCT TTGGGCTTTT CGACCACCTA CGAATTTAG 1440
CCCTCCAAAG AACACCGGCA TGCTATTTTC CCGCTCAAGC TCAACTACAA CCTCTGGGG 1500
CATCAGACAG AAATTTTCCA GGCATTACG GCGAACAATC CCGCCCTGCT GCTCAGCTT 1560
CAGAGTCAGT TCCTTGCTCA AATGGGGTAT ATCTATACG TCAACAAATC CGTTTCAGAG 1620
70 AAAAGTCTCT ATCATCTTTG GATGCAATTC GGAATATCG AGGCAGGCAA TCTCTGAAT 1680
CTGATCTATC TGGCAGCCGG CAAGAAGTAC AGCGACACCA AGAATTTCTG CCGCGTCCCC 1740
TTCTCTCAGT TCATCAAAGC CACGGGAGAA CTGCGCTATT CCTATACCAT AGACCGCAAT 1800
CAGTCACTGG CAACCGTTT CGGACAGGC GTGATATATA GCTATGGCAA TATGCGAGTG 1860
GCACCTTATA GCGAGCAGTT CTATGTAGGC GGTGCCAATA GTATCAGAGC TTTACCGTC 1920
75 CGTAGCATCG GCGCCGAGC GTTCAATCCG GATTCGACA ATCAGTATTC CTATTGGAT 1980
CAGGTGGGCG AATTCAAAC CGAAGCCAAC GTGGAATAA GAGGCAAGCT TTTCGGGAT 2040

129/ 490

(U) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- 5 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
10 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
15 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2601
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

20 ATGAGAAAA GAATTCTACA ACTTTTCCTG ACCGCATTGC TGCTGGCATT AGGCTCCTCT 60
CTCGCCATAG CACAAACAGT GGTGACCGGT AAGGTGATCG ATTCAGAAAC GTCCGAACCG 120
CTCATCGGTG TATCGGTAAG CACCGGTGAG GGAGCATCCG TCCGCGGTGT AACCCACCGAT 180
ATGGATGGTG GCTTCGGATT CGAAGTACCG GCCAAATCTG TCTTGACTTT CCGTTGCGTA 240
GGTATGCTA CCGTAACTCG CTCTATAGGC AGAGGTTCG AAGAAGACCT CGGTACGATT 300
25 CTCCTCGATC CCAGGCCAT CGGCTTGGAT GAGATTCAGG TAATAGCCTC TGTGGTGCCC 360
AAGACCGTA TGACGCGGT ACCCGTTCC AATATCCGTG TGGCTGATAT TCAGGCGAGCA 420
TCGTTGAATG TCGAATTCC CGAAGTGGT AATCCACTC CCTCTACCTA TACGACAAAA 480
GGAAGCGGAG GTTTCGGTGA TGGTCGTACC AATGTGCGTG GATTCCGAC TTACAACTTC 540
GGTGTACTCA TCAACGGAGT TCCTGTCAAT GGTATGGAAG ACGGGAAAGT ATATTGGAGC 600
30 AATTGGAGTG GTCTGATGAA TCAAGCCAGT ACCATTCAGA TTCAGCGCGG ACTCGGAGCC 660
TCCAAAGCTG GTATCAGCTC GGTAGGTGGT ACGATGAACA TTATCAGGAA GACTACGGAC 720
GCCAACACCG GAGGTTCCGC TTATGTCCGT ATGGGTAATG ATGGATTGCA CAAAGAAATCG 780
TTCTCCATT CTACGGGTAT GAACGACGGT TGGGCTATCA CCATTGCAGG CTCGCATATG 840
ACGGGTCTGG GTTATGTGAA GGGGCTGAAG GGACGTGCAT TCTCTACTT CTTCACGTT 900
35 TCGAAGAAGT TCAATGAACG TCATACCCTC TCTCTTACCG GATTCCGTGC ACCCAATGG 960
CACAAACAAC GTTCTCCAA ATATTCTGTA GCGGACTATG ACAAATACGG CATCCGTCAC 1020
AATCAATCCT TCGGCTATCT GCGAGGCGAA CTGACTCCTA CGGCTTATGC TTACAATACG 1080
TACCACAAGC CCCAGTTCTC GCTGAACCA CTCTGGAAGA TGGATGAAA TACCTCTCTT 1140
TATACCGCAN CCTACGCATC TTTGGCTACC GGTGGAGTGC GTCCGCTTA TGGAAAGAAC 1200
40 AGTAAGTGGG TATTGATCAA CTACAACACC GGACAACCT ATGAACAAC AAAGGTGACT 1260
CCCGATGGAC TTATCGACTA CGATGCGTA CTGGCTGCCA ATGCTGCCGC GAGCAATGGC 1320
TCGGAAGCAA TTTTGGCCCT TGGCTCCAC TCTCACAAGT GGTTCGGTCT ACTCTCTTCA 1380
TTCAAGAACA AACTTAATAG TTCGCTGACT TTGACAGCCG GATACGATGG GCGTTACTAC 1440
CGTGGCGACC ACTATGACAA GATCACCGAT CTGCTCGCGG GTAGCTACTA CATAGAGGAT 1500
45 CCCAAGACAA AGCTCGCATA CCATGCGGAA GGTGAGCAAC TGAAGTGGG TGACATTGTA 1560
AATCGGGACT ACACAGGCGA AATCATGTGG CACGCGCTCT TCGCACAGAT GGAGCATTCG 1620
TCCGAATGGA TCGATGCATT CGTATCAGGA TCTATCAACT ACGAACTATA CCGCAATCAC 1680
AATATGGCG GTAGCAAGTC CACCGGCTAC CTGCCCGGCG TATCGCCGTG GAAAAGCTTC 1740
CTTCCGTGGA GTGGCAAGGC AGTCTGAGC TACAAGTTCG CACAGGGACA CAATGTATTG 1800
50 GCCAATGGCG GTTCTCTTAC ACGTGCAACA CTCTTTGGCA ATATCTATGC TGGGGGGGCT 1860
ATCATTCCCA ATGACAAAGC CAATATGGAA AAGGTGCTTA CAGGAGAGGT CGGCTATGGA 1920
TTCAGGAATC ACAAACACTT CGAGTTCAAT ATCAACGGAT ACTATACGAA GTGGATGGAT 1980
CGCGTGACCT CGAAGAGAT CCGAAACGAG TATGTTTATC TCAATGGCGT TGATGCTGTT 2040
CACTGTGGGG TAGAGGCTGA GGTGAGCTAT CGTCTATTG GTCAGATCGA CCTTCGCGGT 2100
55 GCCGGAATG AGACAGGGCA GGAATAACC TATATCAAGG GTTACACTTC TTACGACGAA 2160
GCACAGATGA CCGCTGCTGT ATCGGCAGAC ATAGAGCTGT TCAAGGGTTT CCATGTGATA 2220
GGTAACTACA ACTTCCTTGG CAAGAATCAT GCAGGATTCA ACCCGGCAAC CGGTAATGCA 2280
CAGCAGTACG AAGCGGATGG CAAAGAAATC GTGGAATCAT GGAAGTTGCC CGATGTAGGT 2340
60 CTGTTGATC TGTCTGCATC CTACAATTTT AAGCTTGGT CACTCAGCAC CACATTCTAT 2400
TTCAACATG ACACGTAGC CGACAAGCGA TATGTAGCG ATGCCGACGA CAATATCATC 2460
GGTAAGAAAC ACGATAGGC TCGGCTCTC GTATGGTACG GTTTCGGCCG CACTTGGTCT 2520
ACCGGTATTC GTGTAACCTT C 2580
2601

- 65 (2) INFORMATION FOR SEQ ID NO:192
(1) SEQUENCE CHARACTERISTICS:
70 (A) LENGTH: 1293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
75 (ii) MOLECULE TYPE: DNA (genomic)

130 / 490

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
10 (B) LOCATION 1...1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

15	ATGAAGTTTT CAATCCGCTT TTCTCTCTGC ATCATCTTTC TCCTCTCTGC ATTTATCTCTG	60
	CCTGCTCTCG GACAAAAATC CAAGCAGGTA CAGCGACTTG AGAAGCAACG TAAGGAGGCC	120
	CTCAAAGCCA TCGAAAAAAC CGATCGCGAA CTACGAAATA CCAAGAAAGA CAAGCAAGAC	180
	AAACAAAAGC ATCTCAACCT CCTGAACAAG CAGGTTGCTC AACGCAAGCA GATCGTACAA	240
	CTCTTGAGCA ATGAGGTCAA AGAGTTGCCA TCCGACATTG ATTCCATGAC GGGTGTATGT	300
20	CATCAGCTCT CTGTAGAAGA GAAAGCCCGA TCCGATGAAT ATGCCAAGC TCTACAGTCT	360
	ATGCAAAAAGC GGAAACGCTC GTTGGATCGC ATCCTTTTCA TTTCATCGGC CAAGAGCTTT	420
	GACGAAGGCA TGCCACGGAT GCGTTTCTTG GAACAATACG CTCTGCTATA CAAGCTGGCA	480
	TCTGTCCGGC TCGCGGATAC ACGTAGCAAG TTGGAGACTG AACGTGCGAC TGTAGAAGAC	540
	GCCAAAAAGG AGAAAGGACA TCTCTTAGTC ATCAGAGAAG AGGAAAAAAA GAAACTCGAA	600
25	GGACAGCAG CCGAGCAACG TCGGCAGGTG CAGGCTTTGG GAGCCAAACA AAAAGACTTG	660
	GAAGCGCAGC TCGGAAAGCA GAAAAAGCAA GCGGAAGCTC TGAACAGAAA GATCGAGAAA	720
	CASATTGCCA AGGAAATAGA ACCTGCGGAA CGTCTGCTC GAGAAGAACG TGAACGGTTG	780
	GCACGCGAAG CCAGAGCCAA GGGTAAGCGG GTTCTGCGG AACCGGAACG GAAGCGGAG	840
	ACCAAAGGCG GCTATGCTAT GGATGCTCTT GAGCGTCTC TCTCGGGCAG CTTTGACAG	900
30	AACAAAGGTC GCGTGCCCGG CCCGTTTCGC GGCAGATACC GAATCGTAAG CGACTTTGGC	960
	GTAGCAACAG ACAGTGAGCT GAAAAAGTA CAAGTTAATA ATGGAGGTAT CGACATCGCT	1020
	ATACCGGTTT ATAATTGCGC TACCAGCGTA TTCATGGTG TAGTGTCCAG TGTATTCTGT	1080
	AATCTGAGCA AAGTGTATGT AAATTCGGGC ACTCGTGTA AAACGGGTCA GGCTCTTGGT	1140
	CGTGCCCTATA CGGATCCTTC CAACAACAG ACCATTATTC ACTTCGAAAT CTGGAAAGAA	1200
35	CGCAGCAAAC AAAACCCCAAG ACTATGGTTA CGA	1260
		1293

(2) INFORMATION FOR SEQ ID NO:193

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

60	ATGAAAAAGT ATTTGTTATA TGCCTCGTTG CTAACGAGTG TTTTGCTCTT TTCTGTTC	60
	AAGAACATC CTAACGAGCC GGTGGAAGAC AGATCCATCG AAATTTCTAT AAGGAGTAGT	120
	GATTTACCA AACCGGTGA GGCAGTACGC TATGAAAGGA ATCAAGGAAG TGCTGCCGAA	180
65	AGGCTCATTA CCAATCTTTA CCTCTTGTTG TTGATCAGT CAGGGGCGAA TCCGGCGAAA	240
	TACTATATTA CCGGTAACAC TTTACCCGGA GGGACCTGGC TTCTGACGA TATGAAGTG	300
	AAGTTGATA TGACACAATC CGAGGCCGGA GAGCGCAAG TATATGTCGT AGCCAATGTT	360
	GATAATGCGG TTAACACGGC TCTTGATGCT GTCGCTAACG AAAGCGATTG GCAGACTGTA	420
	AAGAGGACGA CTGCAATGCC GTGGTCGACC GATATAGCCT CTCCTTTCTT GATGTCCGGA	480
70	AACAAGACAC ACGACTTCCT GGCCAATCGT CTTTGGACA ATGTGCCCTT TGTGCGTGCC	540
	ATTGCCAAGG TGGAGCTGAA TATCTCGCTG AGTGAGAAAT TTCAGATTGT GCCGATAATT	600
	GTCATCGTA GTTTGAGTGA GTTCAAGTTC AGATACGTA ACITCGACAA GGAGACCTAC	660
	GATGTAAGC CAACGACCA GCGGACAAT CTCATTAGTT CTGCTAATGG TGTGCGCT	720
	CAGATTACAG ATTGAGCTGT ATGGGGTGCT TCCTTAAATA CTCTCTCTG TCCGGATGCG	780
75	GGCAGAGTTT ATACATTGSA TGCAATGGC AAGGTAACGG CACTACGGAT TGTACCTAT	840
	CTGAATGAGC GCGATAGCAA AGGGGCTACG GTAGAGTCTG CATTGCTCTG TGTGGATGAT	900

GGCACCCTTC CTCCTCCGGA ATTCGGTCCG GAGCTTTATC GTTTGCCTTT GCCGGACVAG 960
ATCCTGCACA ATCATTGGTA CAAGTATGAA GTCGAGATT 999

5 (2) INFORMATION FOR SEQ ID NO:194

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

10

(ii) MOLECULE TYPE: DNA (genomic)

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...945

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

ATGATCAGAA CGATACTTTC ACGATATGTA TCCTCGAACT TTTGGAGTCG GGGAGCTACC 60
TTTTTTTTC ACGATTTCCTC GGCCTTCATC CTCGCCGCTA CTCCTTTGCC GGCTTGTGGA 120
GGGGTACTG CTCAGGCTC CGATCGTACG CTGGCTGTGA CCATCGAGCC ACAGAAATAC 180
TTCATCGAGT CCATTGCGGA TAAGTCGGTG CAGGTGGTGG CATTGGTACC GGCCGGCAGC 240
AATCCGGAGG AATACGACCC TTCGCCTACC GTGATGAAGC GTTTGTCCGA AGCAGATGCC 300
TACTTCTATA TAGGAGGACT GGGGTTCGAG CAAAGAAATC TCGCTGCCAT TCGGGACAAT 360
AACCCTAAGC TCCCTCTTTT CGAAATGGGC AAAGCCTTGG CGGATGCCGG AAGTGCAGAT 420
CTCCACGGCT CCTGCACAGA TCATTCTCAT ACAGACCTGC ATGCCCATGA TCCGCACTAT 480
TGGAGCAGTG TGGTAGGGGC AAAGGCATC AGTCGTGCTG CATACGAGCC GCTTGTGGAG 540
CTTTATCCGA ACGAGAAAGA CAAATGGGAC AAAGGGCAGC ACCGTCTCAA CGGACGTATC 600
GACAGCGTGA AGAGACTCGT CGATACCATG TTTGCCAATG GCAAAGCAGA CAAAGCCTTC 660
GTCATATATC ACCCATCGCT CAGCTTTTTC GCCCAAGAGT TCGGCCTGCG GCAGATCGTC 720
ATAGAGGAAG ATGGGAAAGA GCCTACGGCT GCCCACCTTC GTCGTGTGAT CGATCAGGCA 780
CGTGCCGATG GTGTGAGAAAT CGTATTTATC CAACCGAAT TTGAACGCG TCAGGCGGAG 840
GACATCGCAC GCGAGATCGG TGCTCGTCCG GTAAGGATCA ATCCTCTGCG CAGCTCGTGG 900
GAGGAGGAAA TTTTACATAT TGCTCGCGCT TTGGCTCATG AACGG 945

45

50 (2) INFORMATION FOR SEQ ID NO:195

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

55

(ii) MOLECULE TYPE: DNA (genomic)

60

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

65

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2544

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

ATGATCGGAA AAAAAATCTT TTTTATCTG CTGGCGCTCA TTGGGTTTCA TGGGCTGAAC 60
GCAGCGACAG AACTGAGTT CAAGTACCCG ACCGATGCCA ATATCATCGG TCACGTCAAA 120
GACAGCAAGA CGGGTGAACA CCTTGTGGT ATCACTATTG CTATCAAAGG CACTACCTTT 180
GGTACATCTA CAGATGCAAC CGGGCACTAC TATCTTCTA ACTTGGGTCC GGGTGAGATC 240
ACTTTGATTA TGCGTGGCAT GGCTATAAG AGCCAGGAGC GCGTAGTCCG CSTAGAAAAG 300
GACAGACTA TCGAGGTGAA TTTCAAGCA GAAGAGGATG CCATCAATCT GGACGAAGTC 360
GTGATTTCGG CCAACCGCGA ACTGACGCTT CGCGCTCTT CTCCTACTCT GTTAAATGTA 420

75

	TTGAACGAAA	AAGTCTTCTC	GCAAGTCAAT	GCTTCTAACC	TGGCTCAAGG	CTTGTCATTG	480
	CAGCCGGGAC	TTGGTGTAGA	GAACAACTGT	CAGAACTGTG	GTTTCAATCA	AGTTCGTATC	540
	AATGGACTGG	ATGGTGGTTA	TGCACAGATC	CTCATCGACA	GCCGTCCCAT	CATGAGTGGC	600
5	CTTGCCGGTG	TTTACGGTCT	GGAGCAGATC	CCTGCCAATA	TCATCGAAGC	TGTGGAGGTA	660
	GTACGTGGTG	GAGGATCGGC	CTTGACGGT	TCTTCTGCTA	TTGCCGGAGT	GGTGAATATC	720
	ATCACCAAGG	AACCTTCTCA	CAATTCTTTC	ACATTCAATG	AACTCTGTAG	CTTTACCGGT	780
	TTGAGCAAGC	TGGATAACAA	CACGAACTTC	AATGCCTCCA	TCGTACGCGA	TGACAACCGT	840
	GCCGGTGCCA	TGGTATTGCG	GCAGGCTCGT	TACCGCAACC	ATTGGGATGC	TAACAATGAC	900
10	GGTTATTCCG	AATTGGGTAA	AATAGATGCC	CGCTCGCTGG	GAGCGCATTC	TTATTTGGCG	960
	TTGAGCGACT	ACAGCAAATT	GACGGGAGAG	TTTCACACGA	TCAGTGAATT	CCGCCGTGGT	1020
	GGCGATCGTA	TCGATTTGCC	TCCTCACGTA	GTGGGTGTAG	CTGAACAAAC	TGACCATAGC	1080
	GTATTTAGCG	GAACCTTGAA	ATACGATCTC	TTCTCTTCCA	ACTATAAACA	CCACTTCCAG	1140
	GCTTATACTT	CCGGACAGAT	CGTAAATCGC	AAGAGCTATT	ACGGAGGTAT	CGGAGAGATT	1200
15	GACGTCAATG	GCCACCCCGG	TGGTACGGAA	GGCTACCCTA	TCCCTCAAGA	TCAATACGGC	1260
	AATAATTATG	SCGTGACCAA	AGGCAAGACA	TATATGGGCG	GTATCCAGTA	CAGCTACGAC	1320
	TTGGACAAAT	TCCTCCTCAT	GCCTTCGCAA	CTTTTGTTCG	GAGCCGAATA	TACGCGTGTAT	1380
	GAATCTAATG	ACGTGATGCC	CATCCTTTCA	TGGCAGACCG	GCGAGGATGC	CAATGGGAAT	1440
	ACCATTCGCC	TCTATCCCGA	ATTGGATCAG	AAATATCAACA	ACTACAGCCT	ATTGGGTGAG	1500
20	AACGAATGGA	AAAATGACAG	ATGGAGCATC	CTTGTTGGCG	CTCGCTTGGG	CAAGCATAGC	1560
	GAGGTCAAGG	ATATGATTCT	GAGTCTCTCG	ACCACACTGC	GTTTCAACGT	GAATCCGGAC	1620
	ATCAACCTGC	GCGCTACATA	TGCAAAAGGG	TTCCGCGCAC	CGCAGGTATT	CGATGAAGAC	1680
	TTGACAGTAG	GGGTGTGAGG	CGGTGAGGCA	CAGAAAGTAT	TCAACGATCC	GAACCTCAAG	1740
	CCTGAAATTT	CTCATGCATT	CAGTTTGTAGT	GCCGATATGT	ATCATCGTTT	CGGTAACGTC	1800
25	CAGACCAACT	TCCTTGTGGA	AGGCTTCTAT	ACTCGTTTGC	TGGATGTATT	CACCAACGAG	1860
	GAGCAGCCTG	ATCAGACGSA	TGGCATCAAA	CGCTACACGC	GTATCAACGG	TAGCGGAGCC	1920
	AAAGTATTCC	GTCTCAATCT	GGAAGGTAAG	GTGCGATACA	AGTCTTCCA	GCTCCAAGCC	1980
	GSTCTTACCC	TGGCCAGCAA	CAAATACGAC	CAAGCACAGG	AGTGGGGTCT	GAATACGGTG	2040
	AAAGACACCA	ACGGAGCTTT	TGTTACCGAG	GCCAATGCAA	ATGGACAACA	GGAATACAAG	2100
30	ALCGAATCCA	TGACGGATAC	GCAGATCACC	CGTACCCCCA	GCGTATACGG	TTATTTTACT	2160
	TTGGCCTACA	ATCCTGCTCA	CTCATGGAAC	ATAGCCCTTA	CGGGAGCATA	TACCGGTGAG	2220
	ATGTATGTAC	CCCACGCTAT	CGAATATGGT	GTGAAGTCTG	CCGAACCTGA	TATTATGAG	2280
	AACAATCCTG	AGATTACCGA	CGAAACCGGA	AAGGCTCCCG	GTATTGATGA	GCTGAAGAG	2340
	ACACCTGACT	TCCTCGATTT	GGGCTTGAAA	GTGGGTATG	ACTTCCACGT	ATTCCAGGCT	2400
35	ACTGAGGTTG	AACTCTATGT	AGGTATGAAC	AATATCTTCA	ACTCTTCCA	GAAGGACTTC	2460
	GATCGTGGAG	CTGCACGTGA	CAGCGGATAT	ATCTATGGTC	CTACGCAGCC	GCGTACAGGC	2520
	TACATGGGCT	TGGTAGTGAA	GTTC				2544

40 (2) INFORMATION FOR SEQ ID NO:196

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...606

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

	ATGACAGTAA	AGCGGCGCAGT	GCGAATAGCA	CTTCTCACGC	TGATAGGCAT	TCTTTTTC	60
	TCACCTTCTC	TTGTTGCGGC	GCAAACTCTT	TTCAGCACCG	AACATGTCTT	GCAACTATAC	120
	AACAAGATAC	TCTATGGAGA	GTCCGCGCGG	GATACCGTGG	CAGAGAAAAC	GGCAGGTGAG	180
65	TCGGCATTTG	CTTTTATAGA	CAAACTCATC	AATCTCGGCC	GCACTTTTCT	CGGCAAAACA	240
	TATCGCTATC	GCGGTCCCTT	CCCATGGGCG	ATGGACTGCT	CGGGCTATGT	GTCTTACCTC	300
	TACTCAAAAT	TGCACATCAA	ACTCCACAGT	GGTGCGGCAG	CACAGAGCCA	ATATACGAAT	360
	CCTATCGACC	GCGAGGATGT	TCGTCCGGGC	GACCTCCTTT	TTTTCAAAGG	CCGCAATGCA	420
70	CGCAGCAACC	GTATCGGGCA	TGTAGCTTTG	GTCGTATCTG	TGGATGAAGA	TGATATTACC	480
	ATGATGCACA	GCCGCAATTC	GCGAGCGATC	GTATCGAAAA	AACCTAATCG	CAGTGCATAC	540
	TTCTCCCGTC	GCTTGGTGGG	CTATGGCAGG	GTACCCGGAG	CCAAGAGAGT	GATCCACGGA	600
	AAAAAT						606

75 (2) INFORMATION FOR SEQ ID NO:197

133/490

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGAAACGGA	CAATCCTCCT	GACGGCACTG	ACCGTCCTAT	CTTCGCTCTC	CTTGCTTCGT	60
GCACAAAATG	AATCCGAAGC	ATCAACCAAT	CCGATGTCAG	GCCTCTCCCT	GGAAGACTGT	120
ATCCGGATAG	CCAAGGAGCG	CAACCTGAAT	CTGCGCAGAC	AGGAGATCGA	ACAAAGAAAC	180
CGAATCATTA	GTCTCGATGC	AGCAACGACAC	AGTTTCCTGC	CCTCGGTCAA	TGCAGGCATC	240
GGACACAAC	ATAGCTTCGG	ACGTTTCGAA	GACAAAACGG	GAGTAACCGT	AGATCGCTCC	300
TCGATGAATA	CCAATCTCAG	CATCGGAGCT	TCGGTGGGAA	TATTCAGCGG	CACACGTCGT	360
CTGCACGACC	TCAAGCAGCA	AAAGTACAAC	GTGGAGGATG	GTATAGCCCG	ACTTCAAAAA	420
GCGCGTGAAG	ACCTCAGCCT	GCAAAATCGCG	GCTCTCTATA	TCAATTTCGT	CTTCCGTCAG	480
GAAATGACTC	GTACGGCAGA	AACACAGTTG	GCACTGATTC	GCGAGCAACG	CAATCGCACG	540
GCCGAAATGG	TTCGCGTAGG	TAAATGGGCA	GAGGGTAAGC	TCCTCGACAT	AAATGCCCCAG	600
ATGGCCCAAG	ACGAACAAC	TCTCGTACAA	TATCGTTCCG	AGGAGGAGCT	GGCTCGTCTG	660
GACTTGGGGC	AAGCCCTCGA	ACTGGAGCAC	CCCCAAAGCA	TTGCAGTCAA	GGCTCCCGAC	720
ACAGACGTTT	TCGTAGCAGA	AAGGTTGGGA	TCTCTCCTTG	CTCCCGAAGA	GATCTATCGC	780
ACGGTCTCTG	GCTTGAAACC	GGCACTGCAT	TCGAGCGAGC	TGCAAAATAGC	TTCCGGCAGC	840
GAAGGTCTGG	CCTCGGCTCG	TGCGGCATAC	TTCGGGACGC	TCAGCCTCTC	TGCCGGATAC	900
AGCAACGGTT	ACTTCCGCGA	CCTCGGCAAG	GAGTATGCGG	CCATCAACCC	CTCCTTCTCC	960
GAACAGTGA	AGAACAACGG	CAGCTACAGT	ATCGGACTCT	CTTTGAATAT	CCCCATCTTC	1020
TCTGCCATGC	AAACGCAAGA	TCGCGTTCGG	AGCAGTCGCC	TGCAAAATAGC	CTCAAGCGAG	1080
CTTCGACTCC	TGGAAGAGAA	AAAAGCCCTC	TATAAAGAGA	TCAGGCAAGC	ATACAGCAAT	1140
GCCGTGGGCG	CGGATAAGGC	CATCGCAGCA	GCCGAAAACA	GCAAGGCCGC	TACGCTCAAG	1200
GCATACGAAT	ACGCTCGCGA	CAGCTTCGAG	GCAGGGCGCT	TGTCTGCCCTA	CGAATATGCC	1260
GAGGCAAAAA	CAAAATACGC	CCTCAGCCAA	GTGGAAGAAC	TTGCTGCCAA	GTATGACTTC	1320
ATATACAAAG	CCAAAGTTT	GGATTCTAT	CAGGCAAG	ACTTC		1365

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ATGCGTTTCC	AACATTATCT	CATCTGTACG	GCTGCCGTAG	CGGCTTTGGC	TGCGAATCCC	60
CTTAGGGGCC	AATCGAATAT	GACCTCGAA	GAGTGCATAG	ACTATGCACG	CCGGCAGCT	120
TCGGCCGTGG	CGCTGTCCGC	TGCGGAAC	GAGCAGTCCA	AGGCCGATTA	CCTTCAGGCC	180
GTCCGCAATT	TTCTGCCCGC	TGTATCGGCC	GGAACCGGTG	CTTCGTGGAA	TTTCGGACGC	240
GGATTGGATG	CCGAGACGAA	TACCTACACC	GACATCAACA	GCTTCAACAA	TTGCTACAGC	300

134/ 490

	ATACATGCCA	CGATGACCC	TTTCGACGGT	TTGCAGAGTG	TCTATCGACT	GCGATGGCG	360
	CATGCACGCC	GGGAGGCTTC	GCGCCTCTCC	GTTCGCGAGC	AGCAGGAGCT	GGCAGCTCTC	420
	GGCACCACGG	AGGCTACTA	CGAOCCTCGT	TATGCGCGCC	AAATGCAAGA	GCTGGCCATG	480
5	CAGAAGTACG	AGGAGAGCAG	CCGCTCCAC	CGGCAGACGG	CTCGAATGGA	AGAGCTGGGG	540
	ATGAAGATC	GTCCCGATGT	CCTCGAGATG	CACTCGCGAA	TGGCCGGTGA	CCGTTTGGCC	600
	CTGACTCAAG	CGGACATCA	GTGCATCATC	GCTCTGATCC	GGCTCAAAGA	AAAAATGAAC	660
	TTCCCATCG	ATGACGAAC	CGTCGTAGAC	GATATGCCGG	CTGACAGTCT	CTCCGCCGAC	720
	ATGGCCGAAT	CGGACAGCTC	GGCCGGCGTC	TTGCCCGGTG	CTGCCATCA	TCATCCCGTC	780
10	CTCCTCCGTG	CCAAACTCGA	CGAGCAGGCT	GCCACCGACC	GTTCGCGAGC	CGCGCGAGGT	840
	GCATTCTG	CGAGTGTGTC	GGTATCCGGA	GGATGGAACA	CGGGATTCTC	ACGCTTTTTC	900
	AATGGATCGG	ACTATACGCC	CTTCAGCGAG	CAGTTTCGGA	ACCGTCGGGG	GGAAATACGTC	960
	AGTCTGAATC	TGAGTATCCC	CATCTTTTCG	GGATPCAGCC	TTGTGAGCCA	TCTGCGTCAG	1020
	GCGCGTGGCG	AACGCGAGGC	GGCAATCGTC	CGACGGGGCG	AAGCGGAGCG	CAGGCTCTAC	1080
15	AGCGAGATCG	CCCAAGCCAT	GGCCGACCGG	GATGCCGCTC	TGGCTTCTTA	CCGCCAGGCG	1140
	AAGGAGCATA	CGGACGCCAT	GCAACCGCT	TAGGAAGCG	TCTTGACGCG	TTATGAGGAG	1200
	CGCCTGAATA	CGGCCATCGA	CCTGACCACT	CAGGCCAATC	GGCTCCTGGA	TGCCCGTGTG	1260
	CAGCGACTTA	GAGCGGCCAT	GACCTACCGG	CTCAAATGCA	AACTCATAGC	CTATTACGGC	1320
	TGCCTTTCGG	AC					1332
20	(2) INFORMATION FOR SEQ ID NO:199						
	(i) SEQUENCE CHARACTERISTICS:						
25	(A) LENGTH: 2820 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
30	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
	(iv) AMPLI-SENSE: NO						
35	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
40	(A) NAME/KEY: misc_feature						
	(B) LOCATION 1...2820						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199						
45	ATGAACAAAT	TTTACAAATC	ACTTTTGCAG	TCAGGACTGG	CTGCCCTCGT	GTGATGGCA	60
	ACTGCACTGA	CGCCTTCTGC	ACACATTTTC	TTCCGAGGGG	AACCCCTGAG	TTTCTCTTCA	120
	AGATCCGCGG	GAACGCATTTC	ATTTCGACGAT	GCAATGACTA	TCCGCCTTAC	TCCGGATTTTC	180
	AATCCCGAAG	ACCTGATCGC	ACAGAGCCGT	TGGCAATCGC	AAAGAGATGG	CCGCCCGGTC	240
	CGGATAGGAC	AAGTAATACC	GGTGGATGTG	GACTTTGCAT	CCAAGGCTTC	GCACATCTCT	300
50	TCCATCGGAG	ACGTAGATGT	ATATCCGCTG	CAATTCAGT	TGGAAGGAGC	CAAAGCCATT	360
	ACGCTTTATT	ACGATGCATT	CAATATCCG	GAGGCGCGAC	GCCTCTATAT	CTATACCCCC	420
	GACCATGAAA	TTGTGTTGGG	AGCATATACG	AACGCCACTC	ATCGCCGCAA	CGGAGCTTTT	480
	GCCACAGAGC	CGGTACCGGG	GAGTGAGCTT	ATTATGGATT	ATGAAGTGTC	TGCGGAGGGG	540
	ACTTTGCCCT	ACATCAAGAT	CTCCGCTGCG	GGTTATATAT	TCGACAAAGT	CGGCGGACGC	600
55	CCCGTAACGG	ATAACCATTA	CGGGATCCGT	GAGGACGATT	CCGATTCCGA	TTGCCGATC	660
	AACATCAATT	GTCCCTGAAGG	TGCAGACTGG	CAGGCAGAGA	AGAACCGTGT	GGTGCAAAATG	720
	ATCATGGTAA	AAGGACAGTA	TATCTCAATG	TGCTCAGGCA	ACCTGCTCAA	TAATACGAAA	780
	GGAGACTTTA	CTCCGCTGAT	CATTCTGCG	GGACACTGTG	CTTCCATAAC	AAACCAATTTC	840
	GGTGTAACGC	AATCCGAGTT	GGATAAGTGG	ATCTTCACTT	TCCACTATGA	MAAAAGAGGA	900
60	TGCAGCAATG	GTACATTGGC	CATCTTCCGT	CGCAACAGTA	TCATCGGAGC	TTCCATGAAG	960
	GCTTTCTCTC	CGATCAAAAG	TAAATCCGAT	GGTCTCTTGC	TGCAACTCAA	CGATGAAGTC	1020
	CCCTCGCGCT	ATCGTGTCTA	TTACAATGGA	TGGGACAGTA	CGCCCGATAT	TCCCTCGAGC	1080
	GGTGCCGGTA	TTATCATACC	GGCCGGAGAT	GCCATGAAGA	TTTCCATCCT	AAAGAAGACT	1140
	CCGGCTCTGA	ATACATGAT	CTCCTCCACT	GGTTCCGGAG	GGACTGACGA	TCATCTCTAT	1200
65	TTCAAAATAG	ATCAAGGTGG	TACGGAAGGA	GGATCGTCCG	GTTCCTCTCT	CTTCAATCAG	1260
	AATAAGCAG	TGSTCCGGCAC	ACTGACCGGA	GGTGCCCGCA	ATTGTGGCGG	GACGGAGTTC	1320
	TACGGCAGAG	TGTAACAGTCA	TTGGAACGAG	TATGCATCCG	ATGGCAATAC	GAGCCGATG	1380
	GACATCTATC	TGGATCCCCA	AAACAATGGC	CAGACGACCA	TCCTCAACGG	AACGTATCGT	1440
	GACGGTTATA	AGCCTTTGCC	CTCTGTGCC	CGGCTATTGT	TGCAGTCTAC	AGGCGATCAG	1500
70	GTGCAATTGA	ATTGGACGGC	TGTTCTGTCC	GATCAATATC	CATCATCTTA	TCAGGTGAA	1560
	TACCACATAT	TCCGAATGG	AAAGGAAATA	GCTACGACAA	AGGAGTTGTC	CTATTCCGAT	1620
	GCCATCGACG	AAAGTATTAT	CGGTAGCGGT	ATCATTGAT	ACGAAGTAAG	CGCACGCTTC	1680
	ATTATCCCT	CGCGGTGGGA	TGGAGTGGAA	TCTTATAAGG	ATACGACAA	GACTTCTGCC	1740
	GACCTTGCCA	TAGGAGACAT	TCAGAACCAAG	CTGAAGCCGG	ACGTAAACCC	TCTCCCGGA	1800
75	GGAGGAGTAT	CATTAGCTG	GAAAGTTCCT	TTCTTAAGCC	AGTTGGTTTC	CCGATTCGGA	1860
	GAAAGCCCCA	ATCCTGTGTT	CAAAACCTTT	GAAGTGCCCT	ATGTTTCTGC	CGCAGCCGCA	1920

135/ 490

5 CAAACCCCA ATCCTCCCGT TGCCGTAGTC ATTGCAGACA AGTTTATGGC CGGTACATAT 1980
CCCCAAAAGG CTGCTATCGC TGCCGTITAT GTAATGCCAT CCGCTCCGGA CTCTACTTTC 2040
CACCTCTTCC TCAAGAGCAA CACAAACAGA AGATTGCAGA AGGTGACAAC TCCCTCCGAT 2100
TGGCAGGCCG GAACATGGTT GAGGATCAAT TTGGATAAGC CGTTCCCGGT GAATAATGAC 2160
CATATGCTTT TTGCCGGTAT CAGAATGCCT AATAAGTACA AGCTCAATCG TGCTATCCGT 2220
TATGTAAGAA ATCCGGATAA CCTTTTCTCC ATTACCGGTA AGAAGATTTC ATATAACAAC 2280
GGAGTCTCTT TCGAAGGCTA CGGAATACCC TCGCTCTTGG GCTATATGGC TATCAAAATAT 2340
CTGCTGGTAA ATACCGATGC TCCGAAGATC GATATGTGCG TTGTACAGGA GCCTTATGCT 2400
AAGGGAACGA ATGTGGCTCC ATTCCCGGAA TTGGTCCGCA TATATGTCTA TAAGAACGGA 2460
10 ACATTTATCG GCACACAGGA TCCATCCGTC ACAACTTATT CGGTTTCAGA CGGAACAGAG 2520
AGCGATGAAT ACGAAATAAA ACTGGTATAT AAGGGATCGG GCATTTTCGAA TGGCGTTGCT 2580
CAGATTGAGA ATAACAATGC TGTCGTTGCA TATCCGTCCT TTGTAACAGA TCGTTTCAGC 2640
ATTAAGAACG CTCATATGGT TCACGCTGCC GCCCTCTACT CATTTGGATGG CAAGCAGGTT 2700
CGTTCCTGGA ACAACCTCCG CAATGGCGTG ACATTTCAGT TCAAGGACT TACGGCCGGT 2760
15 ACTTATATGC TCGTTATGCA GACGGCAAAC GGCCTGTGA GCCAAAAGAT CGTGAAGCAG 2820

(2) INFORMATION FOR SEQ ID NO:200

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2010 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
25 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
30 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
35 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

40 ATGAAATATC TTATCAGACT CTTCCTATCA TTGATGTTAC TCTCTCTCTG GACGGGCTGT 60
ACACACGAGG AGCTCTCTAT TTGCGATGGC GAGAATACGC TTGTTTACG CGTAGAGACC 120
GGTAAAGCCC CAAATGCTCG TGCCACAGAA CCGGTCAGG GCATATACAA TGAGAATAAA 180
GTACGGCTCCA TTTCTGTGCT CTCTATTTA GAGGGACAAC TTCGTTGGCA GGTGAAGTCT 240
45 ACAGACTATC AAATCCATGA AGGGGCTAT ATCATTCGG TCAAAGAGCA AATGOGACCA 300
CTATTCATG GCAACAACAA CTTCAGATC TATGTAGTGG CCAATCTCGA TTTCAATGCT 360
CCGGCCACAG AAGCTGGGCT TTCTCAATTT GTGGTAGAGA AATCTATTGA AGTCTCTCT 420
ACGACAGCCC CTGCCGATTT CGTAATGCTT GCTCATGGCA ATAAGCAGAT CAATATGGCT 480
50 ACGACAGAAG SGAAACTGTT GGGGGATTAT AACTCAAAC GAGTGGCAGC AAAGATTGCG 540
ATGATAAAAC CCACCATCAA TGTGCAAGGA TATGAAGTGG TCGGAATAT ACAGGCAAG 600
TTTCGCAATT CGGTAACCAA GGGGTTCTT ACCACAGAAG CTCAGAGAT CCCAGCTGCT 660
GCATCTCTATA AGACATCGGA ATATCTTGAT ATTGCAGAGT CGGCACCTGC CAATTCTATC 720
CATTTCTATT CTACTATAA CAAATGGACA CTCTCCACAC CGGAGAAGCG ACCGGAATTC 780
55 TTATCATG TGAAATTCAA AAAGACAGGA CAGCCGACA ACACAGCCAA ACCGTACTAC 840
TACAGAGTGC CCTCGAATC TCAGGACAAT CAGGTCAAGA GCAATGTCTT CTATAATCTG 900
AATGTGAAAA TCGAAATCTT GGGTCTTTA CAAGAGCCGG AAGCTGTTTC TGTAACCGGC 960
ACACTCGCAA TAGAAGAATG GATTCTCCAT CAGGATGCAT TCAATCTGCC TGCCACCAAT 1020
TACTTGATAG TGGAAACAGCA CGAAATCTTC ATGAATAAGG TGAACACATA CTCGGTGAAA 1080
60 TATCAAACTT CGCAGAAACC AATCAGCAAT AGCATACAGT CAGTTACCTT TAGCTACGTC 1140
TCTTCTGATG GCACTCAGCA CAATGATCTT GTAGCAAGTA GTAGCGACCA GTATCCTACG 1200
ATTACAAGCG ATAATACAAG CATCATAATC ACTTCCAAGA TACCGGTTAA TAACGTACCA 1260
AAGAAGATCG TTTTGTAGGT AACTAATGGG GTAGCCGGTT TGAAGAGAC TGTCACAGTA 1320
TCCCAATATC CTGCACAATT TATTGTCAAT ACATTGGCA CAGCATCGGC ATGGAGACCA 1380
65 GACGGATCTT TGGCTCCGGG GCTTAACAAT AAAGCGATTT ACCATGTCGT AGTACTGGTT 1440
CCACCCGAGA ATTTATTGGA AGATGGGACA CAGACAATCA TCGGTTATCC CCCCAGTGAA 1500
ACAAATTTCTT TCAATAAGAA AGAGAACAAT ACCTATCCGA TAGTATGGTC TGACACAAAT 1560
ACGACAAAAC AGGAACCTGA GACATCAAGA ATGATTTCAC CTTCCTTTGA GTTAGCCTCC 1620
CAACTTGGGG CTACTCTCCC GATGCCCTAT CTCGAGTATT GGCCAGGGAC ATCATATCTC 1680
70 CTGACTATT CGGGAACTA TAATAATAAG AGATACGCCCT TGTTTAATTG CGCTTTTAC 1740
TGGGAGAAAA GAAAGTTAA TAACGAAGAA ATTAATTCG ATGACTGGCG TTTGCCGACA 1800
GAAGCTGAGA TCAAAATTGAT AGATAAGCTG CAACATAATG AGCAGAGTGC TGTCCAAGCT 1860
ATCATGACAG GSAATTATTA TTGGGATAGT TACTCTGCAA ATGGGTCTTA TAAATGCAA 1920
GGAGGAGGGG GCCAAGGAAA TTCCTCCAAA GCCTATGTTT GTTGGCTGCG GATGTGAAA 1980
75 AAGCCGATTC GTGACAACAA GTCAGGTAAG 2010

(2) INFORMATION FOR SEQ ID NO:201

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

25	ATGCGAAAAA TTTTGAGCTT TTTGATGATG TGCTCTCTGC ATTTAGGTCT ACAATCTCAG	60
	ACTTGGCATG GAGATCCGGA CTCAGTGGCA GCCCTACCTT CTATCGGTAT TCAAGAGTCA	120
	AGTTGTACCC GAATCACGTT CGAGGTGTGT TTCCCGGAT TTTATAGTGT GGAACAAACGA	180
	GAAGSCAACCC AAGTCTTTCA GCACATTTCC ATGCCGGGTT GTGGCTCCTT TGGGAATCTG	240
30	GGCGAAGCTG AATTGCCTGT TTTGAAAAAG ATGATAGCCG TTCCGGAATT TTCAACAGCT	300
	AACGTTGCTG TAAAAATCAA AGAGACGGAG ACAATCGACA ATTATAATAT CTATCCTAAT	360
	CCTACCTATG TCGTAGAGGA GTTGCTCTGAG GGGGGGACTT ATCTGGTAGA GGCTTTCGGG	420
	ATAAACAATG ACTATTATAG CCAAAATGTA AGCCTCCCTT CTACTCACTA TGTCTATTCT	480
	CAAGACGGGT ATTTTCGCTC ACAAGGATTT ATCGAAGTTA CCCTGTATCC TTTTCGATAC	540
	AACCTGTCC GACAAGAAAT TCTATTTGCA AAAAAATCG AGGTACAAAT AACTTTCGAT	600
35	AATCCTCAGC CACCTTTACA AAAAAACACC GGCATATTTA ACAGAGTAGC CTCCTCTGCA	660
	TTTATTAAAT ATGAAGCTGA TGGCAAATCG GCGATAGAAA ATGATATGGT GTTCAGTCTG	720
	GGTACACAA CGTACATAAG CGGAAATGTT GCCAGCAACC TCCCTCAGAA CTGTGACTAC	780
	TTGGTTAATT ACGATGATAT GTTCAACGTA AATCAACAAC CACACGACGA AATCAACCGG	840
40	CTGTGCGAAC ATAGAGCCCT CTACAACGSC TTTGATGTAG CTGCTGTAAG TATTAAGGAC	900
	TTCAATTCCT CAGTTTACAA CCAAGCAAT GCGAAGAGGA CTTTAGATGG CAACTGGGGA	960
	TACGTGCTAC TGATCGGAAA ACCATTGAGC AAATATTGGG CTGACACTGA TAATACAAAA	1020
	GTCCCAACCT CTTTATTCCA TAATGTCTCC TTAATTCCAA GTCATCCAAC TTTTGGTTCC	1080
45	ATATGCGCTT CCGACTATTT TTTTAGTTGT GTTTCGCCCC TTGATACTGT CGGCGATTGG	1140
	TTTATCGGTC GATTTAGCGT CACCAATGCT CATGAATTGC ACAATCTGAT TGAAGAGACT	1200
	ATCAACAAG AATCTCATA TAATCCTATT GCACACAAAA ATATTCTTTA CGCAGAAGGG	1260
	AAAGGCTGCG ATGCTCCAAAT CTTACGTTTA TTCTTAAAG AAATCGCCTC TGGTTACACA	1320
	GTCAACTCTA TCTTAAATC TAATCAGGTC TCTGCAATAG ACTCGATATT TGACTGCTTG	1380
50	AATAATGGTT CCCATCATT TTTTAAAC ACTCATGGA TGCCGACTGT TTGGGGGATA	1440
	GGGCAGGGAC TCGACGTCAA TACTCTAACA GCCGATTGA ACAATACATC TTCGCAAGGA	1500
	TTATGTACGA GTCTATCATG TAGTTCGGCT GTAGCAGATT CAACTATTAG ATCGCTTGGG	1560
	GAAGTCCTGA CCACATACGC ACCTAACAG GGATTCTCGG CTTTCTTAGG AGGAAGCAGA	1620
	GCCACCCAAT ATGCCGTTTA TTTAGAAGGC CCTGTCTCTC CGTCAGAAAT TTATGAATAT	1680
55	TTACCTTATT CTTTATATCA CAATCTCTCG ACTGTGTGTT GCGAAATGTT GCTATCATCC	1740
	ATTATCAATA CTAATCTGTG TGATACGTAT TCGAAATTCA ACTTCAATTT GCTTGGCGAC	1800
	CCTGCACTAA ACATTATGGC TCATGGCATG GAGGTTAGTA ATTGTATTAC ACTACCAAAC	1860
	AACACCATTA TAAGCAGTCC GATAACAATA AAAATGGTG GCTGCCTAAA AATACCGGAA	1920
	AAAGGAGTTT TGCATTTTAC TAATAATGGC TCCATACAAG TCAATGTCGG AGGAACCTCG	1980
60	GAAATAGGCA ATCAGGCTAA AATATCCGGA GAGACCGGTG CTAACCCAC CTTTATTACC	2040
	GTTTACGCGG ATGGCTTTGC GATTAAACAG CAGGTAGAGA TAGACAATAT AGACCGACTT	2100
	AACCTGTGTT CTACGCATTC GGTATGCCCC AAATTTCATT TTGACAGTGT GAAATTC AAC	2160
	AGTGCCCCGC TGTATACAA GAACTGTATT GTGGAGATAA GCAATTGCGA ATTTACCAAT	2220
	CGAAGTGACA TTATTTCAA GAATTGTGAC CTAAGCGTTG AAAACAGTAT GTTTAGCAAT	2280
65	TCGGGGATAA CGGTATTCAA GCCTATGGCT ACAAGCTCCA TCACCGGATT ATCTACAAAA	2340
	GCAAGATTA CCGACAATAC TTTTTTTCG ACAGGAACCT TCGCTACCA TATCACAAAC	2400
	ACGCCAGGCT TAACAGCAAC CTCCAATGCT GCCATCAAGT TAGACAAATAT TCCTGAGTAT	2460
	TACATTTCCG GTAATAAAAT AGTCAATTGC GATGAGGCTC TTGTAATAAA TAATAGTGGC	2520
	AACAGAACGA ACAGACTCCA CAATATCACA CGGAATGTGA TAAAAACTG TAGGATTGGG	2580
70	AGCAGCGTTT ATAATTCCTA TGGTATTTAC AACCAGATA AGATCAGTAA CAATCATATA	2640
	GGAGTACGTC TCCTCAACAA CAGTTGTTT TATTTCGATA ATGCTCCTGT AATCAATGAA	2700
	GAAGATAAGC AGACGTTTAT TTCTAATAGG ACTTGGCAGC TCTATTTCATC AAACGGTACA	2760
	TTCCCTCTCA ACTTCCATTA CAACAGCTTG CAGGGGGGAG ATACAGATAC ATGGATTTAC	2820
	AACGACACCT ATACGAATCG CTATATTGAC GTTTCATAA ATCACTGGGG CAACAATGAT	2880
75	TGTTTGTATC CGAATCAGGT TTTCAATACG CCAGACTGT TCATTTGGAT ACCTTTTGG	2940
	GATGGATTGC CAAATGGGAG ATCGGGCAAT AGCTCTGCTG AAGCAGTAGA ATTCAAAAA	3000
		3060

137/ 490

5 GCATTGGACT GTATTGGCAA TAGCGATTAT CTTTCGGCAA AAGTGGCTCT CAAGATGATG 3120
GTGGAACCT ACCCGGAATC CGACTTTGCA ATAGCTGCTT TGAAGGAATT GTTCAGGATA 3180
GAGAAATGT CAGGCAACGA TTACGAAGGC TTGAAAGATT ATTTTCAGATC CAATCCAACC 3240
ATCATCTCTT CCCAGAACTT GTTCCCGACA GCTGATTTCC TGTCTGGCGG ATGCGATATT 3300
GTGTGTGAAA ACTATCAGTC TGCCATCGAT TGGTACGAAA ATCGCTTGAA TAGTGAAATC 3360
TCCTATCAGG ACAGTGTITT TGCAGTCATT GACCTTGGTG ACATTATTG GAATATGCAG 3420
TTAGACTCAC TCAGAGGGAC TGGTATAGAT TTGAACATAC TTCTCTGTGA ACAAGGAAA 3480
TCGCTCGAAA GCCATCAAAA TGTAAAAAAT TATTTGTTGT CAACTCTTCC CGAATCAACA 3540
GGTACTCTCC TGCTCCATT AGAATGCAAC AAATCAAGCC TTGATAAATC CAAGATAATC 3600
10 TCTATTTOGC CCAATCCGGC GAAAGCTGTT GTAACAATAA TCTACTATAC CGATAACCCCT 3660
TCCTGTTCTG TAATAAAAAAT ATATGGAATA AATGGAGCCT CGGCTGATAT AACCGGGTTG 3720
CCCAACATC TATCCGAAGG TTATTACAGC ATACAGTTCA ATACATCCAA CTTTGATCCC 3780
GGTTTCTACC TGGTAACGCT AAATGTTGAT CAGAAAAATA TAGATACGGA AAAATTACGA 3840
ATCAAA 3846

(2) INFORMATION FOR SEQ ID NO:202

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 30 (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...3822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

40 ATGATGTGCT CTCTGCATTT AGGTCTACAA TCTCAGACTT GGCATGGAGA TCCGGACTCA 60
GTGGCAGCCC TACCTTCTAT CGGTATTCAA GAGTCAAGTT GTACCCGAAT CACGTTTCAG 120
GTTGTTTTCC CCGGATTTTA TAGTGTGGAA AAACGAGAAG GCAACCAAGT CTTTCAGCGC 180
AATTCATGCC CGGGTTGTGG CTCTGTTGGG AATCTGGGCG AAGCTGAATT GCCTGTTTTG 240
45 AAAAAGATGA TAGCCGTTCC GGAATTTTCA ACAGCTAACG TTGCTGTAAA AATCAAGAG 300
ACGGAGACAT TCGACAATTA TAATATCTAT CCTAATCCTA CCTATGTCGT AGAGGAGTTG 360
CCTGAGGGGG GGACTTATCT GSTAGAGGCT TTCGCGATAA ACATGACTA TTATAGCCAA 420
AATGTAAAGC TCCCTTCTAC TCACATATGC TATTCTCAAG ACGGGTATT TCGCTCACAA 480
AGATTTATCG AAGTTACCCT GTATCCTTTT CSATACAACC CTGTCGACAG AGAAATCTA 540
TTTGCAAAAA AAATCGAGGT TACAATAACT TTCGATAATC CTCAGCCACC TTTACAAAAA 600
50 AACACCGGCA TATTTAACAA AGTAGCCTCC TCTGCATTTA TTAATTATGA AGCTGATGGC 660
AAATCGGCGA TAGAAAATGA TATGGTGTTC AGTCGTGGTA CAACAACGTA CATAGCGGA 720
AATGTIGCCA GCAACCTCCC TCAGAACTGT GACTACTTGG TTATTTACGA TGATATGTTT 780
AACGTAATC AACCAACACA CGACGAAATC AAACGGCTGT GCGAACATAG AGCCTTCTAC 840
AACGGCTTTG ATGTAGCTGC TGTAAATATA AAGGACGTAT TGAATAGCTT CCCATCAAT 900
55 GCCACCTCAT ACATCAACGA AACTAACTG AAAAATTTCA TTCGCTCAGT TTACAACCAA 960
AGCAATGCGA AGAGGACTTT AGATGGCAAA CTGGGATACG TGCTACTGAT CGGAAAACCA 1020
TTGAGCAAT ATTTGGCTGA CACTGATAAT ACAAAAGTCC CAACCTCTTT TATTCTAAT 1080
GTCTCCTTAA TTCCAAGTCA TCCAACTTTT GGTTCATAT GCGCTCCGA CTATTTTTTT 1140
60 AGTTGTGTTT CGCCCTTGA TACTGTGGGC GATTGTTTA TCGGTGATTT TAGCGTCACC 1200
AATGCTCATG AATTGCACAA TCTGATTGAA AAGACTATCA ACAAAGAAAT CTCATATAAT 1260
CCTATTGCAC ACNAAATAT TCTTACSCA GAAGGGAAGG GCTGCGATGC TCCAATCTTA 1320
CGTTTATTCT TAAAGAAAT CGCCTCTGGT TACACAGTCA ACTCTATCTT AAAATCTAAT 1380
CAGGTCTCTG CAATAGACTC GATATTGAC TGCTTGAATA ATGGTTCCCA TCATTTTAT 1440
TTTAACAATC ATGGAATGCC GACTGTTTGG GGGATAGGGC AGGGAAGTCA CGTCAATACT 1500
65 CTAAACAGCC GATTGAACAA TACATCTTCG CAGGGATTAT GTACGAGTCT ATCATGTAGT 1560
TCCGCTGTAG CAGATTCAAC TATTAGATCG CTTGGAGAAG TCCGAGCAC ATACGCAACT 1620
AACAAAGGAT TCTCGCTTT CTTAGSAGGA AGCAGAGCCA CCCAATATSC CGTTTATTTA 1680
GAAGGCCCTT GCTCTCCTGC AGAATTTTAT GAATATTIAC CTTATTCTTT ATATCACAAT 1740
CTCTCGACTG TTGTTGGCGA AATGTTGCTA TCATCCATTA TCAATACTAA TTCTGTTGAT 1800
70 ACCTATTCGA AATTCAACTT CAATTTGCTT GGCAGACCTG CACTAAACAT TATGGCTCAT 1860
GGCATGGAAG TTAGTAATTG TATTACACTA CCNACAACA CCATTATAAG CAGTCCGATA 1920
ACAATAAAAA ATGGTGGCTG CCTAAAAATA CCGGA/AAAG GAGTTTGTCA TTTTACTAAT 1980
AATGGCTCCA TACAAGTCA GTCCGGAGGA ACTCTGGAAA TAGGCAATCA GGCTAAAAA 2040
TCCGGAGAGA CCGGTGCTAA CCCACCTTTT ATTACCGTTT ACGGCGATGG TCTTGCAT 2100
75 AACAAAGCAG TAGAGATAGA CAATATAGAC CGACTTAACT TGTTTTCTAC GCATTCCGTC 2160

5 ATGCCCAAT TTCAATTTGA CAGTGTGAAA TTCAACAGTG CCCCGCTGTA TACAACGAAC 2220
TGTATTTGGG AGATAAGCAA TTGCGAATTT ACCAATCGAA GTGACATTAT TTCAAAGAAT 2280
TGTGACCTAA GCGTTGAAAA CAGTATGTTT AGCAGTTCGG GATTAACGGT ATTCAAGCCT 2340
ATGCTACAA GCTCCATCAC CGGATTATCT ACAAAGCAA AGATTACCGA CAATACTTTT 2400
TTTGGGACAG GAAACTTCGC CTACCATATC ACAAACACGC CAGGCTTAAC AGCAACCTCC 2460
AATGCTGCCA TCAAGTTAGA CAATATTCCT GAGTATTACA TTTCGGTAA TAAATAGTC 2520
AATTGCGATG AGGCTCTTGT ACTAAATAAT AGTGGCAACA GAACGAACAG ACTCCACAAT 2580
ATCACACGGA ATGTGATAAA AACTGTAGG ATTGGGAGCA CGCTTTATAA TTCCTATGGT 2640
ATTTACAACC GAAATAAGAT CAGTAACRAAT CATATAGGAG TACGTCTCCT CAACAACAGT 2700
TSTTTTTATT TCGATAATGC TCCTGTAATC AATGAAGAAG ATAAGCAGAC GTTTATTCTT 2760
AATAGGACTT GGCAGCTCTA TTCAACAAAC GGTACATTCC CTCTCAACTT CCATTACAAC 2820
AGCTTGACGG GGGGAGATAC AGATACATGG ATTACAACG ACACGTATAC GAATCGOTAT 2880
ATTGACGTTT CAAATAATCA CTGGGGCAAC AATGATTGT TTGATCCGAA TCAGGTTTTC 2940
AATACGCGAG ACTTGTTCAT TTGGATACCT TTTTGGGATG GATTGCCAAA TGGGAGATCG 3000
GGCAATAGCT CTGCTGAAGC AGTAGAATTC CAAACAGCAT TGGACTGTAT TGGCAATAGC 3060
GATTATCTTT CGGCAAAAGT GGCTCTCAAG ATGATGGTTG AAACCTACCC GGAATCCGAC 3120
TTTGCAATAG CTGCTTTGAA GGAATTTGTC AGGATAGAGA AAATGTCAGG CAACGATTAC 3180
GAAGGCTTGA AAGATTATT CAGATCCAAAT CCAACCATCA TCTCTCCCA GAACCTGTTC 3240
CCGACAGCTG ATTCTCTGTC TGCGCGATGC GATATTGTGT GTGAAACTA TCAGTCTGCC 3300
20 ATCGATTGGT ACGAAATCG CTGGAATAGT GAAATCTCCT ATCAGGACAG TSTTTTGTCA 3360
GTCAATGACC TTGGTGACAT TTATTGGAAT ATGCASTTAG ACTCACTCAG AGGGACTGGT 3420
ATAGATTGTA ACATACTTTC CTGTGAACAA AGGAAATCGC TCGAAACCCA TCAAAATGTA 3480
AAAAATTATT TGTGTCAAC TCTTCCCGAA TCAACAGGTA CTCTCTGCC TCCATTAGAA 3540
25 TGCAACCAAT CAAGCCTTGA TAAATCCAG ATAATCTCTA TTTCGCCCAA TCCGGCGAAA 3600
GCTGTTGTAA CATAATCTA CTATACGAT AACCTTCTCT GTTCTGTAAT AAAAATATAT 3660
GGAATAAATG GAGCCTCGGC TGATATAACC GGGTTGCCCA AACATCTATC CGAAGGTTAT 3720
TACAGCATAA AGTTCAATAC ATCCAACTTT SATCCCGGTT TCTACCTGGT AACGCTAAAT 3780
GTTGATCAGA AAATTATAGA TACGGAAAAA TTACGAATCA AA 3822

(2) INFORMATION FOR SEQ ID NO:203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2775 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...2775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

55 ATGCTATCA TGATGAAAG TATTGTTTT AGAGCATTTC TAACGATTTT GCTCTCGTGG 60
GCAGCGATCA CGAATCCGAC TGCTCAAGAG ATCTCAGGCA TGATGCAATC CTGTCTGGCT 120
GCTCGGCTC AACCGGATAC TATCTTATAT GAAAGTTTGG AGAATGGACC TGTTCCCAAT 180
GGCTGGCTTG AGATAGATGC TGATGCTGAT GGTGCCACTT GGGGAAGCCC ATCAGGCTCT 240
TTCTCTGTAC CTTACGGACA CAATGGCCTT TGCACCTACT CCCATATACG TTCCGGTATC 300
TCACACGCGG GCAACTATCT GATTACACCC AATATAGAAG GAGCCAAACG GGTCAAGTAC 360
60 TGGGTATGCA ATCAGTATAG TACCAATCCG GAACATTACG CAGTAATGGT ATCGACAACC 420
GGGACTGCCA TTGAAGACTT TGTTTTGTG TTTGATGATT CCATAACAGG GAAACCGACT 480
CCTCTTSTAT GGCCTAGACG AATCGTGGAC TTACCGGAAG GSACCAATA TATTGCATGG 540
CGACATTACA AAGTCACCGA CTCACACACA GAATCTTGA AATTGGATGA TGTCACTGTG 600
TATAGGTCGA TCGAAGGGCC CGAACCTGCT ACCGACTTCA CAGTAATCAA TATTGGTCAG 660
65 AATGTTGGAC GATTGACTTG GAACTATCCG GAGGATTATC AACCGGAAGG AAAGGGGAAT 720
GAAGAGTTGC AGCTTAGCGG CTACACATC TATGCGAACC GTACACTACT GGCACAAATA 780
AAAGATGTCT CCATAGTGA GTATGTGGAC AGCACTTACT CTTTGCAGGA CAATCCCTTG 840
CAAGTGGAGT ACTGGCTTAC AGCCGTTTAC GATGAAAGCA TAGAATCTTC GACCGTATGT 900
70 GGCACGCTGC ATACCCACG GATGCCATC CTTTATGAAA ATTTTGAGAA TGGACCTGTT 960
CCCAATGTTT GGCTTGTGAT AGAGGCTGAT GGAGATGAT TTAGCTGGGG ACATATTGT 1020
AATGCTACG ACCTTTTTC CGGCCATAAT GGAGGCCATT GCTCCTTGTC GGCTTCTTAT 1080
GTTCCGGGTA TAGGCCCGGT GACTCCCGAC AACTATCTGA TTACCCCAAA GGTGGAAGGA 1140
GCCAAACGTG TCAAGTACTG GGTAAAGCAG CAGGATGCCA ATTGGGCAGC GGAACATTAC 1200
75 GCGGTGATGG CTTGACAAAC GGGGACTGCT GTCGAGATT TCGTCATATT GTTCGAAGAA 1260
ACCATGACAG CGAAGCCGAC CGGCGCATGG TATGAAAGAA CCATCAACTT ACCTGAAGGG 1320

139/490

	ACTAAATACA	TCGCATGGCG	GCATTACAAC	TGTACCGATA	TATATTICTT	GAAGTTGGAC	1380
	GATATCACTG	TATTCGGGAC	TCCTGCATCA	GAGCCCGAAC	CTGTTACCGA	TTTCGTTGTC	1440
	TCGCTTATTG	AAAACAACAA	GGGACGATTA	AAAGTGGAAAT	ATCCTAACGG	CTACGAACCC	1500
5	GATAAGACTG	ATGATAAAGA	CCCATTGCAG	CTTGCCCGCT	ACAATATCTA	TGCAACCGGC	1560
	TCGCTCCTTG	TTACATACA	AGACCCGACT	GTTTTGGAST	ATATCGATGA	GACTTATTCT	1620
	TCACGAGACG	ATCAGGTGGA	AGTGGAAATAT	TGTGTCACTG	CCCTTTATAA	CGACAATATC	1680
	GAGTCCCAAT	CGGTTTGCGA	TAAGCTGATT	TATGATTCTC	AATCGGACAT	TATCTTATAT	1740
	GAAGGCTTTG	AGGCCGGAAG	TATTCCTGAA	GGCTGGTTGT	TGATTGATGC	TGATGGCGAC	1800
10	AATGTTAAAT	GSGACTATTA	TCCTTGGACT	ATGATGGAC	ATGACAGTGA	GAATGTATT	1860
	GCATCCGCTT	CGTACTTACC	GATGATTGGC	GTTTTAACTC	CGSATAACTA	TTTGGTTACA	1920
	CCCAGACTCG	AAGGAGCCAA	GCTTGTCAAG	TATTGGGTAA	GTGCGCAAGA	TGCTGTTTAT	1980
	TCGGCTGAGC	ATTATGCTGT	GATGGTTTCT	ACTACGGGAA	CTGCTGTGA	AGATTTTGTG	2040
	CTCTTGTTCG	AAGAGACAAI	GACCGCTAAG	GCTAACGGTG	CATGGTATGA	GCGAATATT	2100
15	ACATTGCCTG	CAGGAACAAA	ATATATTGCC	TGGCGGCATT	ATGATTGCAC	CGATATGTTT	2160
	TTCTTGCTCT	TGGATGACAT	TACGGTTTAT	CGTCTACTG	AGACTGTTCC	CGAGCCTGTT	2220
	ACTGATTTCG	TTGTCTCGCT	TATTGAGAAT	AACAAGGGTC	GCCTGAAATG	GAATTATCCT	2280
	ACGGGCTACG	AACCCGATAA	GACTGATGAT	AAAAAACCAT	TGCAGCTTAC	CGGCTACAA	2340
	ATCTATGCA	ATGGCTCGCT	CCTTGTTCAC	ATACAGACC	CGACTGTTT	GGAGTATATC	2400
20	GATGAGACTT	ATTCTTCAG	AGACGGTCAG	GTGGAATGG	AATATTGTGT	CACTGCCGTT	2460
	TATAACGACA	ATATCGAGTC	CCAATCGGTT	TGCGATAAGC	TGAACATATAC	TATCACATCC	2520
	TTGGATAATA	TTCAATCTGA	TACAAGCTTG	AAAAATATATC	CTAATCCGGC	ATGATATGTS	2580
	GTAAGGATAG	AGGGATTGAG	TCGGAGCAAG	TCGACAATCG	AGTTGTATAA	TGCGCTGGGA	2640
	ATTTGCATAT	TAAGGGAAGA	GACTCATTCA	GAGAAAACGG	AAATCGATGT	TTCACGTCTC	2700
25	AATGACGGAG	TCTACTTGAT	TAAAGTAGTC	GGTGGAATA	AAACAACAA	CGAAAGGTA	2760
	GAGATAAAGA	GGCCG					2775

(2) INFORMATION FOR SEQ ID NO:204

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2766
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

	ATGATGAAAA	GTATTGTTTT	TAGAGCATT	CTAACGATT	TGCTCTCGTG	GGCAGCGATC	60
	ACGAATCCGA	CTGCTCAAGA	GATCTCAGGC	ATGAATGCAT	CCTGCTCGGC	TGCTCCGGCT	120
	CAACCCGATA	CTATCTTATA	TGAAAGTTTT	GAGAAITGGAC	CTGTTCCCAA	TGGCTGGCTT	180
	GACATAGATG	CTGATGCTGA	TGGTGCCACT	TGGGGGAAGCC	CATCAGGCTC	TTTCTCTGTA	240
55	CCTTACGGAC	ACRAATGGCT	TTGCACCTAC	TCCCATATAC	GTTCCGGTAT	CTCAACAGCG	300
	GGCAACTATC	TGATTACACC	CAATATAGAA	GGAGCCAAAC	GGGTCAAGTA	CTGGGTATGC	360
	AATCAGTATA	GTACCAATCC	GGAAACATTAC	GCAGTAATGG	TATCGACAAC	GGGGACTGCC	420
	ATTGAAGACT	TTGTTTTGTT	GTTTGATGAT	TCCATAACAG	GGAAACCGAC	TCCTCTTGTA	480
60	TGGCGTAGAC	GAATCGTGGA	CITACCGGAA	GGGACCAAAT	ATATTGCAATG	GCGACATTAC	540
	AAAGTCACCG	ACTCACACAC	AGAATCTCTG	AAATTGGATG	ATGCTCACTGT	GTATAGGTGG	600
	ATCGAAGGGC	CCGAACCTGC	TACCGACTTC	ACAGTAATCA	ATATTGGTCA	GAATGTGGGA	660
	CGATTGACTT	GGAACTATCC	GGAGGATTAT	CAACCCGGAAG	GAAAGGGGAA	TGAAGAGTTG	720
	CAGCTTAGCG	GCTACCAACAT	CTATGCGAAG	GGTACACTAC	TGGCACAAT	AAAAGATGTC	780
65	TCCATACTGG	AGTATGTGGA	CAGCACTTAC	TCTTTGCGAG	ACAATCCCTT	GCAAGTGGAG	840
	TACTGCGTTA	CAGCCGTTTA	CGATGAAAGC	ATAGAATCTT	CGACCGTATG	TGGCACGCTG	900
	CATTACGCCA	CGGATGCCAT	CCTTTATGAA	AATTTTGAGA	ATGGACCTGT	TCCCAATGGT	960
	TGGCTTGTGA	TAGACCTGSA	TGGAGATGGA	TTTAGCTGGG	GACACTA/TTT	GAATGCATAC	1020
	GACGCTTTTC	COGGCCATAA	TGGAGGCCAT	TGCTCCTTGT	CGGCTTCTTA	TGTTCCGGGT	1080
70	ATAGGCCCGG	TGACTCCCGA	CAACTATCTG	ATTACCCCCA	AGGTTGAAGG	AGCCAAACGT	1140
	GTCAAGTACT	GGGTAAGCAC	GCAGGATGCC	AATTGGGCAG	CGGAACATTA	CGCGGTGATG	1200
	GCTTCGACAA	CGGGGACTGC	TGTGCGAGAT	TTCGTATAT	TGTTGGAAGA	AACCATGACA	1260
	GCGAAGCCGA	CGGGCGCATG	GTATGAAAGA	ACCATCAACT	TACCTGAAGG	GACTAAATAC	1320
	ATCGCATGGC	GGCATTACAA	CTGTACCGAT	ATATATTCT	TGAAGTTGGA	CGATATCACT	1380
75	GTATTCGGGA	CTCTGCTATC	AGAGCCCGAA	CCTGTTACCG	ATTTCGTTGT	CTCGCTTATT	1440
	GAAAACAACA	AGGGACGATT	AAAGTGGAAAT	TATCCTAACG	GCTACGAACC	CGATAAGACT	1500

140/ 490

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GATGATAAAG ACCCATTTGCA GCTTGCCGGC TACAATATCT ATGCAAACGG CTGCTCCTT 1560
GTTCACATAC AAGACCCGAC TGTITTTGGAG TATATCGATG AGACTTATTC TTCACGAGAC 1620
GATCAGGTGG AAGTGGGAATA TTGTGTCAT GCGGTTTATA ACGACAATAT CGAGTCCCAA 1680
TCGGTTTGGC ATAAGCTGAT TTATGATTCT CAATCGGACA TTATCTTATA TGAAGGCTTT 1740
GAGGCGGGAA GTATTCCTGA AGGCTGGTTG TTGATTGATG CTGATGGCGA CAATGTTAAT 1800
TGGGACTATT ATCCTTGGAC TATGTATGGA CATGACAGTG AGAAGTGTAT TGCATCCOCT 1860
TCGTACTTAC CGATGATTGG CGTTTAACT CCGGATAACT ATTTGGTTAC ACCCAGACTC 1920
GAAGGAGCCA AGCTTGTCAG GTATTGGGTA AGTGCSCAAG ATGCTGTTTA TTCGGCTGAG 1980
CATTATGCTG TGATGGTTTC TACTACGGGA ACTGCTGTTG AAGATTTTGT CCTCTTGTTT 2040
GAAGAGACAA TGACCGCTAA GGTAAACGGT GCATGGTATG AGCGAACTAT TACATTGCCT 2100
GCAGGAACAA AATATATTGC CTGGCGGCAT TATGATTGCA CCGATATGTT TTTCTTGCTC 2160
TTGGATGACA TTACGGTTTA TCGTCTACT GAGACTGTTT CCGAGCCTGT TACTGATTTC 2220
GTTGTCTCCG TTATTGAGAA TAACAAGGGT CCGCTGAAAT GGAATTATCC TAAOCCGTAC 2280
GAACCCGATA AGACTGATGA TAAAAACCA TTGCAGCTTA CCGGCTACAA CATCTATGCA 2340
AATGGCTCCG TCCTTGTTCA CATACAAGAC CCGACTGTTT TGAGTATAT CGATGAGACT 2400
TATTTCTTAC GAGACGGTCA GGTGGAAATG GAATATTGTG TCACTGCCGT TTATAACGAC 2460
AATATCGAGT CCCAATCGGT TTGCGATAAG CTGAACATA CTATCACATC CTGGATAAT 2520
ATTCAATCTG ATACAAGCTT GAAAAATATAT CCTAATCCGG CATCGTATGT GGTAAAGGATA 2580
GAGGGATTGA GTCGGAGCAA GTGCAATATC GAGTTGTATA ATGCGCTGGG AATTGCGATA 2640
TTAAGGGAG AGACTCATTC AGAGAAACG GAAATCGATG TTTCACGTCT CAATGACGGA 2700
GTCTACTTGA TTAAAGTAGT CGGTGGAAT AAAAAACAA CCGAAAAGGT AGAGATAAAG 2760
AGGCCG

25 (2) INFORMATION FOR SEQ ID NO:205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2763 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

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ATGAAAAGTA TTGTTTTAG ASCATTCTTA ACGATTTTGC TCTCGTGGGC AGCGATCAG 60
AATCCGACTG CTCAGAGAT CTCAGGCATG AATGCATCCT GTCTGGCTGC TCCGGCTCAA 120
CCGGATACTA TCTTATATGA AAGTTTTGAG AATGACCTG TTCCCAATGG CTGGCTTGAG 180
ATAGATGCTG ATGCTGATGG TGCCACTTGG GGAAGCCCAT CAGGCTCTTT CTCTGTACCT 240
TACGGACACA ATGGCCTTTG CACCTACTCC CATATACGTT CCGGTATCTC AACAGCGGGC 300
AACTATCTGA TTACACCCAA TATAGAAGGA GCCAAACGGG TCAAGTACTG GGTATGCAAT 360
CAGTATAGTA CCAATCCGGA ACATTACGCA GTAATGGTAT CGACAACGGG GACTGCCATT 420
GAAGACTTTG TTTTGTGTTT TGATGATTCC ATAACAGGGA AACCGACTCC TCTTGATGG 480
CGTAGACGAA TCGTGGACTT ACCGGAAGGG ACCAAATATA TTGCATGGCG ACATTACAAA 540
GTCAUCCACT CACACACAGA ATTCTTGAAA TTGGATGATG TCACTGTGTA TAGGTCGATC 600
GAAGCGCCCG AACCTGCTAC CGACTTCACA GTAATCAATA TTGGTCAGAA TGTGGGACGA 660
TTGACTTGGG ACTATCCGGA GGAATTATCA CCGGAAGGAA AGGGGAATGA AGAGTTGCAG 720
CTTAGCGGCT ACAACATCTA TCGCAACGGT ACACACTGCG CACAAATATA AGATGTCTCC 780
ATACTGGAGT ATGTGGACAG CACTTACTCT TTGCGAGACA ATCCCTTGCA AGTGGAGTAC 840
TGCGTTACAG CCGTTTACGA TGAAGCATA GAATCTTGA CGTATGTGG CACGCTGCAT 900
TACGCCACGG ATGCCATCCT TTATGAAAT TTGAGAATG GACCTGTTCC CAATGGTTGG 960
CTTGTGATAG ACGCTGATGG AGATGGATT AGCTGGGGAC ACTATTGAA TGCATACGAC 1020
GCTTTTCCCG GCCATAATGG AGGCCATTGC TCCTTGTCGG CTTCCTTATG TCCGGGTATA 1080
GGCCCGGTGA CTCCGACAA CTATCTGATT ACCCCCAAGG TTGAAGGAGC CAAACGTGTC 1140
AAGTACTGGG TAAGCACGCA GGATGCCAAT TGGGCAGCGG AACATTACCG GGTGATGGCT 1200
TCGACAAOAG GSACTGCTGT CGGAGATTTC GTCATATTGT TCGAAGAAAC CATGACAGCG 1260
AAGCCGACCG GCGCATGGTA TGAAGAAGC ATCAACTTAC CTGAAGGGAC TAAATACATC 1320
GCATGGCGCG ATTACAACGT TACCGATATA TATTCTTGA AGTTGGACGA TATCACTGTA 1380
TTCCGGACTC CTGCATCAGA GCCCGAACCT GTTACCGATT TCGTTGTCTC GCTTATTGAA 1440
AACAACAAGG GACGATTAAA GTGSAATTAT CCTAACCGGT ACGAACCCGA TAAGACTGAT 1500
GATAAAGACC CATTGCAGCT TGCCGGCTAC AATATCTATG CAAACGGCTC GCTCCTTGT 1560
CACATACAG ACCCGACTGT TTTGGAGTAT ATCGATGAGA CTTATTCTTC ACGAGACGAT 1620
CAGGTGGAAG TGGAAATATT TGTCACGTCC GTTTATAAGC ACAATATCGA GTCCCAATCG 1680

141/ 490

	GTTCGCGATA	AGCTGATTGA	TGATTCTCAA	TCGGACATTA	TCTTATATGA	AGGCTTTGAG	1740
	GCCGGAAGTA	TTCTGAAGG	CTGGTTGTG	ATTGATGCTG	ATGGCGACAA	TGTTAATTGG	1800
	GACTATTATC	CTTGGACTAT	GTATGGACAT	GACAGTGAGA	AGTGATTTGC	ATCCCCITCG	1860
5	TACTTACCGA	TGATTGGCGT	TTTAACCTCG	GATAACTATT	TGGTTACACC	CAGACTCGAA	1920
	GGAGCCAAAG	TTCTCAAGTA	TTGGGTAAGT	GCGCAAGATG	CTGTTTATTC	GGCTGAGCAT	1980
	TATGTCTGTA	TGGTTTCTAC	TACGGGAAGT	GCTGTTGAAG	ATTTTGTCTT	CTTGTTCGAA	2040
	GAGACAATGA	CCGCTAAGGC	TAACGGTGCA	TGGTATGAGC	GAACATTTAC	ATTGCCTGCA	2100
	GGAAACAAAT	ATATTGCCCTG	GCGGCATTAT	GATTGCACCG	ATATGTTTTT	CTTGCTCTTG	2160
10	GATGACATTA	CGGTTTATCG	TTCTACTGAG	ACTGTTCCCG	AGCCTGTTAC	TGATTTGCTT	2220
	GTCTCGCTTA	TTGAGAATAA	CAAGGCTCGC	CTGAAATGGA	ATTATCTTAA	CGGCTACGAA	2280
	CCCGATAAGA	CTGATGATAA	AAAACCATTC	CAGCTTACCG	GCTACAAAT	CTATGCAAAT	2340
	GGCTCGCTCC	TTGTTTACAT	ACAAGACCGG	ACTGTTTTGG	AGTATATCGA	TGAGACTTAT	2400
	TCTTCACGAG	ACGGTCAGGT	GGAAATGGAA	TATTGTGTCA	CTGCCGTTTA	TAACGACAAT	2460
15	ATCGAGTCCC	AATCGGTTTG	CGATAAGCTG	AACATATACTA	TCACATCCTT	GGATAATATT	2520
	CAATCTGATA	CAAGCTTGAA	AATATATCCT	AATCCGGCAT	CGTATGTGGT	AAGGATAGAG	2580
	GGATTGAATC	GGAGCAAGTC	GACAATCGAG	TTGTATAATG	CGCTGGGAAT	TTGCATATTA	2640
	AGGGAAGAGA	CTCATTACGA	GAAAACGGAA	ATCGATGTTT	CACGTCTCAA	TGACGGAGTC	2700
	TACTTGATTA	AAGTAGTCGG	TGGAAATAAA	ACAACAACCG	AAAAGGTAGA	GATTAAGAGG	2760
20	CCG						2763

(2) INFORMATION FOR SEQ ID NO:206

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1779 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1779
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

45	ATGAACAGCA	TCATGAAATA	TCAATTATAT	ACGGCCGCTCA	TAATGGCTCT	CTCTGTATCA	60
	TCCGTTTSCG	GTCAAACCCC	ACGAATATACA	GAACCCRAAC	GCCCCGACAC	GCTCGCGAGG	120
	CAGCTTACTA	TCGTTAATGA	CCAGACTGTG	GAGATGGAGC	ATGCCGATCC	GCTTCCGGCT	180
	GCATACAGG	CCATCGAACC	TCGATTAAAA	CCTTTCGCTC	CGGAATATAA	CAAGCGTACA	240
50	TTCCGATTTC	TCCTGAAAGT	TTCTCTTTCA	GGCAGGAACA	ATCTTCCGAA	TATCCTGCCG	300
	ACCGAAGGTC	ATATGAAGCA	CCGGGGGTAC	CTGAATATCG	GTATCGGCCA	TACGCTAAAC	360
	CAGCGAATGG	ATGCCGGCTA	TCGCTGTGATA	GATGCAGAGC	AGGAGAGACT	GAATCTTTTC	420
	CTCTCCTATC	GTGGGATGAA	ATCGGCTTTC	AATACCGGTG	ACTTCGACGG	CGACAGAAAG	480
	GATAGACGAA	TGATGGCAGG	AGTGGACTAC	GAGCAGCGCA	GGCCTTCCTT	TGTGCTTGCT	540
55	ACCGGCTTGT	ATTATTTCGAA	CCATTATTTT	AATAACTACG	GACGGGGAGC	TACCACCAAT	600
	GTGGGCAGCA	TCCTCAGCT	ATCGACACCT	GTTACTCCTC	AGATGGACAA	CGGGACCCAC	660
	AACGTCCGTG	TATACTTGGG	TGCAAAAAAT	GATGTGATCG	ATGCCAGGAT	CGACTATCGT	720
	TTCTTCGCTT	CTATTCCCTA	TCTGGGTACC	GATCCGATGA	AGGCTCTCAC	AGAACATAGC	780
	CCTCAACTGA	ACGTGACGAT	GAGTAATGAG	TTGTCCGATG	ATATTAAGCT	CGGTGTCGAA	840
60	GTTCTGACGG	GAGGATTTGT	TTTTCGCCAA	AACAGCGAAA	TGATTCAAAC	GGGCGTTCTG	900
	TCCGAAACCG	ACCGAACCT	GTATTATGTG	GAGGGCGCGC	CCACAATCGG	ATTTGTCCGA	960
	GACTCGGACA	ATATGCAATG	GAACATACAG	GCCGGAGTAG	GGATTTCCTC	CCATTTCGGA	1020
	CCCAAAAGGGA	GGTTGTTTTT	CTGGCCATAA	CTGGATGCTT	CGCTTAGTAT	CTTCCCTTCA	1080
65	TGGCGTGTGT	ATCCGAAAGC	CTTCGGGGGT	GTGATTGGA	ATGGTCTCGC	CGATGTTATG	1140
	CRAGAGGAGA	TGCCCTACCT	GATGCCCAAT	ACGATTGTAC	TCCCTTCGCG	CAATGCTTTG	1200
	ACUGCCCAAT	TAGGGGTGAA	GGGGAATATA	GCCGATGTGG	TACGATGGA	GGTTTATGGC	1260
	GACTTCTCCA	AGCTGACAGG	TGTGCTTTTC	TATACTCCGA	CTCTACCCCT	ATATAATCCA	1320
	TCCGACTTST	ATCAGTATAA	TGTGAGTTTC	TTGCCGATAT	ATGCCGACGG	CAGCGCTGG	1380
70	CSGCGAGGTG	GTAAGCTCGA	ATACTCTTAT	CGCGATATGC	TCCGCTTCT	GGTAGACGCA	1440
	TCTATGGCA	AGTGGAAAT	GGATGGAGGA	CTTGTGCGCT	CCATGCAGCC	CGATCTTATA	1500
	TTGAAGGCA	AAGTAGGTGT	TCACTCCATT	GCCCCATTGG	ATGTGACAGT	CCGGTATACA	1560
	CAGCTGAACG	GACGGTATCG	GTATTCTTTC	GGCTCGGCTG	GCTCGGAAGC	CTTGGGATAT	1620
	GGTAATGTAC	ATCTTCTTAG	TGCGGATGTT	TCATACAAGC	TGAAAAAGAA	CTTGAGCCTT	1680
75	TATCTCAAAA	TCGATAATAT	GCTGGCGGAA	ACGACAGAGC	TTATCGGTTA	TTATCCTATG	1740
	CAGCCGTTCC	ATTGTTTCGC	CGGTTTTAGC	TGGACTTTC			1779

142/ 490

(2) INFORMATION FOR SEQ ID NO:207

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1767 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...1767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

25 ATGAAATATC AATTATATAC GGCCTGTCATA ATGGCTCTCT CTGTATCATC CGTTTGCGGT 60
CAAACCCAC GAAATACAGA AACCAACCG CCGGACACGC TGGCGAGGGA GCTTACTATC 120
GTTAATGACC AGACTGTGGA GATGGAGCAT GCGGATCCGC TTCCGGCTGC ATACAGGCC 180
ATCGAACCTC GATTAAAACC TTTCCTCCG GAATATAACA AGCGTACATT CGGATTTGTC 240
CCTGAAGTTT CCTCTTCAGG CAGGAACAAT CTTCGGAATA TCCTGCGAC GGAAGGTCAT 300
30 ATGAAGCACC GGGGGTACCT GAATATCGGT ATGGGCCATA CGCTAAACCA GCGAATGGAT 360
GCGGGCTATC GTCTGATAGA TGCAGAGCAG GAGAGACTGA ATCTTTTCT CTCTATCGT 420
GGGATGAAT CGGCTTTCAA TACCGGTGAC TTCGACGCG ACAGAAAGGA TAGACGAATG 480
ATGGCAGGAG TGGACTACGA GCAGCGCAGG CCTTCCTTG TGCTTGCTAC CGGCTTGAT 540
TATTCGAACC ATTATTTCAA TAACTACGGA CGGGGAGCTA CCACCAATGT GGGCAGCATC 600
35 CCTCAGCTAT CGACACCTGT TACTCCTCAG ATGGACACG GGACCCACAA CGTCCGTGTA 660
TACTTGGGTG CAAAAAATGA TGTGATCGAT GCCAGGATCG ACTATCGTTT CTTCGTTCT 720
ATTCCCTATC TGGGTACCGA TCGATGAAG GCTCTCACAG AACATACGCC TGAACGAAAC 780
GTGACGATGA TGAATGAGTT GTCCGATGAT ATTAAGCTCG GTGTGGAAGT TCGTACGGGA 840
GGATTTGTTT TTGCCAAAAA CAGCGAAATG ATTCAAACGG GCGTCTGTG CGAAACCGAC 900
40 CGCAACCTGT ATTATGTGGA GGGCGCGCCC ACAATCGSAT TTGTGGGAGA CTCGGACAA 960
ATGCATGGA ACATACAGGC CGGAGTAGGG ATTTCTTCCC ATTTCCGAGC CAAAGGGAGG 1020
TTGTTTTTCT GGCCTAAACT GGATGCTTGG CTTAGTATCT TCCCTTCATG GCGTGTGTAT 1080
GCGAAGCCTG TCGCGGTGT GATTGGAAT GGTCTGCGCG ATGTTATGCA AGAGGAGATG 1140
COCTACCTGA TGCCCAATAC GATTGTACT CCTTCGCGCA ATGCTTTGAC CGCCCAATTA 1200
45 GGGGTGAAG GGAATATAGC CGATGTGTA CGTATGGAGG TTTATGGCGA CTTCTCCAAG 1260
CTGACAGGTG TGCCTTTCTA TACTCGACT CTACCTTAT ATAATCCATC CGACTTGTAT 1320
CAGTATATG TGAGTTTCTT GCCGATATAT GCGGACGGCA GCGCTGGCG CGCAGGTGGT 1380
AAGCTGGAAT ACTCTTATCG CGATATGCTC CGCTTCTGCG TAGACGCATC CTATGGCAAG 1440
50 TGGAAATTTG ATGGAGGACT TGTGCGCTCC ATGCAGCCCG ATCTTATATT GAAGGCAGAA 1500
GTAGGTGTTT ATCCATTGCG CCCATTGGAT GTGAGACTCC GGTATACACA GCTGAACGGA 1560
CGGTATCGST ATTCTTTCCG CTCGGCTGCG TCGGAAGCCT TGGGTATCGG TAATGTACAT 1620
CTTCTTAGTG CGGATGTTT ATACAAGCTG AAAAAGAAGT TGAGCCTTTA TCTCAAAATC 1680
GATAATATGC TGGCGGAAC GACAGAGCTT ATCGGTTATT ATCCTATGCA GCGGTTCAT 1740
55 TGTTCGCCG GTTTAGCTG GACTTTC 1767

(2) INFORMATION FOR SEQ ID NO:208

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1038 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...1038

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:208

5 ATGATGGAAA AATGTATCTT TGCTCACTAT CCACATAACC TTGTGTTTAT GATTCGCAAG 60
CATTTCCGTA TCATTTTGGG ATTTCTTTCT CTGTGTGTTT CGGCAGGTGC TCAACAAGAG 120
AAGCAGGTGT TTCATTTTCT GAACCTTCCG GCTACTGCAC AGGCTTTGGC TGGCCGAGGC 180
AAAGCTATCA CCATCGTAGA CGACAATCCC GGACTGGGCTT TTGAGAAATCC GGCTCTGCTC 240
GGATATGAAT CCGGTGGCCG CGCCTTTCTT TCCATTTTAT ATTATATGAG TGGTTCGCAT 300
10 ATGGGCAATG CCTGTTATGC CTCGTCCGTC GGAGAGCGTG GCATGTGGGG TGTGGCATG 360
CGTTTCCTGA ACTACGGGTC TATGCAAGGA TACGATCAGA ATGCGATTGC CACCGGCTCT 420
TTTASTGCTT CGSATATAGC TGTACAAGGA TTTTACAGCC ATGAAGTATG CAACCACTTC 480
CGCGGTGGAG TCAGCCTAAA AGCATTGTAT TCTTCTATCG AGACGTATAG TTCCTTTGGC 540
CTTGGTGTGG ATGTCCGTAT CAGTTATTAC GACGATGACA AAGGATATTC CGCTTCCGCT 600
15 TGGGATTTC AGCTCGGCTT TTCCCGCAGT TTTATCAATG CTCGTTTCG CTTCACATC 660
ACGTTGTTC ATCTGAATCC GCACTATTTC AAGCGTCTTG TACCACGCGA TCTGTCCAAG 720
ATGCAAAAGT TCCTCCGACA CTCTCCGATA GGAGCAGAAT TTACTCCTTC CGAGAGGTTT 780
TGGGTCCGGC TGGGATATAC GCCACAGATT GCACAGGATT TCGAGGTGGA AGCCGCGAAC 840
20 AAATGGGAG GTCTTCCGGC CGGCGTCGGT TTCACITCAG GTGTAGTACG TGTAGGCGTA 900
TCTGCTGCCA CCTATCATCC TGCAGCTCTT TCGTTCAATG GTTCGGTAGG TATCCGTTTG 960
GACGATAAGA GCATCTTC 1020
1038

25 (2) INFORMATION FOR SEQ ID NO:209

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1035 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

30 (11) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GIINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1035

45 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:209

ATGGAAAAAT GTATCTTTGC TCACTATCCA CATAACCTTG TGTTTATGAT TCGCAAGCAT 60
TTCGGTATCA TTTTGGGAT TCTTTCTCTT GTGTTTTCGG CAGGTGCTCA ACAAGAGAAG 120
50 CAGGTGTTTC ATTTTCTGAA CCTTCCGGCT ACTGCACAGG CTTTGGCTGC CGGAGGCAAA 180
GCTATACCA TCGTAGACGA CAATCCCGGA CTGGCTTTTG AGAATCCGGC TCTGCTCGGA 240
TATGAATCCG GTGGCCGGCG CTCTCTTCC TATTATATAT ATATGAGTGG TTGCGATATG 300
GGCAATGCCT GTTATGCCTC GTCCGTCGGA GAGCGTGGCA TGTGGGGTGT TGGCATGCGT 360
55 TTCCCTGAAT ACGGGTCTAT GCAAGGATAC GATCAGAATG CGATTGCCAC CGGCTCTTTT 420
AGTGCTTCGG ATATAGCTGT ACAAGGATTT TACAGCCATG AACTGAGCAA CCACTTCCGC 480
GGTGGAGTCA GCCTAAAAGC ATTGTATTCT TCTATCGAGA CGTATAGTTC CTTTGGCCTT 540
GGTGTGGATG TCGGTATCAG TTATTACGAC GATGACAAAG GATATTCGCG TTCCGCTCTG 600
TTCAAGAAAG TAGGGGCGCA ACTGAAAGGC TATAATGAAG AACGGGAACC GCTCGATTG3 660
GATTTCCAGC TCGGCTTTTC CCGCAGTTTT ATCAATGCTC CGTTTCGCTT GCACATCAGG 720
60 TTGTTCAATC TGAATCCGCA CTATTTCAAG CGTCTGTAC CACGGGATCT GTCCAAGATG 780
CAAAAGTTCC TCCGACACTT CTCGATAGGA GCAGAAATTA CTCCTCCGGA GAGTTTTTGG 840
GTCCGGCTGG GATAACGCC ACAGATTGCA CAGGATTTTG AGGTGGAAGG CGGCAACAAA 900
TGGGGAGGTC TTTCCGGCCG CGTCCGTTTC ACTTCAGGTG TAGTACGTGT AGGCGTATCT 960
65 GCTGCCACCT ATCATCCTGC AGCTCTTTCG TTCATGTGTT CGGTAGGTAT CCGTTTGGAC 1020
GATAAGAGCA TCTTC 1035

(2) INFORMATION FOR SEQ ID NO:210

70 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 990 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

75

144/ 490

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...990
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

ATGATTGCGCA	AGCATTTCGG	TATCATTTTG	GGATTTCCTT	CTCTTGTTGTT	TTCGGCAGGT	60
GCTCAACAAG	AGAAGCAGGT	GTTCATTTT	CTGAACCTTC	CGGCTACTGC	ACAGGCTTTG	120
GCTGCCGGAG	GCAAAGCTAT	CACCATCGTA	GACGACAATC	CCGGACTGGC	TTTTGAGAAT	180
CCGGCTCTGC	TCGGATATGA	ATCCGGTGGC	CGCGCCTTTC	TTTCTATT	ATATTATATG	240
AGTGGTTGCG	ATATGGGCAA	TGCCTGTTAT	GCCTCGTCCG	TGGGAGAGCG	TGGCATGTGG	300
GGTGTGGCA	TGCGTTTCC	GAACTACGGG	TCTATGCAAG	GATACGATCA	GAATGCGATT	360
AGCAACCACT	TCGCGGTGG	AGTCAGCTTA	AAAGCATTGT	ATTCTTCTAT	CGAGACGTAT	420
GCCACCGGCT	CTTTTACTGC	TTCCGATATA	GCTGTACAAG	GATTTTACAG	CCATGAACTG	480
AGTTCCCTTG	GCCTTGGTGT	GGATGTCCGT	ATCAGTTATT	ACGACGATGA	CAAAGGATAT	540
TCCGCTTCGG	CTCTGTCAA	GAACGTAGGG	CGCAACTGA	AAGGCTATAA	TGAAGAACGG	600
GAACCGCTCG	ATTGGGATTT	CCAGCTCGGC	TTTTCCCGCA	GTTTTATCAA	TGCTCCCTTT	660
CGCTTGCA	TCACGTTGTT	CAATCTGAAT	CCGCACATT	TCAAGCGTCT	TGTACCAAGC	720
GATCTGTCCA	AGATGCAAAA	GTTCCTCCGA	CACCTCTCGA	TAGGAGCAGA	ATTTACTCCT	780
TCCGAGAGGT	TTTGGGTCGG	GCTGGGATAT	ACGCCACAGA	TTGCACAGGA	TTTCGAGGTG	840
GAAGGCGGCA	ACAAATGGGG	AGGTCTTTCG	CGCGGCGTGG	GTTCACATTC	AGGTGTAGTA	900
CSTGTAGGGG	TATCTGCTGC	CACCTATCAT	CCTGCAGCTC	TTTGTTTCAT	GTGTTCCGTA	960
GGTATCCGTT	TGGACGATAA	GAGCATCTC				990

(2) INFORMATION FOR SEQ ID NO:211
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...972
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

ATGTGCGCTCG	AACCCATAAT	TGCTCCGATT	TCATCCGAGT	TGCTCGAGCA	GGAGCTGACT	60
GCCGATCGTT	TTCTGCGGAT	GACAAACAAA	GCCGGCAATG	AGATCTATGT	TTTTACGGCC	120
GAAGAAGCTC	CGCATTTGCAT	GAAAGAAGTA	GCCCGACTGC	GAGAAGAAGC	CTTTCCGCAT	180
TATGGCGGAG	GTACTGGCAA	GCGATCGAT	ATAGACGAGT	TGCACACCAT	GCCCGGGAGC	240
TACAAACAGC	TGATCGTATG	GGATCCGCAA	AACAAGGCTA	TACTCGGAGG	CTACCCCTTT	300
ATCTATGGGC	GGGACGTTGC	TTTCGATACC	GATGGCAAGC	CTTTGCTGGC	AACGGCAGAG	360
ATGTTTCSCT	TCAGTGATGC	TTTTTCGAC	GATTATCTCC	CTTACACAGT	CGAATTGGGA	420
CGTTCTGTCG	TGTCGCTCCA	GTACCAATCG	ACACGGATGG	GCACAAAGGC	CATTTTGTG	480
CTGGACATTC	TTTGGGACGG	TATCGGAGCA	CTCACTGTAG	TCAATCCAGA	GGCACTCTAT	540
TTCTATGGCA	AGGTGACCAT	GTACAAAGAC	TATGATCGGC	GAGCTCGCAA	TCTGATCCTG	600
TATTTTCTTC	GCAAGCACTT	CTCCGATCCG	GAAGGCTTGG	TCAAGCCTAT	TCATCCCTTA	660
CCGATAGAGA	TCAGTGCGGA	GGACGAAGCC	TTGTTCTCCT	CATCCGACTT	TGACACCAAT	720
TACAAGACTC	TCAATATAGA	AGTGCGCAAG	CTGGGTATCA	ATATCCCTCC	TCTCGTGAGT	780
GCATATATAG	CTTTGTCTCC	GGAGATGCGT	GTTTTCGGCA	CTGCAGTGAA	TGASTCTTTC	840
GGAGAGGTGG	AGGAAACCGG	CATATTCAAT	GCTGTGGGTA	AGATCCTGGA	AGAGAAAAAA	900
CAACGGCACA	TAGAGAGCTT	CATCTCAGC	CGGAACGAAA	AAAAAGGTCT	CGACAGTAGC	960
AATGGCCGAT	CA					972

(2) INFORMATION FOR SEQ ID NO:212

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

20 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

25	ATGAAACCA TTGTAAGATA CAGCCGCTT CCGGTCGCTC TCTTCTTTG CCTTTTGGGA	60
	GCTGTGCACT TGTCTGTGGA GGCGCAGATG CPCAATACTC CTTTCGAGCT GTCGGATCAG	120
	ATCGTCTCTT CTCCACCGGA AAGGCAATAC AGGGAGATTT GTGTGCAAC GAAAGAAAAA	180
	AGGGGGGCGG ATCTTTTCCC GTTGAGCGAT AAGCTGCGCG ATTCGGCCTA TGTTCGTTTC	240
30	GGCTCGGCCT ATGGCGATAT TGGGGGCGAC TATCTTCCGT ACAACGGCAA TAACTACTCC	300
	TGCTCTCGGC TCGAATCGGG TGGTCGCATC AGTGTCCGTA ACTATGGCAC ATTGCAGGGC	360
	AGTGCTTCCT ACTCAGGTGG CATGCACAAA CGCATCGGCT GGAATGCTCT GCGCAACGCC	420
	GAAGCCTTACT ATCCCTATTT GGTGTCCGAT TCGACCGGCG GAGACTATCA TTTCGAAGAC	480
	TATCGGCTTG CCGGCTACTA TTCTTTTCGC GCGGCGCGCT TGCCCTTCGG TATAGGCTTC	540
35	TCATACAGGG GCGAAGTTGC TTATCGGCTG ACCGATCCGC GTACGACCAA TACGACCGGT	600
	GCATTGGAGC TTCTTTGTGC TACCTCTTTG ACGCTGCCTC GAGAGAACAG GCTATCGCTT	660
	TCGGCTGCGT ATCTCTATCA TAGACAACAC CTCACACAGI ACAACTGGCG TCCCGGGCAG	720
	CAGGACAAAT TCTTCGTCAG CTACGGTTTC GGTACAGTGG ATGTCAGCAA CAGCCCTATC	780
	TGTTTCGGTA TCTCCAGAAT GAACTACGTC AACGGATGGA AGCTTAGCTC CCGTCTGGAT	840
40	ACCCGTAGGG GCGATGCCAT CGGTCTCGAC TACAGCGGCT ACTTCTCGA TACCGAAGAG	900
	AGTCTGCTCA TCAATCTCTT TGCTTTGCTT TACAATCGCC TGGGACTCTA TGGTAGCTGG	960
	CATCTGTCGG ACTTCGATTT TTCAATTTCA GCCGACTATG CTCTGCGCCA AGGGATAGAG	1020
	CGGATATACG AACACTACAA GCCGGATGAT AATTATCATA TCTACGACCT CCGTATCTTG	1080
	GCCATTCGCC GCTGGTATAT GCTCAATGAG TTTTCTGCCC AAGCCCAAGC CTCCTACCGT	1140
45	ATTCGCACGG ATAGAGGTTG TGCCCTGACA GTGAGTGCCG GTAGTGATTT CTACGGCTAT	1200
	GATGACACCT ATCGCAAGCA TGGACATCAT ACCATGAGCG GAATGCTACG TCCTTTTGCC	1260
	GGTATAGCCT ATGACCATGC CGGATCCAAA TTGGATTTTG GACTTTGCTT TTCGGCTGCT	1320
	TATCGAATGG TGCTGACGCA TTCGTATAAG ATTGTTACCA TCCAGAAAGA GCAGCTCGAC	1380
	TATCAGCTGG CCTATTGCCC CTATGCCTAT CGTAATAGAG AAGGCGTGGA GGTGCGTTCC	1440
50	TCCTCTGACG TCTCGATTCC GATGCAGAAT ACCCACCGCC TGATGACAGA GCTGCGGTTG	1500
	TATGGCGACC TGATGAAAG AAAGGACGGT ATAGCCTATG GCAAAACGCC CGGTGTCTATC	1560
	TCACATATCC TGTCCGATCC GCAAGCCGAA CGAACGTCCG GCCATACCAT CGGGGCTATC	1620
	TGCAATATCT CCTACCTCTT C	1641

55 (2) INFORMATION FOR SEQ ID NO:213

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

65 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

70 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2250

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146/490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:213

5 ATGAAAAAAC TTCACATGAT TGCCGCTTAA GCGCTCTGCT CTTTCTGCTT GACGGCACAA 60
GCACCCGCTCT CCAACAGCGA GATAGATAGT CTTAGCAATG TGCAGCTCCA GACCGTACAG 120
GTCTAGCTA CTCGCCGCCAC GGCGAAAAACC CCTGTCGCTT ACACCAAGCT TCGCAAGGCC 180
GAACTTTCCA AGTCCAAATTA TGGTCGTGAC ATCCCTATC TGCTGATGCT GACTCCCTCC 240
GTGGTAGCCA CCAGCGATGC CGGTACGGGT ATCGGATATT CCGGCTTTCG CGTGGGTGGC 300
ACCGATGCCA ATCGCATCAA CATAACTACC AATGGAGTAC CCCTCAACGA CTCCGAATCT 360
CAGTCCGCTCT TTTGGGTGAA TATGCCCGAC TTCCGCTCTT CCATCGAAGA CCTTCAGGTG 420
10 CAGCGAGGTG TGGGTACTTC CACCAATGGT GCCGGAGCTT TTGGGGCAAG TGTCATATG 480
CGTACGGATA ATTTGGGACT GGCTCCTTAT GGCCGTGTGG ATTTGAGCGG AGGTTCTGTT 540
GGCACATTCG GCGGATCGGT CAAACTCGGT AGCGGACGCA TCGGTGCCCA TTGGGCGAGT 600
GATGCCCGCC TGTCCAAAT CGGTTCTGGAC GGCTACGTGG ATAGAGGAAG CGTGGATCTG 660
AAATCCTATT TCGCACAGST GGGCTATTTC GGTAGCAACA CGGCTCTCAG GTTCATCACT 720
15 TTCCGAGGAA AAGAAGTTAC GGGTATCGCA TGGAAACGCT TTTCCAAGGA GGATGAAGCC 780
AAATATGGCC GCGGATACAA CAGTGCCGCT CTTATGTACG TGGACGCGCA AGGAGTACCG 840
CACTACTACC ACAATACCGA CAATTACGAG CAGCGTCACT ACCATGCCAT CATGACGCAC 900
AGGTTCTCTC CTTCCGTTAT CTTCAACCTC ACGGCACACT ACACGGCCGG ATATGGCTAT 960
ACGGACGAAAT ATCGTACCGG ACGTAACTA AAGGAATATG CACTGCAGCC CTATGTGGAA 1020
20 AACAGTGTGA CGGTGAAGAA AACGGATCTC ATCCGTGAGA AGTATCTGGA CAATGACTTC 1080
GGAGGACTCA TCGGTTTCGT TAACGTGGAC ACCGGTGCA TGGGATTGCA GTTCGGGGCC 1140
TCGGGCAATA TCTATAAAGG AGACCACTTC GGCGGTATCA CTTATATCAA AAGTACAAT 1200
CAGCCCTTAG CTCCCGACTT CGAATATTAT CGGAACAGGG CAGACAAAAG AGAAGSTGCA 1260
GCCTTTGCCA AAGCCAACTG CGGATCACT CCGGAACTGA ACATGTATGC CGACCTCCAG 1320
25 TATCGTACCA TCGGTACAC GATAAACGGC ATCAGGACG AAATATGATG GGTACAGGGA 1380
AGATGCAGC ACATCGATTG GGACAAGACC TTCCGCTTCC TCATCCGAA GGCCGCTCTT 1440
ACCTATAGTT TCGACGATGC TCATCTGCC TATGCTTCTG TTGCGGTAGC ACACCGCGAG 1500
CCTAACAGAA CCAATTACAC CGAAGCGGA ATAGGACAGT ATCTACGCC TGAGCGACTG 1560
ATCGACTATG AGCTGGGCTA CCGCTATGCT TCGCCCTCTT TGTGCGCCGG AGTAGGTCTC 1620
30 TATTATATGC AATACAAGGA CCAACTCGTG CTGGATGGCC GTTTGAGCGA TGTGGGACAG 1680
ATGCTCACAA GCAACGTCCC CGACAGCTAC CGTATGGGAC TGGAGCTGAC TCTCGTTGG 1740
CAGATCCTTC CTGCTTGGCT GCGTTGGGAT GCTTCTTTCA CTATGAGTCG CAACAAAATC 1800
GACCGCTACG TACAATATAC ATCCGTATAT GATGCGGACT ACAACTGGCT CGAACTCAAG 1860
GAGGAGACCC TCGAAAGCAC GGATATAGCC TACTCGCCCA ATGTCATGCG CGGCAGCATG 1920
35 CTTACCTCT CTGATGCCGG TTTCGAAATG GCTTGGACGA GCCGCTTCGT CAGCAAGCAA 1980
TATCTGGACA ATACACAGCG CAGCGATCGC ATGCTTCTCT CCTATTGGGT GAACGACCTC 2040
CGCTCCGCT ATGTGCTGCC GGTTCACCTT GTTAAGAGAG TGGCACTGGG CGTACAGCTC 2100
AATAATCTCT TCAACCTCAT GTATGCGTCC AATGCGTACA TCTACGATGC CGGTTACGTA 2160
CAGGCATCCG GAGAACTAAG TGCAATATGC GATCTGCGTT ATTATCTCA GGCCGGATTT 2220
40 AATGCACTGG GTAGTCTGAC AATCGATTTC 2250

(2) INFORMATION FOR SEQ ID NO:214

45 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
50 (11) MOLECULE TYPE: DNA (genomic)
(111) HYPOTHETICAL: NO
55 (1v) ANTI-SENSE: NO
(v1) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
60 (1x) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1482

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:214

65 ATGAAAAGAA GGTTCCTATC GCTGTTACTG CTGTACATAC TCTCTTCCAT CAGCCTTTCT 60
GCTCAGCGGT TTCGATGGT GCAGGGAATC GAGTTGGATA CCGATTCCGT TTTCTCTCTG 120
CCCAAGCGTC CTTGGCGCGC CATCGGTAAA ACGATAGGCG TCATCTGGC CGTATGGGGC 180
70 TTGATCAAT TCATCATGAA CGAGGACTTT GCAGACATCA GTTGGCAGAC TATCAAGAGC 240
AATTTCCAAA CAGGCTTTGG CTGGGACAAAT GACAAGTTTG TCACCAACCT CTTCCGACAT 300
CCTTATCAAG GATGCTCTA TTTCAATGCA GCGAGGTGCA ACCGTTTGA CTTTCAGGCAC 360
TCTGCTCCGT TTGCTTCTT TGGCAGTCTC ATGTGGGAGC TGCTTATGGA AAACGAGCCA 420
CCGAGTATCA ACGACCTCTG TGCCACCACC ATAGGCGGTA TAGCTTTGGG GGAGATGGGG 480
CAGAGGCTGT CCGACCTGCT CATCGACAA CGTACCACAG GGTGGGAACG TATGGGGCGC 540
75 GAGGTGGCTA TCGCTCTGAT CAATCCGATG CGCTTTCTCA ACCGTCTGAC ACGAGGAGAG 600

147/490

GTGACTTCTG TCGGGAGTCG CAGCGGACAG ATATTTTCAGT CTGTCCCCAT AAACATAGTC 660
GTGATGCGG GCTTTCCGCTT TTTGGCAGAC AAGCGGCATG CCGGAACCGG TGCCACGSGT 720
CTGACCCCTGA ATCTGAGATT CGACTAGGGC GATCCATTCC GAAGCGGAGC TTTCTCTCCA 780
TACGATTCTT TCCAATTCAA AGCCGGATTG AGTTTCTCCG AATCGCAACC TCTGCTGAGC 840
5 CAGATCAATC TGATCGGAAT CCTAAGCGGA TGCCAACTGC TCGCACACGA ACGAACGGTT 900
TTGGTGGGAG GTCTCTTTCA GCACTTCGAC TACTACAATT CGGAAAAACG AATAAGCAAA 960
AATTCGGAGG AGGTACTCGT CACCCCATAC CGTATCTCGC AAGTGGCAGC TCTGGGAGGC 1020
GGTCTTATCT TCCAGCACCA CGGAAAAATT CGACGAGTC CTCTGGAGCT ATATGCCGAG 1080
10 ACCTACCTGA ATGTCGTCCC GATGGGAGCC AGTCTGTCCG ATCACTACAA CGTGGACAAT 1140
CGGGACTATA ACCTCGGCAG CGGATTGAGC GGCAAGCTAT ACCTTGGTGC TACGTACAAAT 1200
GATCTGTGGA GCTGGCTCTT GGGAGTCGAA AGCTATCGGC TCTACACATG GATCGGGTAT 1260
GAAGAGCCGC ACCAGAAAAA TACCGATGTC AGCTCTTTTA TGGTGCAGGG GGACGAAAGC 1320
AAGGCCGCC TACTGGTGAC GAGTTCGGAG TTCGCATTTC ATCCTGGCCC CTGGCATGTA 1380
GCCATCGTCG CTCGCCGTTT CATCCGCAA ACAGCCTATC AATTCTACCC TAACGTATCA 1440
15 TTCGATACCG GCGACATACA GCTGCGTGTC GGATTTCAT TC 1482

(2) INFORMATION FOR SEQ ID NO:215

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 882 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 30 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 35 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...882
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

ATGAAACGAC TGATTGTTTT TCTGGCAATG GGTGGCTTGC TGTTCACCCT TGCGAAGCGA 60
CAAGAAGCAA AACTGTCATC TGCACTCCC AAAAAGGACT GGACTATAAA AGGTGTGACC 120
GGACTAAATG CCTCTCAGAC TTCTCTGACC AACTGGGCTG CCGGTGGAGA AAACACGGTG 180
GCAGGTAAAC TCTATTGAA CATAGATGCC AACTACCTGA AAGATAAATG GAGTTGGGAC 240
45 AACGGTTTGC GTACAGACTT CGGTCTGACC TACACAACAG CCAACAAGTG GAACAAAAGT 300
GTAGACAGA TCGAACTCTT CACGAAGGCC GGCTATGAGA TCGGCAACCA TTGGTACGGA 360
AGTGGCGTTT TCACTTTCTT CTCACAGTAT GCCAAAGGAT ATGAGAAGCC CTCGGATCAC 420
TTGACAGGAG TCAAGCATAT CTCTAATTC TTGCTCTCTG CATATCTCAC TCTCGGTATT 480
GGTGGCGGACT ATAAGCCCAA TGAGAAGTTC TCTCTCTACC TCTCTCTCAC AACGGGCAAG 540
50 CTGACTGTAG TAGCAGACGA CTACCTCTCA AGTTTGGGAG CCTTCGGGGT GAAAGTTGGT 600
GAAAGACAA TGTTCCGAAT TGGTGCTTTG GTAGTGGGTT CGGCCAATAT AATCTGATG 660
GAGAATGTCA ATTTGATAAC CAAGGCTTCA TTCTTCTCGG CTTATACGCA CGACTTTGGC 720
AATATTGACA TCAATTGGGA GGCTATGCTG GCCATGAAGA TCAACAAGTT CCTCACGGCT 780
ACGATAGCCA CCAATCTTAT CTACGACGAT GATGTGAAGA TCAACGATGG CCGCAAAATC 840
55 CAGTTCAAAG AAGTTGTGGG CGTGGGTGTT GCGTACACTT TC 882

(2) INFORMATION FOR SEQ ID NO:216

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 612 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:

148/490

(A) NAME/KEY: misc_feature
(B) LOCATION 1...612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

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ATGAAGAAAA TGATTTTGGC AGCTACTATG CTGCTCGCAA CAATCGGTTT TGCAAATGCT
CAGAGTCGTC CTGCTCTTAG ACTGSATGCT AACTTTGTCG GTAGTAACTT AATGCAAAAA
GTGSCAAACA CGAGCGTGAA CAATAAGATG ATCGTAGGCT TACGTGTTGG TGCTGCTGCT
GAGTTCGCTC TTAGCAATGA TGGATTCTAT CTCGCCCCCG GATTGGCCTA TACGATGAGA
GGTGCTAAGA TGGAACTACT AAGTGAAACG ACAACTCGCT TGCATTATCT GCAAATACCG
GTGAATGCCG GTATGAGATT TAGCTTTGCT GACAACATGG CTATTTTCATT GGAAGCAGGT
CCCTATTTG CATATGGTGT CGCCGGAACG ATTAAGACTA AAGTTGCAGG CGTTACGGCT
TCTGTAGATG CCTTTGGTGA TAACGGATAT AACCGTTTCG ACTTGGGCTT GGGCTTGCT
GCTGCCCTGA GCTACGACCG TTATTACGTA CAAATTGGAT ATGAGCATGG ATTGCTTAAT
ATGTTGAAGG ATGCTCCGGA TAAGACTTCT TTGCGTAATC ATGACTTCTT TGTGGGTCTC
GGTGTTCGCT TC

(2) INFORMATION FOR SEQ ID NO:217

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

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ATGAAAAGGA TTTTACTGT AGCCCTTGTG CTACTTGCTT CGGTCACTAT GGCCATCGGA
CAAAGCCGCC CGGCACITCG CGTAGATGCC AACTTCGTAG GCAGCAATCA GAGCATGAAA
AGAGACGGAT ATGTGTGGGA CACCAAAATG AATGTGGGCC TGCGGGTCGG TGCCGCTGCC
GAATTCATGA TCGGATCAAG AGGATTCTAC TTGGCTCCGG GTCTGAACTA TACGATGAAG
GGCTCCAAAA CCGAATGSGA TATACCCGAA ATGGTTCCCT GTACCTATAT TACGATGGTT
TCCACTCGCT TGCACTATCT GCAACTGCCG ATCAATGCCG GCATGCGGTT CGACCTGATG
AATGACATGG CGGTTTCGAT CGAAGCGGGT CCTTTCCTTG CATACGGTAT ATATGGTACA
TATCGGCAGA AGTIGGAAGG ATGGAAGCCG AACCACTACA GCACAGAGTT TTTTGGCCCA
ACGCTTGGTG GCCCAACAAA TATCCGCTGG GACATCGGGG CAAACATAAT AGCCGCATTC
CACTATAAGC GTTATTATAT ACAGATAGGC TATGAACATG GATTGTGGA TATGTGTGCA
GGTGGAGGTT CTGATATTCC CCGACTGAAC GACAATAGGC AATCCTCTTC GACGACCGCT
CTAAGAGAAA AGGGAATAAA CGAATACGCT TATAATCGTG ACTTCTTCGT GGGCATAGGT
TACCGCTTT

(2) INFORMATION FOR SEQ ID NO:218

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature

149/490

(B) LOCATION 1...621

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:218

5	ATGAAAAGAA	TGCTGCTGCT	TCTCGTTGTA	TTATTATATG	GAATTGCAGG	CGGATTGGCT	60
	GCACAAGACG	TTATCAGACC	ATGGTCATTG	CAGGTCGGAG	CGGGATACTC	CGATACGGAG	120
	AACATCCCGG	GAGGATTACG	CTATGGTTTC	TATTTGGGAA	AGCGTATGGG	GAGCTTTCTG	180
	GAAGTGGGGC	TGTCATGTA	CAACTCCACA	CGTCAACAG	CCAACAATGC	AGACTCCTTT	240
	GCATCGAAGC	AAGGAGACGG	ATCTTTTCAG	GTAAATATGT	CTTCTCGGAA	TGAGAAGTGG	300
10	TCATTCTTCG	ATGCAGGCAG	TGCCAACTGC	TATATGATCG	TCGTCCGAGT	CAATCCTCTC	360
	CATCTGTTTT	GGCAGAATAG	CCGGCAACAAT	TTGTTTCTGG	CAGTACAAGC	CGGCCTGTCC	420
	AATAAGCACA	ATATTCAATT	CATCTATGGA	GACAAGGGAG	CCAAAGTCAG	TATCTACACC	480
	AATTGGAATA	CCTACATCGG	TTACGGAGCA	CGTGTAGCCT	ACGAATATCA	AATTCAATAA	540
	AACGTGGGGG	CGGGTGCCGC	TGTAATGTAC	GACCACGGCA	ATAAGATGCT	TACGGCCATG	600
15	GCCACGCTCT	CCACTCATTT	T				621

(2) INFORMATION FOR SEQ ID NO:219

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2853 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 30 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 35 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...2853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

40	ATGAGAGTAT	CGGATCTCTG	TTCCAGACTT	TCATGGTTAT	TACCGGTAAT	CCTTGTCCGA	60
	TTGCTCTGTG	CTACTTTGGT	CGCTGCGGAA	CGTCCTATGG	CCGGAGCAGT	CGGATTGCAC	120
	CACCGTCGGG	ATGCTGCGCT	GTCTGATTCT	ACAGCGAAAG	ACACGGTGCC	TCTCGCAAAA	180
	CCTATTCCCTG	ACAGTGCTTT	TCGAGATTCC	CTTCTGCGOS	ATTCCACCGG	ATCGATGCGG	240
	CAAGATAGGG	TGTATGACGA	TGAATTCGAA	TTGGAAGATA	TAGTGGAGTA	CGAAGCTGCC	300
45	GATTCCATCG	TTTGTCTCGG	ACAGAATCGT	GCCTATCTTT	TCGGCAAGAG	CTATGTGAGC	360
	TATCAAAGGA	GTGCTTTGGA	GGCAAACTTC	ATGTATCTCA	ATACCGACAG	CAGTACGGTT	420
	TATACGCGT	ATGTCCTCGA	TACCGCGGGT	TATCCGATGG	CCTTTCCTGT	TTTCAAGGAT	480
	GGAGAGCAGT	CGTTGGAAGC	CAAGAACTTT	ACCTACAAC	TCGCGCACGA	GAAAGGGATT	540
50	ATCAGCGGAG	TGATCAGCGA	GCAGGGCGAA	GGCTATCTGA	CTGCGGGTAA	GACCAAGAAG	600
	ATGCCCCGAC	ATATCATGTT	TATGCAAGGA	GGGCGTTATA	CGACCTGCGA	CAATCAGGAT	660
	CATCCTCACT	TCTATATCAA	TCTTTCCAA	GCAAAGGTGC	ATCCGGAGAA	AGACATCGTC	720
	ACAGGTCCGG	TCAATCTGGT	TATGCGGAT	ATGCGCGTGC	CGATAGGTCT	TCCTTTGCGC	780
	TATTTTCCCT	TTTCCAACAA	ATACTCTTCC	GGTATATTGA	TGCCACGTA	CGGAGAGGAC	840
55	AATCGCTATG	GATTTTATTT	GAGGAATGGT	GGATATTATT	TTGCCCTCAG	CGACTATATC	900
	GAITTTGGCAT	TGCGTGGGGA	GATCTTTTCC	AAAGGGTCAT	GGGGCAATTC	AGCCCAATCG	960
	AAATATAAGA	AGAGGTATAA	GTACAACGGC	TCGTTGGAAG	CCAATTATCT	GGTATCGAAG	1020
	TCGCGGCGAC	AATACGTGCC	CGGAGACTAC	AGCAAGACCA	CCAGTCTGAA	TATCCGATGG	1080
60	ACACACAGTC	AGGATCCGAA	GGCCAATCCT	TTGCAACGTT	TGTCGGCCAA	TGTCAATTTT	1140
	GCTACGACAC	GAAATTCGGC	CGTGAGCTAT	TGCGGCAAGT	TTCCGGGTAC	TCCTTTTTCG	1200
	ATTACGGGTA	GCAATGGATAT	CAGCCAGAAC	ATGCCGAGTA	CGACGGTGAG	CCTTACCTTG	1260
	CCGAATCTTT	CGATTAATAT	GTCCACGCGT	TATCCTTTCA	AGCCGAAGAC	CCGTGTAGGA	1320
	CCGGAGCGAT	GGTAOSAGAA	STTGAGTGTG	GGCTATTCGG	GTGAGCTTCG	CAATAGTATC	1380
65	TTGACAAAAG	AGAAAGATTT	GCTCCAGAGC	AATCTCGTGC	GCGATTGGAA	GAATGCTATG	1440
	CGTCATTCCG	TACCGATCAG	TTTGAATGTC	CCTTTGTTGG	ATTATATCAA	TCGACTATG	1500
	GGGGTTAACT	ACAATGAGTG	GTGGTACAGG	AAAGGCATAC	GGAAGTCGTG	GAATGAGGAT	1560
	AAGAAACAT	TCCTGCCTTC	GGACACGACC	TATAAATTCC	GCAGACTGTA	CGATTACAGT	1620
	CTGTGCGGAG	GCTTATCTAC	CACATTGTAC	GGTATGTTCA	AGCCTTGGAA	ACCTTTTTC	1680
70	TTGCGAGGCA	ATCTCATTAT	GATCGGTGAT	CGCTTCACGC	CCACTGTCAG	TTTCTCCTAT	1740
	ATGCCGGGACT	TCACGAAACG	CCGATATGGC	TTTTGGGAGC	TTCTTGAGCA	TACGGATCAG	1800
	AACGGCAAGC	TGCATACGCT	GCTCTACICT	CCTTATTTTC	AGCAGATATT	CGGTGCTCCC	1860
	TCCATGGGCA	ATGCAGGATC	TGTCAATTTT	TCTTTTGACA	ACAACTTAGA	GGCCAAGATC	1920
	AAATCCAAT	CGGATTGCAC	AGGGATCAAG	AAGATCAGCC	TGATAGATCA	GTTCACATGG	1980
75	TCTACATCCT	ATAATATGTT	TGCCGATTCC	ATCCGATGGA	GCAATATCTC	GGCTTCGCTG	2040
							2100

150/490

	GCACTTCGCC	TCTCCAAGAG	CTTTACCTTG	CGCTTGTCGG	GTCTGTTCGA	TCCCTATTTG	2160
	ACGAAGTATT	ATCAGGGGAGA	AGATGGGAAG	ATCATTCCCT	ATAAGAGCAA	CGACCTGCCG	2220
	ATTTTAAACG	GCAAGGGGATT	GGCAGCGCTG	ATCAGTACGG	GTACTTCTTT	CAGCTATACG	2280
5	CTCAACAAAG	AGTCGCTCAG	CGGATTGATA	GCTCTTTTCA	GTGGCAAAAA	GGAGCGGAGA	2340
	GATGAAAAGA	AAAACACAGG	GGCTACTGCT	CATGAAGGAG	ACGATGCTGC	CGATATACTT	2400
	GAGGAGGAA	GACCGCAAAA	TGAAAGTGGG	GGGTGCTCC	TCGAGCGCAA	CCGTGAGGGC	2460
	GGAGCAGTG	ATCAGGATGG	TTACTTCGCA	TATTCGATCC	CATGGAGCCT	GTCTTCGAC	2520
	TATAGTTGGA	ATATTGCTAC	CGACTACAAT	AGGTACAATG	TCAATAAGAT	GGAGCACTAC	2580
10	TACCGGGTAA	CGCAGAACT	GAGCTTTCGG	GGCAATATCC	AGCCTACACC	GAAGTGGAGC	2640
	TTCGGATTCA	ATGCGAACTA	CAATTTTCGAC	TTGAAGAAAA	TAACATCGCT	TACCTGCAAC	2700
	GTCACTCGCG	ACATGCACTG	CTGGGCTATC	TCGGCCAGTT	TCATCCCTAT	AGGAGCATAC	2760
	AAGTCCTATA	ATTTCGTCAT	ATCGGTGAAG	AGTTCACCT	TGCAGGATCT	GAAGTATCAG	2820
	CAGAGCAATC	GTCCCATCAC	GAATACTTGG	TAT			2853
15	(2) INFORMATION FOR SEQ ID NO:220						
	(i) SEQUENCE CHARACTERISTICS:						
20	(A) LENGTH: 3678 base pairs						
	(B) TYPE: nucleic acid						
	(C) STRANDEDNESS: double						
	(D) TOPOLOGY: circular						
25	(ii) MOLECULE TYPE: DNA (genomic)						
	(iii) HYPOTHETICAL: NO						
	(iv) ANTI-SENSE: NO						
30	(vi) ORIGINAL SOURCE:						
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS						
	(ix) FEATURE:						
35	(A) NAME/KEY: misc feature						
	(B) LOCATION 1...3678						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220						
40	ATGATGAAC	GATATACAAT	AAATCTTGCA	GTTTTCTTT	TATCTGAC	GGTATTACC	60
	TTTCAAAATA	AAGCTCGCCC	TTATGAAAGA	TTTGCAGATG	TAGAGAAGCC	TTGGATTGAG	120
	AAACATTCAA	TGGATTCTAA	ATTGGTGCCCT	GCAAATAAGG	GTAACTTAAT	TCAAGCTGAA	180
	ATTGTATACC	AATCTGTTTC	TGAACATAGT	GACTTAGTTA	TTTCACTGT	GAACGAAATA	240
	AGGCTGCAA	ATCGTTTCCC	TTGCGATAGG	AAGTCTTTTT	TTGCAGAAAA	TCTACGGGCA	300
45	TCTCCCCCG	TAGTTCCCGT	TGCCGTGAC	AAGTATGCGG	TACCGGTTGC	CAATCCAATG	360
	GATCCTGAAA	ATCCCAATGC	CTGGGATGTG	ACGCTAAAAA	TCACTACTAA	AGCGGTAACA	420
	GTACCTCTCG	ATGTTGGTGT	GGTATCGAC	CAGTCTTCGT	CAATGGGAGG	GCAAAACATT	480
	GCCAGATTAA	AGTCTGCCAT	TGCATCGGGA	CAGCGTTTTG	TGAAAAAAT	GTGCTAAG	540
	GGGACGGCTA	CAGAAGGGGT	CGCATGCGCT	CTGTGAGTT	ATGACCATGA	GCCTCATCGC	600
50	TTATCTGATT	TTACCAAGA	CAGTCTTTTT	CTCTGTCAA	AAATCCGGGC	TTTGAATCCT	660
	ATTGGGGGAA	CACATACCCA	GGGGGGGCTT	AAAATGGCGA	GAACATTAT	GGCCACTTCT	720
	ACTGCTGTGG	ATAAGCATAT	CATATTGATG	TCTGACGGGT	TAGCGACGGA	GCAGTATCCT	780
	GTAAAAAATG	TAACTACTGC	AGACTTCATT	GGCAAACTG	GAAATGCGAA	TGATCCCAT	840
	GATTGGTTA	TACAAGGAGC	AATTAATTTT	CCTACAAAT	ATGTTTCCAA	CAATCCATCT	900
55	ACACCTCTTA	CCCAAAATTA	TCCAATCAT	TCTTCTAAAG	TTGGACGGAG	AAATCTGCGG	960
	GAATCCAAAT	TCGATTATAG	TAACTCTGAGT	GCAAGGATTA	CTTTGATGG	TGTTGTGGC	1020
	GCATTGGTCT	ATGAACCGAG	GTTCCTCAT	CCCTATTATT	ATTATTTCCT	TTGTAACGCT	1080
	GCTATCAATG	AGGCTCAGTT	TGCGAAAAAC	TCTGGTTATA	CAATCCATAC	TATTGGCTAT	1140
	GACCTGGGAG	ATTTTGCCCT	GGCCAAACAT	TCGTTGAATC	TAACCGCTAC	AGACGAGAA	1200
60	CACCTCTTTA	CGGCGACACC	GGCCAAATTA	GCTGCAGCGT	TTGATAATAT	TGCCCCAACT	1260
	ATTAATATAG	GTATACAGAG	GGGGGAGGTG	ACGGACTTTG	TAGCTCCTGG	TTTCATCGTT	1320
	AAAAATCTGA	CGCAATCGGG	AGATGTTACT	CATTTGCTAA	ATGTTTCAA	TGGAACGGTG	1380
	CACATGATG	TCTCTACTAA	AAAACTGACA	TGGACTACTG	GTACTATCCT	GAGCTCATCA	1440
	GAAGCTACCA	TAACTTATCG	TATTTATGCC	GATTGGGATT	ATATACAGAA	CAATGATATT	1500
65	CCGGTAATA	CTACTTCTGC	TATCGGCCCG	GATCTGGTG	GATTGATAC	CAATACCGAG	1560
	GCAAAATTA	CCTATACCAA	TTCCAAATGG	GAACCGAATC	AGCAATTAAT	TTTCCCACGT	1620
	CCGACGGTTA	AGTTAGGTTA	TGGTGTATT	AAGCGGCACT	ATGATTGGT	AAATAAGAC	1680
	GGTCAACCA	TACAGGCAAA	TGGAACAGTT	GTCAATCCC	TAAGCGAGGC	TCATGTTCTA	1740
	CAGTCAACA	ATTTCTTTT	GCCCTCAGGT	GGAGGTGATA	TTGTTCCCAA	ATGGATAAAG	1800
70	TTGGCAAAA	CGACCGAAGC	ATTACAGTAC	TATTCCTGAC	CGCGACTAA	CACGGTCATC	1860
	ACTACTGCCG	ATGGTAAACG	TTATCGTTTT	GTGGAAGTCC	CAGGCTCCAC	CGCGAATCCG	1920
	GGCCAAATCG	GTATCAGTTG	GAAAAAACCG	GCAGGAAACG	CTTACTTCG	TTACAAGCTC	1980
	CTCAATTATT	GGATGGGAGG	AACAACAGAC	CAACAGAGTG	AATGGGATGT	GACGTCCAA	2040
	TGGACAGGAG	CCCAAGTACC	GCTCAGAGGA	GAAGATGTAG	AGTTTGCAAC	GACGAAAAAT	2100
75	TCGGTTCTC	CGCGGTTGAG	CGATTGTCAT	GTCCCGACAA	CCAAACCCAA	AATTATCGGT	2160
	AACCTTATCA	ATAATTCGGA	CAAGGATTTA	GTTGTTACCA	CAAGCAGTCA	ATTGACGATC	2220

151/490

	AACGGCGTGG	TTGAGGATAA	CAATCCGAAT	GTCGGTACGA	TGTCGTGAA	GTGTCGAAA	2280
	GACAAATCCTA	CGGGGACATT	GCTTTTGGCC	AATCCGGGCT	ATAATCAAAA	TGTAGGGGGG	2340
	ACCGTCGAGT	TTTACAAATCA	GGGATATGAT	TGTGCCGATT	GTGGTATGTA	TGCGAGGAGC	2400
	TGGCAGTATT	TCGGTATCCC	TGTCAATGAA	TCAGGTTTTC	CAATTAATGA	TGTGGGCGGA	2460
5	AACGAGACCG	TCAACCAATG	GGTTGAGCCT	TTCAATGGCG	ATAAGTGGCG	GCCAGCACCT	2520
	TATGCACCTG	ATACAGAGCT	TCAAAAATTC	AAGGGCTACC	AGATCACGAA	TGACGTGCAG	2580
	GCACAGCCTA	CGGGAGTTTA	CAGCTTCAAG	GGTATGATT	GTGTGTGCGA	TGCCTTCCTG	2640
	AATCTGACAC	GCACGTCCGG	TGTCAACTAC	TCGGGCGCCA	ACTTGATCGG	CAACTCATAC	2700
	ACTGGAGCCA	TCGACATCAA	GCAGGGTATT	GTCTTCCCGC	CGGAAGTCGA	GCAGACGGTG	2760
10	TATCTGTTCA	ACACGGGAAC	ACGCGACCAG	TGGCGTAAGC	TTAATGGAAG	CACGGTTTCA	2820
	GGCTATCGAG	CCGGTCAGTA	CCTCTCTGTA	CCTAAGAATA	CAGCGGGTCA	GGACAATCTT	2880
	CCGGATCGTA	TTCCATCGAT	GCATTCTTTC	TTGGTGAAGA	TGCAGAACGG	AGCGTCTTGT	2940
	ACGTTGCAHA	TCTTGTACGA	TAAGCTGCTC	AAGAACACGA	CTGTAAACAA	CGGTAATGGT	3000
	ACGCAGATCA	CATGGCGATC	CGGCAACTCC	GGATCGGCGA	ATATGCCGTC	ACTTGTGATG	3060
15	GATGTTCTTG	GTAACGAGTC	GGCCGACCGT	TTGTGGATCT	TTACCGATGG	GGGTCTTTCT	3120
	TTCCGATTTCG	CAACCGGCTG	GGATGGTCCG	AAGCTGACTG	AAAAAGGTTT	GTCACAACTT	3180
	TATGCGATGT	CTGACATCGG	TAATGATAAA	TTCCAGGTTG	CAGGGGTTC	GGAGTTGAAT	3240
	AACCTGCTGA	TCGGCTCGA	TGCGGATAAG	GATGGTCAAT	ACACGTTGGA	GTTTGTCTTT	3300
	TCGGATCATT	TTGCGAAAGG	GGCTGTTTAC	CTGCACGATC	TTCACTCAGG	AGCCAAACAC	3360
20	CGTATTACGA	ATTCTACGTC	GTATTCATTC	GATGCCAAGC	GGGGAGATTG	CGGGGCTCGT	3420
	TTCCGCTTGT	CATATGGATG	TGATGAGAAC	GTAGATGATT	CGCATGTGCT	GAGTACAAAT	3480
	GGCCGTGAAA	TTATAATTCT	GAATCAGAT	GCTCTTGACT	GCACGTGAAC	CTTATTCACA	3540
	ATAGAAGGTA	AGCTTCTTCG	CCGCTTGAAA	GTATTAGCTG	GTCTAGAGA	AGTCATGAAA	3600
	GTGCAGACCG	GAGGGGCCCTA	TATTGTGCAT	CTTCAAAATG	CTTTCATAA	TGATGTGCAT	3660
25	AAGGTGCTTG	TTGAGTAT					3678

(2) INFORMATION FOR SEQ ID NO:221

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3675 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3675
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

50	ATGAAACGAT	ATACAATAAT	TCTTGCAATT	TTTCTTTTAT	TCTGCACGGT	ATTACCTT	60
	CAATAAAAG	CTCGCCCTTA	TGAAAGATT	GCAGATGTAG	AGAAGCCTTG	GATTGAGAAA	120
	CATTCAATGG	ATTCTAAAT	GGTGCCTGCA	AATAAGGGTA	ACTTAATTCA	AGCTGAAATT	180
	GTATACCAAT	CTGTTTCTGA	ACATAGTGAC	TTAGTTATTT	CACCTGTGAA	CGAAATAAGG	240
55	CCTGCAAAATC	GTTTCCCTTC	GCATACGAAG	TCITTTTITG	CAGAAAATCT	ACGGGCATCT	300
	CCCCCGTAG	TTCCCGTTGC	CGTCGACAAG	TATGCGGTAC	CGGTTGCCAA	TCCAATGGAT	360
	CCTGAAATC	CCAATGCCTG	GGATGTGACG	CTAAAAATCA	CTACTAAAGC	GGTAACAGTA	420
	CCTGTCGATG	TGGTGATGGT	TATGACACAG	TCTTCGTCAA	TGGGAGGGCA	AAACATTGCC	480
	ASATTAAGT	CTGCCATTGC	ATCGGGACAG	CGTTTGTGA	AAAAAATGTT	GCCTAAGGGG	540
60	ACGGCTACAG	AAGGGGTGCG	TATCGCTCTT	GTGAGTTATG	ACCATGAGCC	TCATCGCTTA	600
	TCTGATTTTA	CCAAAGACAC	TGCTTTTCTC	TGTCAAAAAA	TCCGGGCTTT	GACTCCTATT	660
	TGGGGAACAC	ATACCCAGGG	GGGGCTTAAA	ATGGCGAGAA	ACATTATGGC	CACCTCTACT	720
	GCTGTGSATA	AGCATATCAT	ATTGATGTCT	GACGGGTTAG	CGACGGAGCA	GTATCCTGTT	780
	AAAAATGTAA	CTACTGCAGA	CTTCATTGGC	AAAACCTGGA	ATGCGAATGA	TCCCATTGAT	840
65	TTGGTTATAC	AAGGAGCAAT	TAATTTCCCT	ACAAATTATG	TTTCCAACAA	TCCATCTACA	900
	CCTCTTACCC	CAATTATACC	AACTCATTTCT	TCTAAAGTTG	GACGGAGAAA	TCTGCCGGAA	960
	TCCAAATTCG	ATTATAGTAA	TCTGAGTGCA	AGGATTACTT	TTGATCGTGT	TGCTGGCGCA	1020
	TTGGTCTATG	AACCGAGGTT	TCTCATCCCT	TATTATTATT	ATTTCCCTTG	TAACGCTGCT	1080
	ATCAATGAGG	CTCAGTTTGC	GAAAAACTCT	GGTTATACAA	TCCATACTAT	TGGCTATGAC	1140
70	CTGGGAGATT	TGCGCTTGGC	CAACAATTCG	TTGAAACTAA	CCGCTACAGA	CGAATCNC	1200
	TTCTTTACGG	CGACACCGGC	CAATTTAGCT	GCACGCTTTC	ATAATATTGC	GCAAACTATT	1260
	AATATAGGTA	TACAGAGGGG	GGAGGTGACG	GACTTTGTAG	CTCCTGGTTT	CATCGTTAAA	1320
	AATCTGACGC	AATCGGGAGA	TGTTACTCAT	TTGCTAAATG	TTTCAAAATG	AACGGTGAC	1380
	TATGATGTCT	CTACTAAAAA	ACTGACATGG	ACTACTGGTA	CTATCCTGAG	CTCATCAGAA	1440
75	GCTACCATAA	CTTATCGTAT	TTATGCGGAT	TGGAATTATA	TACAGAACAA	TGATATTCG	1500

5 GTAAATACTA CTTCTGCTAT CGGCCCGGAT CTTGGTGGAT TCGATACCAA TACGAGGCA 1560
 AAATTGACCT ATACCAATTC CAATGGCGAA CCGAATCAGC AGTTAATTTT CCCACGTCGG 1620
 ACGGTTAAGT TAGGTTATGG TGTTATTAAG CGGCACATATG TATTGGTAAA TAAAGACGGT 1680
 CAACCCATAC AGGCAAAATGG AACAGTTGTC AGTTCCCTAA GCGAGGGCTCA TGTCTACAG 1740
 TCACAAGATT TCTTTTGGCC CTCAGGTGGA GGTCAATATG TTCCCAATG GATAAAGTTG 1800
 GACAAAACGA CGGAAGCATT ACAGTACTAT TCCGTACOSC CGACTAACAC GGTCACTACT 1860
 ACTGCCGATG GTAAACGTTA TCGTTTGTG GAAGTCCGAG GCTCCAGGCC GAATCCGGGC 1920
 CAAATCGGTA TCAGTTGGAA AAAACCGGCA GGAACGCTT ACTTCGCTTA CAAGCTCCTC 1980
 AATTATGGGA TGGGAGGAAC AACAGACCAA CAGAGTGAAT GGGATGTGAC GTCCAATTGG 2040
 10 ACAGGAGGCC AAGTACCGCT CACAGGAGAA GATGTAGAT TTGCAACGAC AGAAAATTTT 2100
 GGTTCCTCGG CGGTAGCCGA TTTGCATGTC CCGACAACCA ACCCCAAAT TATCGGTAAC 2160
 CTTATCAATA ATTCGACAA GGAITTAGTT GTTACCACAA GCAGTCAATT GACGATCAAC 2220
 GGCCTGGTTG AGGATAACAA TCCGAATGTC GGTACGATCG TCGTGAAGTC GTCGAAAGAC 2280
 AATCCTACGG GGACATTGCT TTTTGCCAAT CCGGGCTATA ATCAAAATGT AGGGGGGACC 2340
 15 STCGAGTTT ACNATCAGGG ATATGATTGT GCCGATTGTG GTATGTATCG CAGGAGCTGG 2400
 CAGTATTTCG GTATCCCTGT CAATGAATCA GGTITTTCCAA TTAATGATGT GGGCGGAAAC 2460
 GAGACCGTCA ACCAATGGGT TGAGCCTTTC AATGGCGATA AGTGGCGGCC AGCACCTTAT 2520
 GCACCTGATA CAGAGCTTCA AAAATTCAAG GGCTACCAGA TCACGAATGA CGTGCAGGCA 2580
 20 CAGCCTACGG GAGTTTACAG CTTCAGGGT ATGATTTGTG TGTGCGATGC CTTCCTGAAT 2640
 CTGACACGCA CGTCCGGTGT CAACTACTCG GGCGCCAACT TGATCGGCAA CTCATACACT 2700
 GGAGCCATCG ACATCAAGCA GGGTATTGTC TTCCCGCCGG AAGTCGAGCA GACGGTGTAT 2760
 CTGTTCAACA CCGGAACACG CGACCACTGG CGTAAGCTTA ATGGAAGCAC GGTTCAGGC 2820
 TATCGAGCCG GTCACTACCT CTCGTGACCT AAGAATACAG CCGGTGAGGA CAATCTTCCG 2880
 25 GATCGATTTC CATCGATGCA TTCCTTCTTG GTGAAGATGC AGAACGGAGC GTCTGTACG 2940
 TTGCAHATCT TGTACGATA GCTGCTCAAG AACACGACTG TAAACACGG TAATGGTAGC 3000
 CAGATCACAT GGCATCCGG CAATCCGSA TCGGCGAATA TGCCGTCCT TGTGATGGAT 3060
 GTTCTTGGA ACGAGTCGGC CGACCGTTG TGGATCTTTA CCGATGGGG TCTTTCTTTC 3120
 GGAITTCGACA ACGGCTGGGA TGGTCGCAAG CTGACTGAAA AAGGTTTGTG ACAACTTTAT 3180
 30 GCGATGTCTG ACATCGGTAA TGATAAATTC CAGGTTGCAG GGGTTCCGGA GTTGAATAAC 3240
 CTGCTGATCG GCTTCGATGC GGATAAGGAT GGTCAATACA CGTTGGAGTT TGCTCTTTCG 3300
 GATCATTTTG CGAAAGGGGC TGTTTACCTG CACGATCTTC AGTCAGGAGC CAACACCGT 3360
 ATTACGAATT CTACGTGCTA TTCAATCGAT GCCAAGCGGG GAGATTCCGG GGTCTGTTTC 3420
 CGCTTGTCAT ATGGATGTA TGAGAACGTA GATGATTCG ATGTCGTGAG TACAAATGGC 3480
 35 CGTGAATTA TAATTCTGAA TCAAGATGCT CTGACTGCA CTGTAACCTT ATTACAATA 3540
 GAAGGTAAGC TTCTTCGGC CTGAAAGTA TTAGCTGGTC ATAGAGAAGT CATGAAAGTG 3600
 GAGCCGGAG GGCCTATAT TGTGCATCTT CAAATGCTT TCACTAATGA TGTGCATAAG 3660
 GTGCTTGTTG AGTAT 3675

40 (2) INFORMATION FOR SEQ ID NO:222

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 50 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 55 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1275
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222

65 ATGGAAGTGA AGAAAAACAC AGTGGTGCTA CGCCTTCTGA TTTGGTTCGT GGCCATTCTT 60
 CTCTTCCACT CCTCACGCT GTGGGGACAG GAAGGGGAGG GAGTGCCCG ATACAGATTC 120
 AAAGGATTTC TGGATACCTA CCATGCCGTA CGCAGCTCTT CTCCTTTTGA TTTATGAGC 180
 TCAGGTACGA GAGTGAGAGG TGAGCTGGAG AGGTCGTTCC GTAATTCGAA AGTAGCCGTA 240
 TCGGTCAATG CCACCTACAA TGCTCTACTG AAAGACGAGA CCGGCTTACG TTTACGTGAA 300
 GCGCTTCTCG AGCATCAGGA AGAGCATTGG GGGTTGCGCC TCGGACGACA GATTGTCAAT 360
 70 TGGGGGCGTG CCGACGGTGT GCGCATCAGC GATCTGATCT CCCCGATGGA TATGACCGAG 420
 TTTCTGGCAC AGGATTACGA TGATATTGCT ATGCCGGTCA ATGCATTGGC TTTCTCTGTC 480
 TTCAACGAAT CGATGAAAGT GGAAGTCGTG GTACTGCGTG TATTCGAGGG GTACCGCTG 540
 CCTGTGGATC CTGCAATCC TTGGAATATC TTCTCCCTTT CGCCCATTCG TCAGGGGATG 600
 AATATCGTCT GGAAAGAAGA AGCCGGCAAA CCGGCCTTCA AGGTTGCCAA TATCGAGTAC 660
 75 GGTGCGCGAT GGAGCACTAC GCTCTCCGGT ATCGACTTCC CTTTGGCTGC ATTGCATACA 720
 TGGAAACAAGA TGCCCGTCAT CGAAGTACAG GGCATTGTGC CGACGGAAAT CATCGTTAGC 780

153/490

5 CCTCGCTATT ATCGTATGGG ATTTGTCCGG GGGGACCTCT CCGTACCCGT CGGACAGTTT 840
GTTTTCAGGG GAGAGGCTGC GTTCAATATC GACAAACACT TCACCTATAA GAGTCATGCC 900
GAGCAAGAGG GTTTCACAAAC AATCAATTGG TTGGCCGGAG CCGATTGGTA TGCTCCCGGT 960
GAATGGATGA TCTCAGGACA ATTCTCAATG GAAAGCATAT TCAGGTATAG GGATTTTCATC 1020
TCCCAAAGAC AACATTCTAC CCGATTACT CTCAATGTTT CCAAGAAATT CTTCGGCAGT 1080
ACACTCCAAC TTTCGGACTT CACCTACTAC GACCTTACGG GCAAGGATG GTTCAGTCGC 1140
TTTGAGCTG ACTATGCCCTT GAACGATCAG ATACATCTGA TGGCCGGATA TGA CTGGTTC 1200
AGTAGTAAGG GCAGCGGTAT ATTCGATCGC TACAAAGACA ATTCGGAAT CTGGTTCAAA 1260
10 GCCCCTACA GCTTC 1275

(2) INFORMATION FOR SEQ ID NO:223

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
20 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

35 ATGTCTCTCT GTGAGGTGGC TTATTTTTC CTAAGCCGA TCGATCTGCA GAACATCCGC 60
GAACGGAATC ACTCTTCCGA CATCGCGCTT TCCAATTAT TAGACAATTC GAATCAGCTA 120
TTAGCTACTA TTCTGATCGG GAATAATGTG ATTAATGTAG CCAATCGTAT CCTTTCCAAT 180
TATGCCATCG AGCAGACATT CGTTTCTCT TCTCCGATCA TTGGATTCT GATCCAGACG 240
ATACTCCTGA CCAGTGTCTT TTTGCTGTTT GGAGAGATTC TGCCGAAAGT GTATGCGCGG 300
AAGAATCCGC TGCAATACTC GCGCTTTTCT GCTGCAGCTA TGTCGGTAT CTATAAGATA 360
TTGTACCCGT TTTCAAAATT GCTGGTCAAA AGTACCGGCA TCGTTACCAG AGGTATCAGC 420
AAGAAGAAAT ACGATATGTC CGTGGATGAG CTCTCGAAAG CCGTAGCCCT CACCACTACG 480
GAGGGAGAGC CGGAGGAGAA AGAAATGATT AACGAAATCA TCAAATTCTA TAATAAGACA 540
GCCTGCGAAA TCATGGTTCC CGGTATCGAT ATTGTGGATG TGGATCTGAG CTGGCCATT 600
45 CTTAAGATGC TTGACTTCGT TGTTTCGTG GGTATTCCA GACTTCCCGT TTCAGAGGGG 660
TCAGAGACA ATATCAAAGG GGTGATTAC ATCAAAGAT TAATCCACA CATGGATAAA 720
GGCGATGAAT TCGACTGGCA TCCTCTGATT CGTAAAGCAT ATTTGTCCC CGAAAACAAG 780
CGCATAGATG ATTTGCTCGA GGAGTTCAGA GCCAATAAGG TGCATGTCTC CATCGTTGTG 840
GATGAGTTCG GTGGCACTTG CGGACTGATC ACAATGGAGG ACATATTGGA AGAGATCGTC 900
50 GGCAGATTA CGGACGAGTA CGATGAGGAA GAACTCCCTT TTAAGGTTT GGGGGATGGC 960
AGTTATCTTT TCGAAGGAAA AACGCTCTC TCCGATGTTT GACACTATCT TGACCTTCCG 1020
GAAATGCTT TCGGTGAATT GGGGGACGAG GTAGATACGC TAAAGTGGCT CTTCCTGGAA 1080
ATCAAGCAGG AACTCCCCCA TGTGGCGGAT ACAGCAGTGT ACGAGCCATT CCGCTTCAA 1140
GTGACCCAAA TGGACAAGCG CCGAATCATC GAAATCAAGA TTTTCCCTTT CGAGCGCACT 1200
55 TGGGAGGTCT AA 1212

(2) INFORMATION FOR SEQ ID NO:224

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
65 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
70 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
75 (ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...780

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:224

5
ATGAAACTAT TACTTTATCT CCTATTGGTC TTGTGACTC TATCCCCGAT GTATTGCGAA 60
ATGCTCTTCT CAGAGAATCT CACANTGAAT ATAGACAGCA CCAAACCAT ACAAGGAACG 120
ATATTGCCCG TACTGGATT TCAAACCGAA AAGGAAATG TGTTCACCTT CAAAATACT 180
GCCANTCTCA ATCTGCTGAT AAAGCACGGT CAAGTAATCA ACTTAATTAA TAAGCTTGAG 240
10 TTTTCTACCT ATGGCAATAA AGTAACCGTA AGTGGAGGAT ATGTACACAC CGAATACCGC 300
TAITTTGTTGC ATCATGTTTT TGAGGTTTAT CCTTATGTCG AGTCGCAATG GGCAGAAAGT 360
ACAGGAATGA AATATAAGGT TTCTACGGGA TTACAGTTCG GTTATCGGCT GGTAAATAGT 420
GATAACTGTC TCATGTTTGC AACATTGGGG GTATTTTTCG AATTGGAATA GTGGGAACAG 480
CCAGCCACTA GCCTCTTTGC AGGAACGTAT GCATACAGCC GAAGTATCAA AAGCCACCTG 540
15 TCTATCAGTT TCAGACATCG GTTGGGTGAA CATTTGGGAAT TTACAACCTAC GGCTATTAC 600
CAGGCAAAAG CTGACAGTTA TTITAAGAAG GCACGTTTTG GAGGAGCTAT CGACCTCAAA 660
TACCATATCA CACCTACGAT AGGAATACGC GGGGCTATC GGATCATCTA CGATACTGCC 720
CCTATTGTAC CTGTGCGGAA AGATTACAAC ACCGTTGATG TTGGTATCGA TATTTCGTTT 780

(2) INFORMATION FOR SEQ ID NO:225

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 2502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

40 (A) NAME/KEY: misc feature
(B) LOCATION 1...2502

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:225

45 ATGAAACGAA TCGTTTTATC ATCTTTCTCG TTCGTTCTGT CCATACCTTC TTTGATGGCA 60
CAGAACAAATA CCCTCGATGT ACACATATCC GGTACGATCA AGGATGCCTC CTCGGGGGAA 120
CCAGTGCCCT ATGCCACTGT AAGCATCCGG CTGACAGGAG CAGATACCAC ACAGGTGTTT 180
CGACAAAGTA CTGACGGCAA CGGCTACTTC GTCATAGGCC TGCCGGCAGC TCCCTCCTAT 240
CACCTGACAG CTTCGTTCTG AGGTATGAAA ACCCATAGCA TGCAGATTAG TCGGGGAAAT 300
50 GGACAGCAGC ACATCAAATC CATCGACATT TCTCTCGAAT CCGAGGACAA ACAACTCTCC 360
ACCGTCACCG TATCGGCAGC AGCAACCTGC TCGAAATGCT GCGCAACGTT 420
AATATGAAG ATGACCCCGC AGCCAAGACG AACCAACCTGC TCGAAATGCT GCGCAACGTT 480
CCTTTGGTAA CGGTGGATGG TCAGGGCAAT ATCCAGGTGA AAGGATCTTC CAACTTCAA 540
ATCCACCTCA ATGGCAGGCC CTCGACCATG GTGAGCAGCA ACCCGAAGGA GGTCTTTCCG 600
55 TCCATTCTCG CCCATACGAT CAAACGGGTG GAGGTCTATC CCGATCCGGG TGTAAGTATC 660
GATGCGGAAG GCACAAGTGC CATCTGGAC ATCGTCACGG AAGAAGGTAA GAAGCTGGAA 720
GGATATTGAG GTTCCATCAC GGCAGTGTG ACACAACATC CCACAGCCAA CGGTAGTATC 780
TTTCTGACAG CAAAGTCCGG CAAAGTCCGG CTGACTACCA ACTATACTA CTACGGTGGC 840
AAAAACAAGG GCTCTCGCTA CTTTACCGAA CGTACTACAT CCATGCTCCA AACGATAGAA 900
60 GAAGGCAAGG GGCAGAAAC CTTTGGCGGA CACTTCGGCA ATGCCCTCCT CTCATTTCAG 960
ATAGATTTCG TCAATCTCTT TACGGTGGGC GGCATGTATC GCCTTTGGGA GATGACCACC 1020
GACCGGAACA GCGTAGAAAA AAGCTTTGCC GGCAGCAACC TCATGTCCTA CATAGACAGA 1080
AAACTCAAAA CACAGATGGA TGCCGGATCA TACGAGCTCA ATGCCGACTA TCAGCACAGC 1140
ACTCGCTGCG CGGGCGAATT GCTCACCGTT TCCTACCGCT TCACTCACAA TCCTAATAAT 1200
65 AGCGAGACCT TCATTGACCA ATGGAAGCGC GATCCGCTCA ACACAGCTAA TACGATCCAG 1260
TACGCGGGCC AGCACTCCAA ATCCGATGCG GGCATGGAAG AACATACGGC ACAAGTGGAC 1320
TATACACGTC CCTTAGGACA AGCACATTCT TTGGAAGCAG GGTGTAAGTA CATCTATCGT 1380
CATGCCACGA GCGATCCTCT CTATGAGATA CGACCATCCG AAGATGCTCC GTGGCAGCCC 1440
GGCTCTCTAT ATGCACAGAA TCCGTCGAAC GGAAGTTTCC GCCACGATCA ATACATCGGA 1500
70 GAGGCTATG CCGGCTACAA CTATCGTAAG GATCAGTATT CTTTGCAGAA CCGCCTCCGA 1560
GTGGAAAGCA CGAGGCTGAA AGCACTCTTT CCGCAAAACG CAGCAGCAGA TTTCTCCAC 1620
AACTCGTTGG ACTGGGTGCC ACAGCTCAGC CTCGGCTATA CCCCCTCGCC CATGAAGCAG 1680
CTTAAGCTGG CCTATAACTT CCGAATCCAA CGTCTGCAA TCGGCCAACT GAATCCCTAC 1740
CGGCTACAGA CCAACGATTA TCAAGTACAG TATGGTAATC CCGACCTAAA GTCCGAGGAG 1800
CGTACCAAG TCGGTCTCTC CTATAATCAA TACGGAGCCA AGGTATGCT TACAGCATCG 1860
75 CTCGACTACG ACTTCTGCAA CAACGCCATC CAGAATTACA CTTCTCCGA CCGGCCAAT 1920

155 / 490

5 CCCAATCTCT TCCACCAGAC CTATGGCAAT ATCGGACGAG AGCATTCTTT CAGCTTGAAT 1980
ACCTATGCCA TGTACACGCC GGCCGTATGG GTCAGGATTA TGCTCAACGG AAATATCGAT 2040
CGCACATTCC AAAAGAGCGA AGCACTGGGC ATTGATGTCA ATTCATGGTC CGGCATGGTA 2100
TACTCAGGCC TGAAGTTTAC CCTGCCGAAG GATTGGACTG TGAATCTCTT CGGAGGTTAT 2160
TATCATGGGG GAAGAAGCTA CCAGACGAAG TATGATGGCA ATGATTCTAA CAATATCGGT 2220
ATAGCCAAAC AGCTTTTCCA CAAAAATTG AGAGTCTGCG TGAGCGCMAA CAACATTCAT 2280
GCGAAGTATT CGACATGGAA GAGCCGGACC ATCGGCAATG GATTTACTAT TTATTGGGAA 2340
AATGCCGGTA TACAACGGAG TGTTCCCTC AGCCTCACCT ACAGCTTCGG TAAGATGAAT 2400
10 ACACAAGTGC GCAAGGTAGA GCATACGATC GTCAACGACG ACCTCAAGCA AACCTCATCC 2460
CAAGGACAGC AGGGTGGCGG ACAAGGAAAT CCTACCGGCA AT 2502

(2) INFORMATION FOR SEQ ID NO:226

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 20 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 25 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

35 ATGAGACTCT CTGCCATTCT TATCGCTTTG ATTGTGATGC TGCCTGCTGT GCTTAGCGGG 60
CAGCATTATT ATTCCATGGC GGGAGAGCGA CTGGAGACGG ACAGCATTCG TCCGAACGAA 120
CTCTCGGCAT CGATCCGAAG TGCCGTTTTC TTTCGGACAA ATGAATACAA TGACAGTTTCG 180
GTCAAAGGTT ATACGTTGCC GGGTGACGGG GTTTCGGCTT TTGCTCTTA CTGCTGCTCG 240
40 GCAGCACATG GTGTGAAGCT TTCGCTCGGA GTATCTACCC TGAACACTCG GGGGGCAAGT 300
CGCTATCCGG CCGGTATCGC TTATTCGGAT TTACCTTATT GGAACGACTA TAACGACTAT 360
GTACGCTTGC GTATCCTGCC TTATGTACAG GCCATGCTGA AGCCGACGGC CACGACTGCT 420
CTCATGCTGG GCATATAGC CGGTGGTACG GCTCACGGAC TGATCGAACC GATCTACAAT 480
CCTGAGTTGG ATTTGACGGC TGATCCTGAA GCCGGTGTGC AATTTCGGGG TGATTGGACA 540
45 CGTTTCCGAA TGGATGTTTG GGTCAATTGG ATGAGCATGA TTTTCAAAAA TGACAATCAT 600
CAGGASTCGT TTGTCTTTGG CTGTCCACT ACTTCGAAAT TGTTATCGGG TGAAGGCAAA 660
TGGGCACTCG AACTGCCCTT GCAGGCTATT GCCACGCATC GCGGCGGGGA ATACAACCTG 720
GGCAGCAGG ATACCGTGCA TACATGGGTC AATGGAGCTG TCGGACTTAA GCTTTCGTAT 780
50 CGCCCTCGTA CCGACAAACC CATGCAGATT TGGGGATCTG CTTATGGTGT GGCAGCCTTG 840
TCAAGCGGAG GATACTTCCC TTACGAAAGA GGGTGGGGCG GTTATCTTTC TCTCGGAATG 900
GACTTGGAGC ACTTCGCTTT TCGTACCGAC TATTGGTACG GCAGGCATTA CGTTTCTCCC 960
TTTGTGCAC CTTTCGCCAA TTCCCTGACG TATGACAAAC AGCCTCTTAC GAACGTTTGG 1020
GGCGATTATA TTCGTCTCTA TGCCGACTAT TCGTGGCGCA TGGCAGGAAG TGTTTCGTTG 1080
GCGGCTGTTG CTCGGGTATG GTTCCAGCCT TCGGATCGTT TTGCGATGAG CCACGCCTTG 1140
55 GAAGTACGCA TGGGTATCGA TCCCAAAATC CCAATAGCTT TTCTGAAAGG CAATCAT 1197

(2) INFORMATION FOR SEQ ID NO:227

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 65 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 70 (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 75 (ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...1146

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:227

5
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25
ATGAACAAAT CGCTATTATC ATTGGCATGC CTCATCCTGT GCGGTATGCC GGCCATCGCC 60
CAACAGACAG GACCGGCCGA ACGCAGCGGC GAGCCTTCTC TGGCCGAACG TGTATTGGGT 120
CTGGAGCAGA AGCAGAAAAA GCTGAAGGTG TACTTAGGCA TACAGTCGTT CTACGACCAG 180
CCGCTTGTCC ATGACGAATC CCATATCGGA CACTTCAAGG TACAGGAGCT GCGGATGTCT 240
GCTCATGGCG AACTGAACCG CCACCTCAGC TTGACTGGC GACAACGTCT CAACCGTGCC 300
GCCGACGGCA CTTCGTTTGC CGACAATCTC TCCAATGCCA TCGACATCGC AGGTGTGGAC 360
TGGCACCCGA ACGACAAGGT GTCTTTCTTC TTCCGACGTC AGTACGCGCG TTTCGGAGGG 420
ATAGAATACG ACATGAACCC CGTAGAGATC TACCAGTACA GCGACCTTGT GGATTACATG 480
ACCTGCTATA CTTCGGGCGT GAACTTCGCA TGGAACTTCC ACCCCGAACA GCAGCTGCAG 540
CTACAGGTAC TCAATGCTTA CAACAACCGC TTCGCGGACC GCTACCAAGT GACACCCGAT 600
GTCGCTACCG CCACGAGCTA CCGGCTCCTC TACTCGGCAC AGTGGAAACG TACCCTCCTC 660
GGAGGAGCAC TGCATATGCG TTACGCCGTG TCGATGGCTC ATCAGGCCCA AGAGCGTAAT 720
ATGTGGTACT TCACTGCGGG CAACCTGTTC AATCCGGGCA AACGGATCAA CGGATACTC 780
GACCTCACT ACTCGATCGA GGGATTGGAC GACAAAGGCA TTATGACTGC TCGCTACGGC 840
AAGGGCAAGA CCCTCACGGA CGTCAAGTAC TATGCTCTGG TATCGAAGTG GAACTTCGCG 900
ATTTTCGATC AGGTCAATCT CTTCCTCAA GGCATGTACG AGAACGGCTA TGCSCCTGCC 960
CAATACGGCG AGAGCAGCCA CACGCGCCAC TCCTACGGCT ATATGGGAGG GGTGGAAATAT 1020
TACCCTACGG AGACCAACTT CCGTCTGTTC GTACCTACA TAGGACGGCA TTACCGGTAC 1080
AGTGGGACCG AGACGGAAAG CACCAATGCT CTTCGCGCCG STGTGATCTA TCAGATACCT 1140
TTCTTA 1146

(2) INFORMATION FOR SEQ ID NO:228

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 666 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
35 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
40 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...666

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:228

50
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60
65
ATGAACATT TGTTTAAGTC GACATTAGTA CTCTTTGTG CTCTTTCTTT TTCCGGTACC 60
TATACCTTTG CACAAGAAAA TAATACAGAA AAGTCACGAT TTGATTTTTC TGTTAGGCTG 120
GGACAGGGAT ATATTGCAGG TTCAACTACC AACCTGATGT ATGGGTATAC ATCTGCTAAC 180
GATAGACTTT TGTCGGGTGC AATTATCTG GGCCTGACAC CAAGTAAGAA AGAAAAATGA 240
ACCGGCGTAG CATTTGTTT CTATCNCCTC TCTCCGGGTT ATTATGCGA TATATCCGGC 300
AAAGAAAAATA CCTTGAATTA TGCCTTTTAC GTTGTGCGAG CATATAATAG AATAGCCATT 360
CCTATACGCC CTATCAAAAA TTTTAATTTC ATCTTCTCTA CAGAAGTCGG AATGGCTTGG 420
ATGAGTCGTC ATGAGCAAAAT TTACAATTCT ACTTCGCAGA CTTGGGATAA GCAGCGCAAG 480
TCGAGGTCCG GACTGGATTT TGGTCTCGGG ATGCATCTGC AATHCCACAT TAATAAGACC 540
GTTTACTTTA TGGCAGGAAC CGATCTTACG TCTTGCATGT TCGGAAAAAG GATCAATGAC 600
TACCAGCAAA AGGATCGAAC CTTCATTGCA CTTATCGACA ACAGTATTGG CATAGGATTA 660
AACCTC 666

(2) INFORMATION FOR SEQ ID NO:229

70 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
75 (iii) HYPOTHETICAL: NO

157/ 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

ATGATTATCA	AGAAATGCT	GAAAAATAAA	TTGGCCCCCT	TGGCCATACT	GTTCCTTTT	60
GCTCCAAAGG	CTATGAAGGC	TCAGGAGCAA	CTGAATGTGG	TACACACCTC	TGTGCCATCG	120
CTGAATATCA	GTCCGGATGC	ACGTGCGGCC	GGTATGGGGG	ATATAGGTGT	GGCAACGACG	180
CCGGATGCGT	ATTACACAGTA	TTGGAATCCG	AGTAAATATG	CTTTCATGGA	TACGAAAGCC	240
GGTATTAGCT	TCTCATATAC	ACCCTGGCTG	TCCAAGCTGG	TCAATGATAT	TGCCCTGATG	300
CAGATGACCG	GTTTCTACAA	ATTGGGAACA	GACGAGAATC	AGGCTATTAG	TGCTTCTCTG	360
CGTTATTCCA	CATTAGGAAA	GTTGGAGACT	TTGCGAAT	TGGGCGAATC	CATGGGAGAG	420
GCCCATCCCA	ATGAATTTGC	TGTCGATTG	GGCTATAGCC	GCCAGTTGTC	GGAGAACTTC	480
TCCATGGCTG	TTGCATGCG	TTACATCCGC	TCAGACCAAA	GCACTCACAA	CACCGGAGAG	540
AATCAGGCCG	GAAATGCCTT	TGCGGCGGAT	ATAGCCGGTT	ATTTCAGAAA	GTATGTGCTA	600
CTGGGTAAATG	CGGAGAGCTT	GTGGTCGTTG	GGTTTCAACG	TAAAGAATAT	CGGAACGAAG	660
ATCTCCTATG	ACGGAGGTGT	CACGAGTTTT	TTTCATCCCTA	CTTCGTTGAA	TCTCGGGACG	720
GGGCTGTTGT	ATCCGATCGA	TGACTATAAC	AGCATCAATT	TCAACCTTGA	ACTTAGCAAG	780
CTGCTGTGAC	CCACTCCTCC	TATCATGGAT	CAAAACGATC	AGGCCGGGTA	TGAGGCTGCA	840
CTCAAGAAAT	ATCAGGAAAC	TTCTTCGATC	AGCGGTATAT	TCTCTCTTTT	CGGTGATGCG	900
CCGGGAGGAC	TCAAGGAAGA	ATTCCGTGAG	ATTACATGGG	GACTTGGGGC	TGAATATAGC	960
TATGACGATA	AATTTTTTGT	TGTCGCCGGA	TATTCATACC	TGCACCCAC	CAAGGCAAT	1020
TTGCAGTACT	TCACGGCCGG	TGCCGGCTTC	AAAATGAACA	TATTCGCTAT	CGATGCTTCC	1080
TACCTGTGTG	CTACGATCCA	GAGTAATCCG	TTGGATCAGA	CTCTGCGGTT	TACGCTTGCT	1140
TTGATATG	ATGGATTGCG	CAATTTGTTT	CAC			1173

(2) INFORMATION FOR SEQ ID NO:230

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

ATGAAACAA	CAGTTCAACA	AATTATTCTG	TGCTGGGCTT	TAATGATGTC	AGGTGTATTG	60
GGCGGAAACG	CACAGAGCTT	TTGGGAAGAA	ATAGCTCCTC	CTTTTATCAG	TAATGAGCCT	120
AACGTCAGT	ATATAATTCC	CAATATGGGG	ATTGATTCAA	AGGGAACAAT	CTATGTAACC	180
GTGACAAAAA	GGATTACGCA	GGGAGCAAA	TATACTTCTG	AGCAATTGGG	TATGTACTAT	240
CGACCATTAG	GTGATAATGA	ACAGTGGTGG	AAACATGATC	CGTATTTTGA	TGACAAGATA	300
GTTCGGGATA	TTGACACAGA	TGCATATGGC	AGAGTTTATG	TATGTACGAC	TTCTTCTCGA	360
GATCAAGAGT	ATCAACTTTA	TATAAACGAG	CAGAACGAAT	GGAGGTGTAT	ATTCAAAACT	420
TCTGTGCTTA	CATATGAGCA	TGGTATGGCT	GTTTTCGCT	CTTCGACAGG	GGTGACTTAT	480
ATAGGTACCA	GGCATCACAT	CTTCGATCA	GGTGTAATG	ATTTCGAGTT	CAACACTATC	540
TATGAGACT	CTACACCTAT	GAGCTGTGCG	TTTGACAGG	CTACGAATAG	TGGCACCATC	600
TATCTGSCAT	TGATGCATGA	AACCACAATG	TCTACGACTA	TCCTTACTTA	TCAAAACGGT	660
GAGTTCGTG	ATATCTCGGA	AAGTGAATTG	AGTAACTCGA	TTATTGCATC	CATGTGCTCT	720
AATAAGAGAG	GTGATATAAT	AGCTCTTGTT	ACTTCATAIA	CAGGATTTAT	GAGTGGAAAC	780
CTTGGGATCA	GAAAAGCAGA	TGAAGGCCAA	TGGCAACTTG	TTGGCGGAGA	TATACAGAA	840
GCGATCGSTT	AAAAATATG	CATGATGGAC	GACAACAAGA	TTGCTTGTGA	AGTCTTCGGG	900
ACTCCTAACG	CAGTAGATGG	TGGGACAAGG	GTTCGTGTTT	CTGACGCATC	TGTCTTGAT	960
TTTGAATGGT	ATGAAGATGA	AATATACGGA	GGCCTGATAT	TTGACACTTT	CTTCTATAGC	1020
CCTTGGGACA	AACCTCTTTA	TGCGAAATTT	GGTGGGATTA	TGCTCAGGAG	TAAAGAGTCT	1080

158/ 490

TTTATAACCT CTTTCATTTC TCCGACAGTT GTACAAGGAG TGGATGTCTA TACTTTGGCC 1140
GGGAAGATAA GGATCGAAGG TGAACTCCG GTGCTGAGG TGTGCTTTT CGACCTGGCT 1200
GGCAGGATGG TACTTCGGCA AACCATTGAT AATAAATCT ATTCGGACAT AGATACTAAC 1260
GGACTAAAGC GAAGCGGTAT TTACGTAGTC TCGGTGCGGC TCTCTCCGG ACAGGTATTC 1320
5 AGTCATAAGG TGCAGGTA 1338

(2) INFORMATION FOR SEQ ID NO:231

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 25 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

30 ATGATAATCC GGTGTCTTAT CCGTGTCCG AGAACCGTCC TGTTCGGGTT GATATTCGTG 60
GTAGGTCTTT TCTCTGCGAT GGCAGCAAGAG AAAAAGGATA GTCTCTCTAC GGTTCAGCCA 120
GTGCCGAATA GCAGCATGGT GGAGCAGACC CCTCTTCTCT CCATTGATCA CCCCGTCTCG 180
CCCGCTTCTT TTCAGAATAC CCGTACACTG AAAAGGTTTA GAGACAAACA TCTTCCGAT 240
35 GCTTTGCTCA ATGGATTGAA GCCTCATCGC TCATCTTTGC AATTGAATGA GGAACCAAC 300
TTCGCGGCAG AGCGTCGGGA TTTCGTTTCT CCGCTCTTGC AAACCTCGCA CGCTGCCGGT 360
GTCTTTTCAT GSCGACCGAC CGATAGGATG CATTTTATA CATCGGCAAT TATCGGTCTT 420
GGCCATGATT TATTGACCGG TGTGCGCAAG GACTTCGGAT GGAATGCTGG TGCCGACTTC 480
TTGCTGAGTC AAAATCTTAC GGCACATGTC CAAGGCGGTT GGCAGCAGAA TTTCCGGCTT 540
40 ATACCTATGA CGGCTGTCAA TGGCCAACCTG CGTTGGCAAG CCACCGAGAG ATTGAGTTTT 600
ACCACCGGTA TCGATTATCG ACAGGTACAG TGGAAATGCT TCGATAATAG AACGTTCTCG 660
CTTAAAGGAA GTGCTCGATA CGAAGTGATG GACAATGTCT TTGTCAATGG ATTTGGCAGC 720
TATCCTTCTT ACAGCAGTAC GCGCTCAGGA CTCAATATGG CTGTTCCGAT GCATGGATTG 780
GGCCCTCAGT ACGGTGGATC GCTTGAGCTG AAAGTCTCCG AGCGATTCCG CTTTGCCGTC 840
45 GGTATGGAGC GCGAATACAA TATCTGGACT CGTCGGTGGG AAACGCATTA CTTTGCTTAT 900
CCTGTATTCT ATGGCGATAA GAAG 924

(2) INFORMATION FOR SEQ ID NO:232

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 55 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 65 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

70 ATGAAAACGA ATAGACGATA CGCATTGTGT TTGCCGCTTC TGCTACTCAC CGGATTGTTG 60
GCATGGGGGC AGGATTCCTC CCACGGTAGC AATACAGCGT TTGCAACTGA TTCTTCGAGT 120
AGAGAGTTGC CCACGGAGCA GTCCGCTTAC CGCATTGATT CTGCCATATAT GGTGCGTGGT 180
75 GCGGGAAGCA TAACCGCGCA CACCTATTTG TCACCCCTTC GTTATGGAGG ATGGACACTG 240

159/ 490

5 AATTGTGTGG GAGAGAAGAC GTTCCCTCTC AAAGCCTCCG ATTCCCGTTG GATGATCCGT 300
ACCGGSCATG AGCTGGATTT TGCCCTGATG GACAATCCGG CCAATAATGC TCATTTCTAT 360
TCCCTGCTGT ATAACGGTTC CGCTGCGGCT CTTACCGCC TTGGCGCTAA GCATCTGCGA 420
GCCGCGTGGA TGGACAATCT GCGCTTCGCA TTCGGCCCGG GCTTGGAAAT CGGGCTTGGA 480
GSAATTTATA GTACACGCAA CGGCAATAAT CCTGCGACAT TGAAGCTCTA CACCAATGCC 540
ATCGCCCAAG CCTCGATAGG ATACTACGTC CCTCCGAAA CTTTCCCTT GTATTTTCGG 600
TTGCTCTCCC AGATCAATCT CTTCCGTATA GCCTATGGAA ATGGTTTGG TGAGAGCTAT 660
TAGGAGAATT TTTTGCTCAA TAACGGCATT GCAGGCTCCC TGCATTTTAC TTATCCGGGC 720
AAGTTTACTC GGTTCACGAC ACTCATACG GCGGATATTC CCATTCCGAA CTTCTGTAGG 780
10 CTTGCTGTCG GTTATCGCTA TTCCCATTTG GGCTCTTCGC TTAACGCATT GGATACTCGA 840
ATCCACAGTC ATACGGCTTT TATCGGTTTC GTCACGGAGT TTTACCGATT CCGTGGGCGC 900
AAAGCCATGA ATACCGGTG GAGAACCAGT CTTTACTATC ATGAT 945

15 (2) INFORMATION FOR SEQ ID NO:233

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 855 base pairs
20 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

25 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

35 (B) LOCATION: 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

40 ATGGTAGTGA CGCTGCTCGT AATTGTCCGT ATTGTGGTAG TAGTGGGTA CTCCTTCCGC 60
GTCCACGTAC ATAAGACCGG CACTGTTGTA TCGGCGGCCA TATTGGCTT CATCCTCCTT 120
GGAAAGACCG TTCCATGCGA TACCCGTAAC TTCTTTTCCT CCGAAAGTGA TGACCTGAG 180
AGCCGTGTG CTACCGAAAT AGCCACCTG TGCGAAATAG GATTTCAGAT CCACGCTTCC 240
TCTATCCACG TAGCCGTCCG AACCGATTTT GGACAGGCGG GCATCCACTG CCCAATGGCG 300
ACCGATGCGT CCGCTACCGA GTTTGACCGA TCGGCGGAAT GTGCCGAACG AACCTCCGCT 360
45 CAAATCGACA CGGCCATAAG GAGCCAGTCC CAAATTATCC GTACGCATAT TGACACTTGC 420
CCCAAAGCT CCGGCACCAT TGGTGGAAAT ACCCACACCT CGCTGCACCT GAAGGTCCTC 480
GATGGAAAGG CGGAAGTCGG GCATATTAC CCAAAGACG GACTGAGATT CGGAGTCGTT 540
GAGGGGTACT CCATTGGTAG TTATGTTGAT GCGATTGGCA TCGGTGCCAC GCACGCGAAA 600
GCCGGAATAT CCGATACCGG TACCGGCATC GCTGGTGGCT ACCACGGAGG GATCAGCAT 660
CAGCAGATAG GGGATGTCAC GACCATAATT GGACTTGGAA AGTTCCGCCT TGGGAACGTT 720
50 GGTGTAGCG ACAGGGGTTT TCGCCGTGGC GCGAGTAGCT ACGACCTGTA CGGTCTGGAG 780
CTGCACATTG CTAAGACTAT CTATCTCGCT GTTGGAGACG GGTGCTTGTG CCGTCAGGCA 840
GAAGGCGAGG ACGGC 855

55 (2) INFORMATION FOR SEQ ID NO:234

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1797 base pairs
60 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

65 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

70 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

75 (B) LOCATION: 1...1797

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:234

5 ATGGGAAACT TAAAGAACAT TCAGCCCGAG GAGGATTTC AACTGGGAAGA GTTTGAGGCC 60
GGTGGCGTCC ATGCTGCCGT GAGTCGTGAG GAGCAGGAAG CTGCTTATGA CAAAACGCTC 120
AATACCATCA AGGAAAAGGA AGTGGTAATG GGTAGGGTAA CTGCTATCAA CAAGCGTGAA 180
GTGGTTATCA ATGTAGGGTA CAAATCGGAA GGTGTGGTAC CTGCAACAGA ATTCGGCTAC 240
AATCCCGAAC TCAAAGTGGG AGACGAAGTG GAATTTATA TCGAGAATCA GGAAGATAAG 300
AAGGGCCAGC TCGTCTTGTC TCACCGCAAG GGTCTGTCGG CTGCTCTTG GAGCGCGGTG 360
AAGGGGCTCG TCGAAAAGA CGAAATCGTA AAGGGCTATG TGAAGTGTG TACCAAGGGT 420
GGTATGATCG TCGATGTATT CGGTATCGAG GCTTTCTCTC CGGGATCACA GATCGACGTG 480
CGCCCCATTC CGGACTACGA TGCATTCTG GAGAAGACGA TGGAGTTCAA GATTGTGAAA 540
ATCAATCAAG AATATAAGAA TGTAGTTGTT TCCCAACAGG TGCTCATCGA AGCAGAGCTC 600
GAACAACAGA AGAAAGAAAT CATCGGCAAG CTCGAAAAAG GGCAGGTACT CGAAGGTATC 660
GTCAAGAATA TTAATTCTTA CGGAGTATTT ATCGACCTCG GTGGAGTGA TGGTCTTATC 720
CATATCACTG ACCTTTCTAT GGGTCGTGTG GCTCATCCGG AAGAAATCGT ACAGCTGGAT 780
CAGAAGATCA ATGTCTTAT CCTCGACTTT GATGAAGATC GCAAGCGTAT CGCTCTCGGA 840
CTCAACACAG TGATGCTCA TCCTTGGGAT GCTCTCGACA GCGAGCTTAA GGTAGGCGAT 900
AAGGTGAAGG GTAAAGTTGT GGTGATGGCA GATTACGGTG CTITCGTTGA GATTGCACAG 960
GGCGTTGAAG GTCTTATCCA CGTAAGCGAA ATGTCTATGA CACAGCACTT GCGTCTCTGT 1020
CAGGACTTCC TGCATGTAGG CGACGAAGTG GAAGCCGTGA TCCTGACGCT CGACCGCGAA 1080
GAACGCAAAA TGTCGCTCGG TCTGAAGCAA CTCAGCCGG ATCCTTGGGC CAATTTCTGT 1140
ACTCGTTTCC CTGTAGGCTC TCGTCAACAT GCTCGTGTTC GCAACTTCAC CAATTTCTGT 1200
GTATTCTGTG AGATCGAAGA GGGCGTAGAT GGCCTTATCC ATATTTCCGA CCTTTCTTGG 1260
ACGAAGAAGA TCAACACCCC CAGCGAGTTT ACGGAAGTAG GTGCTGATAT CGAAGTTCAG 1320
GTAATCGAGA TCGACAAGGA AAACCGTCGT CTCAGCTTGG GTCACAAACA GTTGAAGAG 1380
AATCCTTGGG ATGTATTGGA GACGGTATTC ACTGTAGGAT CTATCCACGA AGGAACGGTA 1440
ATCGAAGTGA TGGACAAGGG TGCTGTCTTT TCTCTGCTT ACGGTGTGGA AGGTTTGTCC 1500
ACTCGAAGC ACATGGTGAA GGAAGATGCC TCACAGGCTG TACTCGAAGA GAAGTTACCT 1560
TTCAAGGTTA TTGAGTTCAA TAAGGATGCC AAGCGAATCA TTGTATCTCA TAGCCGTGTA 1620
TTCCGAAGATG AGCAGAAATG GGCTCAGCGT GAAGCCAAAT CAGAGCGTAA GGCTGAAGCC 1680
AAGCGGCTCG AGAAGAAAGC TGCTGCCGAA GCTGCCAATC CTGCACAGGC TGTAGAGAAA 1740
GCCACTCTCG GAGACCTCGG CGAGCTGGCC GCTTTGAAAG AAAAGCTTTC AGAAAAAC 1797

35 (2) INFORMATION FOR SEQ ID NO:235

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1650

55 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:235

60 ATGGGTAGGG TAACTGCTAT CAACAAGCGT GAAGTGGTTA TCAATGTAGG GTACAAATCG 60
GAAGGTGTGG TACCTGCAAC AGAATTCGCG TACAATCCCG AACTCAAAGT GGGAGACGAA 120
GTGGAAGTTT ATATCGAGAA TCAGGAAGAT AAGAAGGGCC AGCTCGTCTT GTCTCACCGC 180
AAGGTCGTG CCGCTCGCTC TTGGGAGCGC GTGAACGAGG CTCTCGAAA AGACGAAATC 240
GTAAAGCGCT ATGTGAAGTG TCGTACCAAG GGTGGTATGA TCGTCAATGT ATTCGGTATC 300
GAGGCTTTC TCCCGGCATC ACAGATCGAC GTGCGGCCCA TTCGCGACTA CGATGCATTC 360
GTTGAGAAGA CGATGGAGTT CAAGATTGTG AAAATCAATC AAGAATATAA GAATGTAGTT 420
GTTTCCACA AGGTGCTCAT CGAAGCAGAG CTCGAACAAC AGAAGAAAGA AATCATCGGC 480
AAGCTCGAAT AAGGGCAGGT ACTCGAAGGT ATCGTCAAGA ATATTACTTC TTACGGAGTA 540
TTTATCGACC TCGSTGAGT GGATGGTCTT ATCCATATCA CTGACCTTTC ATGGGGTCTG 600
GTGGTTCATC CGGAAGAAAT CGTACAGCTG GATCAGAAGA TCAATGTGCT TATCCTCGAC 660
TTTGATGAAG ATCGCAAGCG TATCGCTCTC GGACTCAAAC AGCTGATGCC TCATCCTTGG 720
GATGCTCTCG ACAGCGAGCT TAAGGTAGGC GATAAGGTGA AGGGTAAAGT TGTGGTATG 780
GCAGATTACG GTGCTTCTGT TGAGATTGCA CAGGGCGTTG AGGGTCTTAT CCACGTAAAG 840
GAATGTCTAT GGACACAGCA CTTGCGTTCT GCTCAGGACT TCCTGCATGT AGGCGAGCAA 900
GTGGAAGCCG TGATCCTGAC GCTCGACCGC GAAGAACGCA AATGTCTGCT CGGTCTGAAG 960
CAACTCAAGC CGGATCCTTG GGCTGATATC GAAACTCGTT TCCCTGTAGG CTCTCTGTCAC 1020
75 CATGCTCGTG TTCGCAACTT CACCAATTTC GGTGTATTCT TTGAGATCGA AGAGGGCGTA 1080

161/ 490

5 GATGGCCTTA TCCATATTTC CGACCTTTCT TGGACGAAGA AGATCAAACA CCCCAGCGAG 1140
 TTTACGGAAG TAGGTGCTGA TATCGAAGTT CAGGTAATCG AGATCGACAA GGAAAAACCGT 1200
 CGTCTCAGCT TGGGTCACAA ACAGTTGGAA GAGAATCCTT GGGATGTATT CGAGACGGTA 1260
 TTCACGTAG GATCTATCCA CGAAGGAACG GTAATCGAAG TGATGGACAA GGGTGCTGTC 1320
 GTTTCCTGTC CTTACGGTGT GGAAGGTTTT GCCACTCCGA AGCACATGGT GAAGGAAGAT 1380
 GGCTCACAGG CTGTACTCGA AGAGAAGTTA CCTTTCAGG TTATTGAGTT CAATAAGGAT 1440
 GCCAAGCGAA TCATTGTATC TCATAGCCGT GTATTGGAAG ATGAGCAGAA AATGGCTCAG 1500
 CGTGAAGCCA ATGCAGAGCG TAAGGCTGAA GCCAAAGCGG CTCAGAAAGA AGCTGCTGCC 1560
 10 GAAGCTGCCA ATCCTGCACA GGCTGTAGAG AAAGCCACTC TCGGAGACCT CGGCGAGCTG 1620
 GCCGCTTTGA AAGAAAAGCT TTCAGAAAAC 1650

(2) INFORMATION FOR SEQ ID NO:236

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 20 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 25 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
 30 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1374
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

35 ATGATCGTCG ATGTATTGGG TATCGAGGCT TTCCTCCGGG GATCACAGAT CGACGTGGCG 60
 CCCATTCCGG ACTACGATGC ATTCTGTGAG AAGACGATGG AGTTCAAGAT TGTGAAAATC 120
 AATCAGAAT ATAAGAATGT AGTIGTTTCC CACAAGGTGC TCATCGAAGC AGAGCTCGAA 180
 CAACAGAAGA AAGAAATCAT CGGCAAGCTC GAAAAAGGGC AGGTACTCGA AGGTATCGTC 240
 40 AAGAATATTA CTTCTTACGG AGTATTATC GACCTCGGTG GAGTGGATGG TCTTATCCAT 300
 ATCACTGACC TTTTCATGGG TCGTGTGGCT CATCCGGAAG AAATCGTACA GCTGGATCAG 360
 AAGATCATTG TCGTTATCCT CGACTTTGAT GAAGATCGCA AGCGTATCGC TCTCGGACTC 420
 AAACAGCTGA TGCCTCATCC TTGGGATGCT CTCGACAGCG AGCTTAAGGT AGGCGATAAG 480
 GTGAAGGGTA AAGTTGTGGT GATGGCAGAT TACGCTGCTT TCGTTGAGAT TGCACAGGGC 540
 45 GTTGAGGGTC TTATCCACGT AAGCGAATG TCATGGACAC AGCACTTGGC TTCTGCTCAG 600
 GACTTCCTGC ATGTAGGCGA CGAAGTGGAA GCCGTGATCC TGACGCTCGA CCGCGAAGAA 660
 CGCAAAATGT CGCTCGGTCT GAAGCAATC AAGCCGGATC CTTGGGCTGA TATCGAAACI 720
 CGTTTCCCTG TAGGCTCTCG TCACCATGCT CGTGTTCGCA ACTTCACCAA TTTCGGTGTA 780
 TTCGTTGAGA TCGAAGAGGG CGTAGATGGC CTTATCCATA TTTCCGACCT TTCTTGGAGC 840
 50 AAGAAATCA AACACCCAG CGAGTTTACG GAAGTAGGTG CTGATATCGA AGTTACAGTA 900
 ATCGAGATCG ACAAGGAAAA CCGTCGCTC AGCTTGGGTC ACAACAGTT GGAAGAGAAT 960
 CCTTGGGATG TATTCGAGAC GGTATTCACT GTAGGATCTA TCCACGAAGG AACGGAATC 1020
 GAAGTGATGG ACAAGGGTGC TGTCGTTTCT CTGCCTTACG GTGTGGAAGG TTTTGCCACT 1080
 CCGAAGCACA TGGTGAAGGA AGATGGCTCA CAGGCTGTAC TCGAAGAGAA GTTACCTTTC 1140
 55 AAGGTTATTG AGTTCAATAA GGATGCCAAG CGAATCATG TATCTCATAG CCGTGTATTG 1200
 GAAGATGAGC AGAAATGGC TCAGCGTGAA GCCAATGCAG AGCGTAAGGC TGAAGCCAAA 1260
 GCGGCTCAGA AAGAAGCTGC TGCCGAAGCT GCCAATCTG CACAGGCTGT AGAGAAGGCC 1320
 ACTCTCGGAG ACCTCGGCGA GCTGGCCGCT TTGAAAGAAA AGCTTTCAGA AAAC 1374

(2) INFORMATION FOR SEQ ID NO:237

- 65 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 70 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 75 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

5 (A) NAME/KEY: misc_feature
(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

10 ATGGAGTTCA AGATTGTGAA AATCAATCAA GAATATAAGA ATGTAGTTGT TTCACACAAG 60
GTGCTCATCG AAGCAGACCT CGAACACAG AAGAAAGAAA TCATCGGCCAA GCTCGAAAAA 120
GGGCAGGTAC TCGAAGGTAT CGTCAAGAAT ATTACTTCTT ACGGAGTATT TATCGACCTC 180
GGTGGAGTGG ATGGTCTTAT CCATATCACT GACCTTTCAT GGGGTCTGTG GGCTCATCCG 240
GAAGAAATCG TACAGCTGGA TCAGAAGATC AATGTCTGTA TCCTCGACTT TGTGAAGAT 300
CGCAAGCGTA TCGCTCTCGG ACTCAAACAG CTGATGCTC ATCCTTGGGA TGCTCTCGAC 360
15 AGCGAGCTTA AGGTAGGCGA TAAGGTGAAG GGTAAAGTTG TGGTGATGGC AGATTACGGT 420
GCTTTCTGTT AGATTGCACA GGGCGTTGAG GGTCTTATCC ACGTAAGCGA AATGTCATGG 480
ACACAGCACT TCGCTTCTGC TCAGGACTTC CTGCATGTAG GCGACGAAGT GGAAGCCGTG 540
ATCCTGACGC TCGACCGCGA AGAACGCAAA ATSTCGCTCG GTCTGAAGCA ACTCAAGCCG 600
GATCCTTGGG CTGATATCGA AACTCGTTT CCTGTAGGCT CTCGTACCA TGCTCGTGT 660
20 CGCAACTTCA CCAATTTCGG TGTATTCGTT GAGATCGAAG AGGGCGTAGA TGGCCTTATC 720
CATATTTCCG ACCTTCTTG GACGAAGAAG ATCAAACACC CCAGCGAGTT TACGGAAGTA 780
GGTGCTGATA TCGAAGTTCA GGTAAATCGA ATCGACAAGG AAAACCGTCG TCTCAGCTTG 840
GGTCACAAAC AGTTGGAAGA GAATCCTTGG GATGTATTTC AGACGGTATT CACTGTAGGA 900
TCTATCCACG AAGGAACGGT AATCGAAGTG ATGGACAAGG GTGCTGTCTG TTCTCTGCT 960
25 TACGGTGTGG AAGGTTTTC CACTCCGAAG CACATGTTGA AGGAAGATGG CTCACAGGCT 1020
GTACTCGAAG AGAAGTTACC TTTCAGGTT ATTGAGTTCA ATAAGGATGC CAAGCGAATC 1080
ATTGTATCTC ATAGCGGTGT ATTCGAAGAT GAGCAGAAA TGGCTCAGCG TGAAGCCAAT 1140
GCAGAGCGTA AGGCTGAAGC CAAAGCGGCT CAGAAAGAAG CTGCTGCCGA AGCTGCCAAT 1200
30 CTGACACAGG CTGTAGAGAA AGCCACTCTC GGAGACCTCG GCGAGCTGGC CGCTTTGAAA 1260
GAAAGCTTTT CAGAAAAC 1278

(2) INFORMATION FOR SEQ ID NO:238

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

40 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

45 (iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

50 (A) NAME/KEY: misc_feature
(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

55 ATGAAAAAG CTATTCCTTC CGGAGCGGCC TTGCTCCTCG GCCTATGTGC CAACGCACAA 60
AACGTGCAGT TGCACTACGA TTTGGGTCTT TCCATCTACG ACGAAGTAGA TGGACGTCCC 120
AAACTGACTA CCACAGTGGG AAACCTTACA CCAGCAAAAT GGGGAAGCAC GTTCTTCTTC 180
ATCGACATGG ATTACACGGG CAAGGGTATC CAGTCGGCCT ATTGGGAGAT TTGCGCGGAA 240
CTGAAGTTTT GGCAGCTCC CGTTTCCATT CATTGGAGT ACAACGGAGG CCTCTCCACA 300
AGCTTTACTT TCGGACACGA TGCTCTAATC GGTGCCACCT ACACCTACAA CAACCCCTCC 360
TTTACACGTA GATTACGAT CAGCCCATG TACAAGCATC TGGGTGCGCA CGACTTCCAC 420
ACCTATCAGA TCACCGGCAC TTGGTACATG CACTTCTGAG ACGGTCTGCT TACCTTCAAC 480
GGCTTCTCTG ATCTTTGGGG TTTCCTCCAA GAGAACCCAA TCGGGGGGCC TGTGCTCAAA 540
65 GAAGGGGATA AGTTCTGATT CTGTCTCGAA CGCAGTTCT GGATCAACCT CAATCGCATC 600
AAAGGCATCG ACAAGGATTT CAATCTCAGC ATAGGGACAG AGATGGAAT CAGCAGGAAC 660
TTGCTCGCA TGGACAAATT CTCTGCTATC CTTACTCTTG GGTCAAAAT GACTTTCAAC 720

(2) INFORMATION FOR SEQ ID NO:239

(i) SEQUENCE CHARACTERISTICS:

75 (A) LENGTH: 1302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

163/490

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1302

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

20 ATGTATAAAG ACTATAAGGG TTGTATGCG TCGCTTCGGT GGTATGCCCT GATCATTGGG 60

TTGCTATTTG CAGCAGACGG TATACAGGCT CAGAACAACA ACTTTACCGA GTCGCCCTAC 120

ACTCGCTTCG GCCTTGGCCG TCTCGGAGAA CGGACGACTA TTAGTGGGCA TTCCATGGGA 180

GGACTCGGCG TCGTCTGCG TCGAGGCACA TACGTCAATG CGGTCAATCC TGCTTCATAC 240

TCGGCTGTGG ATTCSATGAC GTTTATCTTC GATTTCGGTG CATCTACCGG AATTACGTGG 300

TATGCCGAGA ACGGGAAAAA GGACAATAGG AAAATGGGAA ACATTGAGTA TTTCGCCATG 360

CTTTTTCCTA TTCCAAATC CATTGCTATG AGTGGGGGAG TGCTTCCTTA CTCGCGATCC 420

25 GGGTACCAGT TCGGATCCGT TGATCAAGTG GAAGGAGGCA GCGTCCAGTA CACCGGTAAA 480

TACTTGGGGA CAGGCAATCT GAACGATCTC TATGTCGSTA TAGGTGCAAC CCCGTTCAAA 540

AACTTCTCAA TAGGAGCUAA TGCTTCATCC CTTTTCGGGC GATTACACA CAGCAGGCAG 600

GTAACTTCT CACGCGAGGC TCCTTACAAT CCGGTACATC TCTCGACGT GTACTTGAAG 660

30 GCTGCCAAGT TCGACTTCGG TATGCAATG CACCTTCTTC TCAAATCAGA TCGTTCGCTC 720

GTATCGGTG CCGTCTATTC TCGCGGGGTG AAGATGCATA GCGAGCTGAC TCAGATAAAG 780

AATCAGGTTT AGAACGGTGT AGTAGTGGAG AGCGAAACCC AAGAATATAT CAAGGGAATG 840

GACTATTATA CCCTGCCTCA TACATFGGGG ATAGGTTTTT CTTATGAAA GAAAGATAAA 900

CTTCTCTTAG GAGCAGACGT CCAATATAGT AAATGGAAG GCGAGAAATT TTATAAATCC 960

35 GATTGCAAA TCCAGGACAG AATACGGSTA TCTCTCGGCG GAGAGATCAT ACCGGATATA 1020

AATGCCGTTG GATGTGGGCC TAAAGTTCCG TATCGCTTCG GTTTACATGG TGAAATTTCT 1080

TACCTGAAAG TCCCGACTAA AGGCGGTGTA TATCAAGGAT ACCATATCGT AGGTGCTGTA 1140

TTCCGTATAG GAATCCCGCT CAATGACAGA CGTTCGTTCC TAAATGTCTC TCTTGAATAT 1200

GACCGATTGA TCCCGAAGGA GGTATGATC AAAGAAAATG CTCFGAAATT GACCTTCGGC 1260

40 CTCACGTTCA ACAGTCATG GTTTAAAAAG CTGAAACTGA AC 1302

(2) INFORMATION FOR SEQ ID NO:240

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2778 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

50 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

60 (A) NAME/KEY: misc_feature

(B) LOCATION 1...2778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

65 ATGCGATCGA TTTATCAATT ACTGTTGTCA ATACTCCTTG CTTCTCTTGG TTTCGTGGG 60

CTGGAAGCCC AACAGCCGG AGTAGCAGGT AGAGTATTGG ACGAAGAAG CAACCCCATG 120

ATTCAAGCCA ACGTACAGCT TGTACAGAGT ACCGGCCAAG TAGCCGTGTC CGCAGGTGCC 180

ACTAATGAAA AAGGGTTGTT CAGCCTGAAA ACCTCACAGG AGGGTGACTA CATCTCTGCG 240

70 GTTTCATATG TAGGTTACAC TACCCACGAC GAAAAAATAT CTCCTAGAAA CGGGCAAAAC 300

ATTACGCTCA AAGATATATC CATGAACGAA GATGCCCGTC TTCTACAGAG TGTGACGGTG 360

CAGGCTAAAG CGGCAGAGGT CGTGGTACGC AACGATACGC TCGAATTCAA TGCCGGATCC 420

TATACCGTAG CACAGGGAGC TTCTATCGAG GAAGTGAATC AGAAGCTACC CGGAGCAGAG 480

ATCGGATCCG ATGGGAAGAT CACCATCAAC GGCAGGACA TTAGCAAGAT CCTTGTGAT 540

75 GCCAAGAGT TTTTCTCAA AGATCCACAG GTGGCAATTA AGAATCTTCC GCGCGATATG 600

GTCATAAAG TACAGGTACT GAACAAACTG AGCGAGCTGT CGCGGATGAG CGGTTTCGAT 660

WO 99/29870

PCT/AU98/01023

164/ 490

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5  GATGGAGAAG AGGAGACCGT AATCAACCTG ACGGTGAAGC CCGAAAAAAA GAAAGGCCTC 720
   TTCGGAACGC TTCAGGCCGG CTACGGTACC GACCAACGCT ATATGGCCGG AGGGAACGTC 780
   AATCGGTTTC ATGGAAATAA GCAATGGACA TTGATCGGTA GTGGGAACAA TACGAACAAT 840
   ATGGGCTTTA GCGAGATGGA CAGCGAGATG GGATCCATGA CCTTCTTCTC TCCCCAAGGC 900
   GSTGGTCGAC GCGGCTTCGG CAATAGTGGG GGTGTACGT CTTGTGAT GCTGGGGGGC 960
   AACTTCAGTG TCGAATTCCT CTCTGCCCTT AATACAGGAG GCGATGCACG CTACGGATAC 1020
   AACGACAAGG CCATAGAGAC GACCAACGCG GTGGAAATA TCCTCGCCGA AGGGAATACT 1080
   TATATGGAGC AATATATAT GGAACGCTCT TTCTCTCACA ATGGTCAGGC GCGATTTAGG 1140
   ATGCAATGGA AACCGTCCGA ACGTACCGAA GTGGTATTCT AGCGGATCTT TTCGATATCC 1200
10 AAGATCGATG GGTTCCTTAA CGACACATAC GAGACGAAAG ATGCCACCGG AATCTCTATC 1260
   AACAAAGGTT CTATCCACCA AACTACACAA GGAAACAACT TCAGACTGAA CCGAGAATTG 1320
   GATATCAGTC ACAAGCTCAA CGACGAAGGC CGTACGATCA GTGCCTCCGT CAGTGGCGGT 1380
   CTGACCGAGC AAGACGGAGA TGGCATATAT CAGGCTGTGC TCCAAAGCGT GGAGACGAAT 1440
   CAAAAGCAAT TCAACGACAA CTCCAACCTG CAATATCGGC TTGCTCTCTC GTATGTGGAA 1500
15 CCGTTGGGTA AAAACTACTT CGCACAGCG ATTCTGAACA GACGTTTCTC CCGTCGCAAT 1560
   TCGGATCGTG AGGTGTACCG ACTGGGCGAT GACGGGCAAT ACTCCATATT AGACAGTCAG 1620
   TACGACTCT CTACAGTAA CGAGTTCACC CAGTATCGCA TCGGACTCAA CCTCAAGAAG 1680
   ATTGCCAAAA CGTGGGACTA CACCGTAGGA TTCAATGTGG ATCCCAACAG AACTGTCTAGC 1740
   TATCGGAGCG TAGCGGAGT AGAGCAGGAC AAACCTGGCTT TCAATCGTGT CAATCTCTCC 1800
20 CCGATGCTCC GAATCAACTA CAAACCGAGC AGGACTACCA ACCTCCGAGT GGAATACCGA 1860
   GGACGACGCA CACAACCATC CATCAATCAG ATCGCTCCCG TTCAGGACAT CACGAATCCG 1920
   CTATTCGTGA CCGAAGGCAA TCCCGGTCTG AAGCGAGCT ATTCCAACAA TGTGATGGCC 1980
   ATGTTCTCGG ACTTCGATGC CAAAAGTCAG CGAGCTTCA ACATTGTTT CTTCGGCAAC 2040
   TATACATTCC AGGACATCGT CCCCATAACG CACTACGATC CGTCTACAGG GATCCGTACC 2100
25 ACTCGTTACG AAAACGCCCT CCGTACGTTG CAAGCGAATC TTCATGGGAC ACTATCGCTT 2160
   CCACTCAAGA ACAGGGCATT TTCTTTCAGC ATGTCTCTGT TCAACAGGTT GGCCGAAGGA 2220
   CAAGCTTCA TCAATGACGA TAAGAACAAA GCTCTCTCTT TCCGAACGAG GGAACGCCCT 2280
   ACCGTGACCT ATCGCAACAA TTGGATCGAT ACGAGTATCG GTGGCAATAT CGGATTCTAT 2340
   ATGGCGAATA ATAGTCTGAG CGGACAGAAA GATTCTCGCA CATACGATTT TGGCGGCAAT 2400
30 TATCAAGTTG CCTAACGCT TCCCTATGGA TTCCGTATCG ACAGCGATGT TGAATACAAT 2460
   ACGAATCTCC GTTACAGCGG AGGATTCAGT CTGGACGAAT GGCTTTGGAA TGCTTCGCTT 2520
   TCATACAGCT TCCTCCGTGA CAAGGCCCGT AACTGCGTGT TCAATGGCTA TGACATCTCT 2580
   GGTGAGCGGT CAAGTATCAG CCGTTCTGCT TCGGCCATCA ATATAGAAGA GAGCATGTCC 2640
   AATACGATCG GACGCTACGT GATGGTGGAC TTTATCTACC GATTCAACGC CTTCAGTGGT 2700
35 GGTGGATCTC CGAGCGATCA TCAGCGTGGC AATATGAATC GTCCGGGCCC ACCTTTCGGC 2760
   GGTGGCAGAC GACCGTCC 2778

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40 (2) INFORMATION FOR SEQ ID NO:241
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1200 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: circular
45
    (ii) MOLECULE TYPE: DNA (genomic)
    (iii) HYPOTHETICAL: NO
50
    (iv) ANTI-SENSE: NO
    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55
    (ix) FEATURE:
        (A) NAME/KEY: misc feature
        (B) LOCATION 1...1200
60
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

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65 ATGGTTATGA AGCTGATTAA AAGAAGTTTG CTCCTGCTTG GAGCGGTAAT GCTGATTACG 60
   CTTCTCTCGT ACTCGCAGAA TGATGACATC TTCGAAGATG ACATCTATAC ATCGCGAAAA 120
   GAAATACGTA AACAAACCA AGTTAAAGAC TGGCAAAACC AAGAGGACGG ATACGGCGAC 180
   GATACGGAAT ATACAGTGGC TTCCGATCGG GACATTGACG CCTACAATCG TAGAGATGGC 240
   CAGTCCCTACG ATGGGAAAAA GTTGTCCAAA GACAAGAAAA GAGACTCCAC TCGTTCTTCT 300
   GTTCCCGGTC GCTATAGTCG CGGCTTCGCT CGATTCTATA AGCCGAATAC GATCGTCATT 360
   TCAGGTGCGG ACAATGTATA TGTAACGATG GATGGTGAGT ATTTCGTCTA TGGAGACGAA 420
   TACTATATAG ACGCGTCGTC TGTAACATTT TACATCAACA GTCTTCTGCT CGATCCGTTT 480
70 CTTTATACGT CATGGTATCC ATCTTCTTCC GGCTGGTACA ACTATACGTG GAACATATCA 540
   TGGTTCTACT ACGGTAGCCA TATCCGATGG GGCGGTATT ACCCCGGATA TAATTGGTAT 600
   TGGAGCTACT ACTATGATCC TTTCTACAA CCCTATGGAA TCGGTATGGG TTGGGGATAT 660
   CCTTATGGCT GGGGACGCTA TTACGGTTGG GGTGGCTATC CCGGAGTGAT ACATCACTAC 720
   CACCACTACC CCAAGAAGAC CTATTCCAAT GGTGAGCATT CCGGAGCTTA CTATTCTTAT 780
75 GGCGGACCGA ATCGTATCAA AGGTGGAACG TCCCGTGCCA AACTTGGGAC AGGACGCTAC 840

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165 / 490

5 GATAGAATTC AAAATTCGTC TTCGCAAAAA AATAAGTTG GATTGCAGTC GAACAAACCC 900
AATAAATATC TGCAAAATGT CAAGTCGGGA CGTACCGGCC GAGCCAATAG AGACCGAAAT 960
ATAGAAACGG TAACTCCAAA CAACGGGCAA AAGCAGAATC GTCCCGTATT CCAGCAGAAT 1020
CAGTCCGGCA ATGACCGACC GACCGGACGG AATATCCGCA GCGAGAGACA GCGGGAAAAAT 1080
AACGATAGGA CATTTTCGAC TCCTTCTCGT AGCAATAGTA ACGGTGGCTT CTCCACGCCCT 1140
TCTCGCTCTT CTCCGGCTC TATGAGCGGA GGTGGCGGAC GTAGTGGCCG GGGACGCAAT 1200

(2) INFORMATION FOR SEQ ID NO:242

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

15

(ii) MOLECULE TYPE: DNA (genomic)

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...1194

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ATGAAGCTGA TTAAGAAG TTTGCTCCTG CTTGGAGCGG TACTGCTGAT TACGCTTCCT 60
GCSTACTCGC AGAATGATGA CATCTTCGAA GATGACATCT ATACATCGCG AAAAGAAATA 120
CGTAACAACA ACCAAGTTAA AGACTGGCAA AACCAAGAGG ACGGATACGG CGACGATACG 180
GAATATACAG TGGCTTCCGA TCGGGACATT GACGCCTACA ATCGTAGAGA TGGCCAGTCC 240
TACGATAGGA AAAAGTTGTC CAAAGACAAG AAAAGAGACT CCACCTCGTC TTCTGTTCCT 300
GGTCGGCTATA GTCGCCGCTT GGCTCGATTC TATAAGCCGA ATACGATCGT CATTTCAGGT 360
GCCGACAATG TATATGTAAAC TGATGATGGT GAGTATTTTC TCTATGGAGA CGAATACTAT 420
GATGACGGCT CGCTGTGAAA CATTTACATC AACAGTCCTT GGTGCGATCC GTTCCCTTAT 480
ACGTATGCT ATCCATCTTT CTCCGGCTGG TACAACATA CGTGGAACTA TCCATGGTTC 540
TACTACGGTA GCCATATCGG ATGGGGCGGT TATTACCCCG GATATAATTG GTATTGGAGC 600
TACTACTATG ATCCTTTCTA CAATCCCTAT GGAATCGGTA TGGGTTGGGG ATATCCTTAT 660
GGCTGGGGCA GCTATTACGG TTGGGGTGGC TATCCGGGAG TGATACATCA CTACCACCAC 720
TACCCCAAGA AGACCTATTC CAATGGTCAG CATTCCGGAG CTTACTATTC TTATGGCCGA 780
CGAATCGTA TCAAGGTGG AACGTCGGT GCCAAACTTG GGACAGGACG CTACGATAGA 840
ATTCAAATTT CGTCTTCGCA AAAAATAAAG TTCGGATTGC ATTCGGAACA ACCCAATAAT 900
AATCTGCAAA ATGTCAAGTC GGCACGTACC GCGCGAGCCA ATAGAGACCG AATATAGAA 960
ACGGTAACCT CAAACAACGG GCAAAAGCAG AATCGTCCCG TATTCCAGCA GAATCAGTCC 1020
GGCAATGACC GACCGACCGG ACGGAATATC CGCAGCCAGA SACAGGGGGA AAATAAGSAT 1080
AGGACATTTT CGACTCCTTC TCGTAGCAAT AGTAACGGTG GCTTCTCCAC GCCTTCTCGC 1140
TCTTCTCCG GCTCTATGAG CGGAGGTGGC GGACGTAGTG GCCGGGGACG CAAT 1194

55

(2) INFORMATION FOR SEQ ID NO:243

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1743 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

60

(ii) MOLECULE TYPE: DNA (genomic)

65

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

70

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...1743

75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

166/490

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ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGGG 66
GTACCAACCG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC 120
TCTTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTCAGTATT 180
CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC 240
TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC 300
TATAAGCCCC TGCCCGGACA TGAACCGAG ATGGGGCGTG GCGTTCCTCA CATGTAITGT 360
AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC 420
GGTATGSTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGGTAGC 480
GGACGTATAG TACTCACTCC TTTTGATGGA GTGCGTGTCA AGGGTATTGC AGCACAGCAG 540
CGTAACCTACT TCGACCGCAC GGGCAAGGTA TTCAATTCGG GCCGAGGCTA CCTACTGGGT 600
TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGGCGGACAA TGAATATCAT 660
TTGGGTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGST 720
GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCOGATTAT GGGCCTGCGC 780
ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT 840
CCCTCGGCAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCCTCA 900
TACTCCAAAA AAGGGATGAG TATCCTGTTG CAGGCCAAAC GTTGTGAGAA CTTTGCTTTT 960
CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC 1020
CAAGCTCACA CTTATACGCT GCGCGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA 1080
TGGGCTTTCC AAGGTGAAGT GCGTTACAACT TTTGCTCGCC GSACAGCTCT CGGTGGACCG 1140
TACGGTACCG GCTTGCGTAT CAACGTTTCC CATGTGCGTG GTCTGGACAA AAAGATGCTC 1200
AAAGAGATC CCGACGAAGT GATCGGAACG GATGGCTACA CCGTTTCTTT CTTCCGCATG 1260
GGCGACCTCT ATTATTCGGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC 1320
AATTTACGCG TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC 1380
GGAGAGAAGC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG 1440
AGTAATAAGG TAGCCCTCCG TACCGAAGTG CAATATTTCG ACACGAAGCA GGATCAGGCT 1500
GACTGGATCT ACGGCTAGGC CGAGCTCTCT ATCCTGCCTT CTCTGATGCT TTCCCTCTCG 1560
GAGCAGTATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT 1620
CAGGAGCAGC ATCGASTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGAT GAACCTGCTG 1680
30 GAGGGTGTAT GTCGTGGGT CCTGAGACT CAGGGATTCT ACCTTTCTTA TAGCACCAAT 1740
CTG 1743

(2) INFORMATION FOR SEQ ID NO:244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

ATGCGTTCTT TATTTTGTAG CGCGTTGCGC AGCTCCTCTC TCCATGGTTC AGAGCGACGC 60
AGTCGGATTA GTTCTTCTGT AGTCATGTCA ATAAGGCAGA AAATAAGGTT ATTCCATCTC 120
TCGGTATGCG CCCAAACGCA TGATCATCTC ATCGAAATCC ACTTGGTGTG CATCGAATTC 180
GGGGCCATCG ACACAGACGA ATTTGCTCTG TCCTCCACG CTTATACGAC AAGCCCCACA 240
CATACCGGTG CCATCCACCA TAATTGTATT GACAGAAGCT ATGGTCGGTA TCTCGTAACG 300
TTTGGTCAGG AGAGAAACGA ACTTCATCAT CACAGCCGCG CCGATCGTAA CGCAGAGGTC 360
TACCGTTTCC CGTTTGATAA CGCTTTCCAC TCCATCCGTT ACGAGGCCCT TCGTCCCAT 420
AGACCATCG TCTGTATGA TGATCACTTC ATCGCTATTG GCTCGCATTT GTTCTTCAAG 480
GATAACCGA TCTTTAGTTC TGGCAGCCAA TACGACAAIT ACACGGTTGC CTGCTTTGTG 540
GAAAGCCTCC ACGATCGGGA GCAAAGGAGC CACACCCACA CCGCCTCCGG CACAAACCAC 600
TGTGCCGACC TTTTCGATAT GCGTAGCTCT TCCAGCGGA CCTACCACAT CCGTGATATA 660
GTGCGCGACT TCGAGTTCGG CCAATTCTCTT GGAAGATTG CCCACGGCCT GAACCCAC 717

(2) INFORMATION FOR SEQ ID NO:245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid

167/490

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

20	ATGTCAATAA GGCAGAAAAT AAGGTTATTC CATCTCTCGG TATGCGCCCA AACGCATGAT	60
	CATCTCATCG AAATCCACTT GGTGTGCATC GAATTCGGGG CCATCGACAC AGACGAATTT	120
	CGTCTGTCTT CCCACGCTTA TACGACAAGC CCCACACATA CCGGTGCCAT CCACCATAAT	180
	TGTATTGAGA GAAGCTATGG TCGGTATCTC GTAACGTTTG GTCAGGAGAG AAACGAACTT	240
	CATCATCACA GCGCGCCCGA TCGTAACGCA GAGGTCTACC GTTTCGGTT TGATAACGCT	300
25	TTCCACTCCA TCCGTTACGA GGCCTTTCTG CCCATAAGAC CCATCGTCTG TCATGATGAT	360
	CACCTTCATCG CTATTGGCTC GCATTGTTC TTCAAGGATA ACCAGATCTT TAGTTCTGSC	420
	AGCCAATACG ACAATACAC GGTTCCTGTC TTTGTGGAAA GCCTCCACGA TCGGGAGCAA	480
	AGGAGCCACA CCCACACCGC CTCGGGCACA AACCAGTGTG CCGACCTTTT CGATATGCGT	540
30	ACTCTGTCCC AGCGGACCTA CCACATCGGT GATATAGTCG CCGACTTCGA GTTCGGCCAA	600
	TTTCTTGGAA GATTTGCCCA CGGCCTGAAC CAC	633

(2) INFORMATION FOR SEQ ID NO:246

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...2343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

55	ATGATCGTC CTAAGCCTTC ATATATTGTT CGAATAGCAG CCATTCTCTG CTGTTTGTG	60
	GGCAGGCGCTT TGTTTGCGCA GAGCTATGTG GACTACGTG ATCCGCTGAT CGGGACGCTA	120
	AGTTCTTTTG AGCTGAGTGC GGGCAATACC TATCCGGTGA TCGGTTTACC GTGGGGAAATG	180
	AATAGCTGGA CACCGATGAC CCGGTGATCC GGTGACGGCT GGCATATATC CTAAGCTGGA	240
60	CACAAGATTG GCGGATCAA ACAGACCCAC CAACCCAGTC CTGGATCAA CGACTACGGC	300
	CAATTCTCCC TTCTTCCCCT TACGGCACCG CAGAAGCCAT CATCGAACGA CTCATAGCT	360
	CTGACTAAAT GGTGCAAGCA ACTCTTTTCG GACGAACAGA CCTCGTGGTT CTCGCACAAA	420
	GCGGAGACGG CGACGCCATA CTATTATAGT GTCTATTGCG CCGATTACGA CACACGGGTG	480
	GAGATGGCTC CGACCGAGCG TGCAGCTATC TTTCGCATAC GTTATTCCGG CAATACCGAA	540
65	AGTGGCTCCG GTCGATGGCT TCGTCTTGAT GCCTTTACCG GTGGTTCCGA GATTAGCATC	600
	GTGGATCCTC ACACCGTAGT GGGCATATCT CGCAAGAATA GCGGAGGTGT GCCGGCTAAC	660
	TTCCGCTGTT ATTTCATCCT CGAGTCCGAT ACTCCTATGG CCGATGTCCT GCTTGAGACA	720
	GATACCGGCA AGTCAGACGA AGGCACAAGG GCATGGGCGAG CCTGTGCTT CGATTCCGAA	780
	GAAGTTACCG TCGGGGTGGC ATCTTCTTTT ATCAGTGTGG AGCAGGCCGA AAGAAATCTT	840
70	GCGGAAGTCA AAGGGCAGAG TTTCGACCGG ATCAGACTTG CCGGTGCGCA AGCTTGGAAAT	900
	AAGGTGCTCG GACGCATACA TGTGGAAAGG GGAACGAAGG ATGAGCGCAC TACATTCTAT	960
	TCGCGACTCT ATCGCTGTCT GCTTTTCCCG CGTCGCTTCT ATGAGGAGGA TGCTTCCGGC	1020
	AATTTTGTGC ATTACAGCCC CTACAATGGA GAGTACTTTC CCGGTTATCT CTATACCGAT	1080
	ACCGGATTTT GGGACACTTT TCGAGCCCTT TTCCCCCTGC TCAATCTGCT GTATCCCGAT	1140
75	GAAGACATTA AAATTCAGGA AGGTCTGCTG AATGTATATC GCGAGAGTGG CTTTTTCCCG	1200
	GAATGGGCCA GTCCGGGCCA TCGGATGTGT ATCATAGGCA ACAACTCTGC TTCTGTTCTG	1260

168/490

5 GCGGATGCGT ACCTCAACGG TGTTCGGGTA GAAGATACCC GTACACTGAT GAACGGACTC 1320
TTGCATGCTA CGAAAGCCGT CCATCCGAAA ATCTCCTCCA CGGGTCGCAA AGGTTGGGAG 1380
TGGTACAACCT CCTTAGGTTA TGTTCGGGCT GATGCAGGCA TCGACGAAAG TGTGCCCCGT 1440
ACGCTCGAAT ATGCTTATAA CGATTGGTGC ATCCTCCGAC TGGGGCGCAC ATTGGGTTGG 1500
GATAGAGCTG CATTGGACAC GTTGGCTCAT CGTTCGATGA ACTATCGTCA TCTGTTCCGAT 1560
CCGSAACCA AACTCATGCG CGGTAGAAAT CAGGATGGTA GTTTCGGGAC ACCTTTTTC 1620
CCTTTCAAAT GGGGAGATGT ATTACCGGAG GGCAATGCCT GGCACTACAC TTGGTCGGTC 1680
TTTCATGATG TGCAGGGGCT TATCGACCTG ATGGGAGGAG ATCGCCCGTT CGTGTCTATG 1740
10 CTCGATTTCG TATTCAATAC TCCTCCTATG TTCGATGAGA GCTATTACGG ATTTGTCTATC 1800
ATACAGCATA TGATATATCT GTATAATCAT GCCGGTCATC CATGGAAAGC TCAGGAGAGA 1860
CTACGCGAAG TGATGGGGCG GCTCTATCGT CCTACTCCGG ATGGGTATTG CGGCGATGAA 1920
GACAAACGAC AGACTTCGGC TTGGTACGTT TTCTCTGCTT TAGGCTTCTA TCCTGTTACA 2040
15 CCGGCTACGG ATCAGTATGT GCTCGGTTCC CCGATTTTTT CCAAGGTAAT ACTCTCTTTT 2100
CCGACGAGAC ACAAACGGT GTTGCATGCT CCGGCCAACA GTGCCGATAC GCCTTACATC 2160
CGCTCGATCA CGGTAGAAGG AAAAGAATGG AGCTGCAATT ACCTGACTCA CGAACAGCTT 2220
CGCTCTTCTG CATCCATTCA ATGGATGATG GACACGAAAC CCAATTATAA TCGTGGTATG 2280
AAGGAAAGTG ACAGACCTTA TTCTTCTCC ACGGAGCAAC AGCGTCGCGC TAATCACACT 2340
20 AAT 2343

(2) INFORMATION FOR SEQ ID NO:247

- 25 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 30 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 40 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

45 ATGATGAAT CCATGCGCAG CGTGCTGTTG CTACTCTTTC CATTGTCTTT GATCACTGCT 60
TTGGGCTGTA GCAATAACAA AGCTGCCGAA TCGAAGTCTG TCTCTTTTGA TTCGGCCTAT 120
CTCGAACGCT ACATCCCTCT GCGGGCAGAC ATAGATACGC CATCGCTGCA TGTGATGATC 180
AGCTACGCTT ATCCTTCGGG AGATGATATG CTCACAGAGA TTTTCAACGG TTTGCTCTTC 240
50 GCGCACAGCC TGATGGATTG CTCTTCGCGG GAGAATGCCA TGGAAAGGCTA TGCACAGATG 300
CTGGGAGAAG ACTATCGCTC TAACAATGCC GAAGCCAATC TGCAAGGGCT TCCTTCTGAC 360
CTTTTGGACT ATATCTACAA GCAGGAAAAT ACCATCGCTT ATTGCGATAC GGGATTGATC 420
TCCACGCGCA TCAATACATA TACTTACGAA GCGGGTGCAAC ATACGGAGAA TACAGTCCGG 480
TTTGCCAAACA TCCTTCGCAC CACCGGCAAG GTGCTCGAAG AGCGAGATAT ATTCAAGATC 540
GACTATGCGG AARGGCTGTC CGCACTCATC ATAGGCAAT TGGTGACGA TTTGCGCAAG 600
55 ACCACACCTG CCGAATTGGA TGCAATAGGT TTCTTCAAG CAGAAGAAAT ACAGCCCAAT 660
GGCAATTTTA TGATCGATGA CAAAGGTCTC ACATCTGTT TCAATGAGTA TCAGATAGCT 720
GCTTATGCCA GAGGTGCTGT CTATGTCCTG CTGGGATATG ACGTATTGGC TCCTTTGCTA 780
60 AGGGATGATT CCCCACTAAA GCGTTACTTG CCG 813

(2) INFORMATION FOR SEQ ID NO:248

- 65 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 70 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 75 (vi) ORIGINAL SOURCE:

169/ 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

5 (A) NAME/KEY: misc_feature
(D) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

10 ATGAAATCCA TGGCGAGCGT GCTGTTGCTA CTCTTTCCAT TGTCTTTGAT CACTGCTTTG 60
GGCTGTAGCA ATAACAAAGC TGCCGAATCG AAGTCTGTCT CTTTCGATTC GGCCTATCTC 120
GAACGCTACA TCCCTCTGCG GGCAGACATA GATACGCCAT CGCTGCATGT GATGATCAGC 180
TACGTCTATC CTTGGGAGAG TGATATGCTC ACAGAGATTT TCAACGGTTT GCTCTTCGGC 240
GACAGCCTGA TGGATTCTCT TTCGCCGCGAG AATGCCATGG AAGGCTATGC ACAGATGCTG 300
GGAGAAGACT ATCGCTCTAA CAATGCCGAA GCCAATCTGC AAGGGCTTCC TTCTGACCTT 360
15 TTGGACTATA TCTACAAGCA GGAATAATACC ATCGCTTATT GCGATACGGG ATTGATCTCC 420
ACGGCATCA ATACATATAC TTACGAAGGC GGTGCACATA CGGAGAATAC AGTCCGGTTT 480
GCCAACATCC TTCCGACCAC CGGCAAGGTG CTCGAAGAGC GAGATATATT CAAGATCGAC 540
TATCGGAAA GGTGTGCGC ACTCATCATA GGACAATTGG TGCACGATT CCGCAAGACC 600
ACACCTGCCG AATTGGATGC AATAGGTTTC TTCAACGCAG AAGAAATACA GCCCAATGGC 660
20 AATTTTATGA TCGATGACAA AGGTCTCACA TACTGTTTCA ATGAGTATCA GATAGCTGCT 720
TATGCCAGAG GTGCTGTCTA TGTCCGTCTC GGATATGACG TATTGGCTCC TTTGCTAAGG 780
GATGATTCCT CACTAAAGCG TTACTTGCCG 810

25 (2) INFORMATION FOR SEQ ID NO:249

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

45 (A) NAME/KEY: misc_feature
(B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

50 ATGCGCAGCG TGCTGTTGCT ACTCTTTCCA TTGTCTTTGA TCACTGCTTT GGGCTGTAGC 60
AATAACAAG CTGCCGAATC GAAGTCTGTC TCTTTCGATT CGGCCTATCT CGAACGCTAC 120
ATCCCTCTGC GGGCAGACAT AGATACGCCA TCGCTGCATG TGATGATCAG CTACGTCTAT 180
CCTTCGGGAG ATGATATGCT CACAGAGATT TTCAACGGTT TGCTCTCGG CGACAGCCTG 240
ATGGATTCTT CTTCCGCCGA GAATGCCATG GAAGGCTATG CACAGATGCT GGGAGAAGAC 300
TATCGCTCTA ACAATGCCGA AGCCAATCTG CAAGGGCTTC CTTCTGACCT TTTGGACTAT 360
55 ATCTACAAGC AGGAAAATAC CATCGCTTAT TGGGATACGG GATTGATCTC CACGCGCATC 420
AATACATATA CTTACGAAGG CGGTGCACAT ACGGAGAATA CAGTCCGGTT TGCCAACATC 480
CTTCGCACCA CCGGCAAGGT GCTCGAAGAG CGAGATATAT TCAAGATCGA CTATGCCGAA 540
AGGCTGTCCG CACTCATCAT AGGACAATTG GTGCACGATT TCGGCAAGAC CACACCTGCC 600
GAATTGGATG CAATAGGTTT CTTCAACGCA GAAGAATAC AGCCCAATGG CAATTTTATG 660
ATCGATGACA AAGGTCTCAC ATACTGTTTC AATGAGTATC AGATAGCTGC TTATGCCAGA 720
60 GGTGCTGTCT ATGTCGTCTC CGGATATGAC GTATTGGCTC CTTTGCTAAG GGATGATTC 780
CCACTAAAGC GTTACTTGCC G 801

65 (2) INFORMATION FOR SEQ ID NO:250

(i) SEQUENCE CHARACTERISTICS:

70 (A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

75 (iii) HYPOTHETICAL: NO

170/ 490

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

ATGAAAAAAA	CTACTTTGAC	AGGATCGATA	TGTGCTTTAC	TCCTGTTTTT	GGGTCTCTCG	60
GCCCAATGCCC	AATCGAAGTT	AAAGATCAAG	AGCATTGAGG	CAGCTACCCAC	TTTCAGTTTCG	120
GCCACGGCOG	GAAATGGTIT	TGGTGGCAAT	ATCTTCGGCA	TGGACATGAG	CATACGGATG	180
AGGSTACACC	ACAGCATTCT	GCCCGAAGGG	TTGGATTTTT	CGGTAGGAAT	ACATGAAAGA	240
AGAGCACACT	GGGAAGAGGC	CGGAAGTCCG	AAGCTCATGT	ATACGAATGT	CCCAAGTATC	300
ATTGGTATTG	TTGAAAAGGT	AATAGTCTTC	GAAGACGCG	AAGACTTTTT	TGACAAAAAA	360
GCTCTCGGCC	GCTTCCTCAT	CAGTTTGGGG	ATATCCTATA	CCAAGCATCT	GGGAGCGTAT	420
TGGGGATGGA	CCAATGACGC	CCATATTCTT	TTCTCACCAG	TACCCAAGAG	CAAGGTCCAC	480
TATGACACCT	ACACAAGAGC	TGGCAGTGAC	CTTGTACTTC	AGTCCGAAGA	TGTTGCCACA	540
GTGAGCAATG	GCTTTTCACC	GGGGATCGGA	CTCAAAAGTT	CTATTGGGTG	GAAATGCCCC	600
ATCAAGAGCA	AATATGATTT	TGCCTCGGT	TTCAAGCCTG	GCTATGAGTA	TCTGAACCTG	660
CTATATCCGT	ATCGTAATTT	CAAGCTGGAT	GGAAATAAGC	CGCTTTCAGC	ACTATCTCCT	720
CGCATGAACC	ACATCGGCCA	TGTGGGCTTC	AACCTTACCG	TGGGTCTTTG	GACTAAT	777

(2) INFORMATION FOR SEQ ID NO:251

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...3798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

ATGGGCAAGT	ATAAAGAGC	TAAGTACGCG	TATGGCTTT	TTCTTTCTG	TTGGGATTAT	60
TATACCTTTG	AGGGAGTTAC	TTTTTTATGC	GCATCTGAAG	ATATGACAAC	CAAGAAACCC	120
CAAGCCATTT	TAGACTTAGA	GAAGGCCTAT	AACATTGAAA	TTCTTGATCT	CTCCTCACAA	180
GAAGGGATAA	GCTGGTCGGT	AAATAGATAT	TTCAAGCAAG	ATTCTTCGGG	TGCAGTCGTT	240
GAGCTTTGCT	TGGCAGAAATG	TCAGATAGAA	AGCATGACTT	GGCTTATTGA	TTTTCTCTGCT	300
CTAAAAAAGC	TTGATCTATC	GTATAACCAA	ATCAGTAAGC	TAGAGGGTCT	AGAAGCTCTT	360
ACTTCGTAA	CAAAACTTCG	TCTAAGAGT	AAACCAATCC	GTAAGCTAGA	GGGCTTGGAT	420
AGTCTCACCT	CGCTAACAAA	ACTTCTCTC	TCCGATAACC	AAATCAGTAA	GCTAGAGGGT	480
CTGGAACGTC	TCACCTCGTT	AGCGGAGCTT	TATCTTTTGG	ATAACCAAT	CAGTAACTA	540
GAGGCTCTGG	AACGCTCAC	GTCTTACCA	ACGCTTGAAC	TATCGGGTAA	CCAAATCCGT	600
AAGCTGGAGG	GTCTGGAACG	TCTCACGTCC	TTAGCAACGC	TTGAATATC	GGGTAACCAA	660
ATCCGTAAGC	TAGAGGGTCT	GGAAACGTCT	ACTTCGTAA	CAAAGCTTCG	TCTAAGAGT	720
AACCAATCA	GTAAGCTAGA	GGGTCTGGA	CGTCTCAGT	CCTTAGCAAC	GCTTGAACCTA	780
TCGGGTAAAC	AAATCCGTAA	GCTGGAGGGT	CTGGAACGTC	TACGTCCTT	AGCAACGCTT	840
GAACCTGTCG	GTAACCAAT	CAGTAAGCTA	GAGGGTCTGG	AACGCTCTCT	TTCTGTTAACA	900
AAAGCTTCGTC	TAAGAAGTAA	CCAGATCAGT	AAACTAGAGG	GCCTGGAACG	TCTCACCTCG	960
CTAACAAAAC	TTTCTCTCTC	CGATAACCAA	ATCAGTAAGC	TAGAGGGTCT	GGAACTCTCT	1020
ACCTCGTTAG	CGGAGCTTTA	TCTTTTGGAT	AAACCAATCC	GTAAGCTGGA	GGGCTTGGAA	1080
CGTCTCACT	CGTTAACAAA	GCTTCGTCTA	AGAAGTAACC	AAATCAGTAA	ACTAGAGGGC	1140
CTGGATAGCT	TACCTCGCT	AACAAAACCT	TCTCTCTCCG	ATAACCAAT	CAGTAACTA	1200
GAGGGCTCTG	AACGCTCTAC	GTCTTAGCG	GAGCTTTATC	TTTTGGATAA	CCAAATCCGT	1260
AAGCTGGAGS	GTCTTGATGG	TCTTGCTTCC	TTAACAAAGC	TTAGTCTAAG	GCGCAACCAA	1320
ATCAGTAAGC	TGGAAGGACT	AGACAGACTA	AAGGTTTGA	GAAAACCTGA	TGTTTCGGGC	1380
AATGATATTC	AATCTATTGA	TGATATTAAG	CTATTGGCTC	CGATTCTGGA	GCAAACTTCT	1440
GAAAACTGA	GAATCCATGA	CAATCCATTT	GTTGCATCAT	CAGGCTTGAT	ACTCTCTCCT	1500
TATGATAATC	ATTTCGGGGA	GATTAAAGCT	CTTCTTGAAA	AAGAAAAAGA	AAAACAGAAA	1560

171/ 490

5 AAGACTTCAG TTGAATATCA CCCATTTTGC AAAGTAATGC TATTGGGAAA TCATTCTTCG 1620
GGTAAACAA CATTTCTTAG TCAATACGAT ACAAATTATA CGTATCAGAA AAATACACAT 1680
GTGTTGTCGA TACATCGAAG CAATAACCCT AATCGGATCT TTTACGACTT TGGGGGACAG 1740
GACTATTATC ATGGGATTTA CCAAGCCTTT TTTACCACCC AATCGTTATA CCTTCTCTTT 1800
TGGGATGCTA AGAAGGATCG AAACCTTTGTG AGCGTAGATG ATAAAGAATA TCAGACTCTT 1860
AATTTCAATC GCCCCTATTG GTTAGGACAG ATAGCCTATG CCTGCAATCG TTGTATGTCC 1920
GTTGGAGGAA ATCCTGATGG CAAGGACACA CCACAGACCA CAGACGATAC AATTATCATT 1980
CAGACTCATG CCGATGAAAC GGGCGCTAAG CAGCAACCT TAGGCTGTGC AGCCGAGAAT 2040
GGAGTATTGG AAGAAATCTA TGTATCCTTA GAGCCCAAGG CGAATAGTGC CGTACATGGG 2100
10 CTCAACTATC TGAATGAGCG GGTGCGAGAA GTTGTGCGAA GCAGGAGTAA ATCAATTGAG 2160
ATCACAGAAA AAGATAAGGG ATTGTACGAA GCTCTTCCCA CAATCGCCGG TGATAATAAA 2220
CACATGCCCTA TCTCTCTCGA AGCTCTTGCG GCTCAATTGA ATAAGGGAAG AGCTGAAAAT 2280
GATCTTTACA CCATAGAGTA TCTACAGACC GAATTGAACC AGCTTAGTCT GCGAGGGGAG 2340
GTGCTTTACT ATCGTGAGAA TGAGAAGCTG AACAAATTATG TCTGGTTAGA TCCGGCAGCT 2400
15 TTTGCCAAA TGATTATGG AGAAATCCTC CAAAAGACA ACATCAATAG AGGAACAGTT 2460
CCTAAAGACA TTTTGAATG CAACTGCAAT AATCTAAGTT CCGGAAGTAT ATTTGAAGAA 2520
GATGCCAAA ATGGTAATAT GATCTTGCG AGCTCTTGCG AAGAGCTGAT CGTATATGAA 2580
GATAAGGACT GCTATGTGAT ACCGGGCTAT CTCCCTTTGC ATTCCGATGA CGAAGCCTAT 2640
20 AAATGGCTTA CTTTGGGATT CGAGAGSCCC AATTTTGTCC TCAAAATCGA ACCTTTTATC 2700
CCCTTTGGCC TGATCAACCA GATTATAGCC TACTATGGCC GGGAGAAGG TGCTCTAAG 2760
CGGTATTGGC GAGATCAGGT CATCTTCACA GCAGGCCGTG AGATGGATAG GCAAACGCTT 2820
GAGCAAGAAG AAGAGAAAGA GGGTTTGGCC AAGACGAATG CCGAGGATTA TCAGATCTGG 2880
ATCAAGCTCG ACTTTACCGA CTTGGCCATA TCCGTATTCA TCAAGAGACA GAGAAAGACA 2940
25 TCAGCTAAGG ATATGACGG GAAAGAGGCT ACTATCCTCA GTGATATGTT GGATATGTAT 3000
TGGAACAATA TCCCTCCGAG GGAGCAAATA GGAGATAAGG ATACGGACCA AACGAGAAGC 3060
ACTATTCTGT AAACAACAG AAAGAAGAGA CCCATCCAGG ATCTCTACCT CTCTGTGCC 3120
CAAGCGGATA AAGATTGAC GGAGTCTCAT TATATCCATT TGGGCACGCT GGACGATGAA 3180
AGCAAGACTA CGGCGAGGAT TGCAGCCTAT CCGTTGAAGA ACGCGGTTAT CGATAAAGAG 3240
CGGGTGCGAG AAGTATCGAC TCGTCCCTAC AAACATCTTT CCGTCAATAA AAATCTGGCT 3300
30 ACTGCAAAA ACATCTTTAT TTCTTATCC AAAGAGGATC AGACTGAATC GGAGACCTGT 3360
CTGCAATTTT TCAACCCCTT GGAGAAGAAT GGTGAGATCG AGATCTACTA TGATAAGTTG 3420
ACTAAGTTTG AAACACCTAT TCACCCCTGAA ATAAAGAAAGC GTATTGTGGA AGCCGAGTGT 3480
ATAATCGCTT TGATCAGCCA ACGCTATCTG GCCACGGATT ACATCCTGGA TCATGAGTTG 3540
35 CCTGTATTTC GGGAGTATAA CAAGACCATA GTGCCSATAT TGATCAAGCC TTGTACATT 3600
GAAGACGATG AGTTCCCTCG GGAGAAATAT TTTGCTCAGA AAGCTCAAT AATCAATCTT 3660
GGAAAGAGG GAAACCAAT TAAAGCTTAT GATAGTATTA CGGCATCAGC CCATCGTGAT 3720
GAAATTTGGG TGGCAGTAGT CAGAGAGTTC AAAGAGAAGA TATTAAGAAAT AACAAAACAG 3780
GAGGTAAATA CAGATGAA 3798

(2) INFORMATION FOR SEQ ID NO:252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION: 1...3696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

65 ATGACAACCA AGAAACCCCA AGCCATTTTA GACTTAGAGA AGGCCTATAA CATTGAAATT 60
CCTGATCTCT CCTCACAAGA AGGGATAAGC TGGTCGGTAA ATAGATATTT CAAGCAAGAT 120
TCCTCCGGTG CAGTCGTTGA GCTTTGCTTG CGAGAATGTC AGATAGAAAG CATGACTTGG 180
CTTATTGATT TTCTGCTCT AAAAAAGCTT GATCTATCGT ATAAACCAAT CAGTAAGCTA 240
GAGGCTCTAG AACGCTTAC TTGTTAACA AAACCTCGTC TAAGAAGTAA CCAATCCGT 300
70 AAACCTAGAGG GCCTGGATAG TCTACCTCG CTAAACAAAC TTTCTCTCTC CGATAACCAA 360
ATCAGTAAGC TAGAGGGTCT GGAACGCTC ACCTCGTTAG CGGAGCTTTA TCTTTTGGAT 420
AACCAATCA GTAACCTAGA GGGCTGGAAC CGTCTCACGT CCTTAGCAAC GCTTGAACTA 480
TCGGGTAAAC AAATCCGTAA GCTGGAGGGT CTGGACGCTC TCACGCTCTT AGCAACGCTT 540
AACTATCGG GTAACCAAT CCGTAAGCTA GAGGGTCTGG AACGCTCTAC TTGTTAACA 600
75 AAGCTTCGTC TAAGAAGTAA CCAATCAGT AAGCTAGAGG GTCTGGAACG TCTCAGTCC 660
TTAGCAACGC TTGAACATC GGTAACCAA ATCCGTAAGC TGGAGGGTCT GGAACGCTCT 720

ACGTCCTTAG CAACGCTTGA ACTGTGCGGT AACCAATCA GTAAGCTAGA GGGTCTGGAA 780
CGTCTCTCTT CGTTAACAAA GCTTCGTCTA AGAAGTAACC AGATCAGTAA ACTAGAGGGC 840
CTGGAAACGTC TCACCTCGCT AACAAAACCT TCTCTCTCCG ATAACCAAT CAGTAAGCTA 900
GAGGGTCTGG AACGCTCTAC CTCGTAGCG GAGCTTTATC TTTTGGATAA CCAATCCGT 960
AAGCTGGAGG GCCTGGAACG TCTCAGCTCG TTAACAAAGC TTCGTCTAAG AAGTAACCAA 1020
ATCAGTAAAC TAGAGGGGCT GGATAGTCTC ACCTCGCTAA CAAAACCTTC TCTCTCCGAT 1080
AACCAATCA GTAAACTAGA GGGCCTGGAA CGTCTCAGT CCTTAGCGGA GCTTTATCTT 1140
TTGGATAACC AATCCGTAA GCTGGAGGGT CTTGATGGTC TTGCTTCCTT AACAGGCTT 1200
AGTCTAAGGC GCAACCAAT CAGTAAGCTG GAAGGACTAG ACAGACTAAA GGTTTTGAGA 1260
AAACTTGATG TTTGGGCAA TGATATTCAA TCTATTGATG ATATTAAGCT ATTGGCTCCG 1320
ATTCTGGAGC AAACTTTAGA AAACTGAGA ATCCATGACA ATCCATTGT TGCATCATCA 1380
GGCTTGATAC TCTCTCTTA TGATAATCAT TTGCCGGAGA TTAAGCTCT TCTTGA AAAA 1440
GAAAAGAAA AACAGAAAA GACTTCAGTT GAATATCACC CATTTTGCAA AGTAATGCTA 1500
TTGGGAAATC ATTCTTCGGG TAAAACAACA TTTCTTAGTC AATACGATAC AATTTATAGG 1560
TATCAGAAAA ATACACATGT GTTGTGATA CATCGAAGCA ATAACCTTAA TCGATCTTT 1620
TACGACTTTG GGGGACAGGA CTATTATCAT GGGATTTACC AAGCCTTTT TACCACCCAA 1680
TCGTTATACC TTCTCTTTG GGATGCTAAG AAGGATCGAA ACTTTGTGAG CGTAGATGAT 1740
AAGAAATATC AGACTCTTAA TTTCAATCGC CCCTATTGGT TAGGACAGAT AGCCTATGCC 1800
TGCAATCGTT GTATGTCGT TGGAGGAAAT CCTGATGGCA AGGACACACC ACAGACCACA 1860
GACGATACAA TTATCATTCG GACTCATGCC GATGAAAGCG GCGCTAAGCA GCAAACTTA 1920
GGCTGTGCAG CCGAGAATGG AGTATTGGAA GAAATCTATG TATCTTAGA GCCCAAGGCG 1980
AATAGTGCCG TACATGCGCT CAACATCTG AATGAGCGGG TGCGAGAAGT TGTGCGAAGC 2040
AGGAGTAAT CAATTCAGAT CACAGAAAA GATAAGGGAT TGTACGAAGC TCTTCCACA 2100
ATCGCCGGTG ATAATAACA CATCCCTATC TCTCTCGAAG CTCTTGGGCG TCAATTGAAT 2160
AAGGGAAGAG CTGAAATGA TCTTTACACC ATAGAGTATC TACAGACCGA ATTGAACCAG 2220
CTTAGTCTGC GAGGGGAGGT GCTTTACTAT CGTGAGATG AGAAGCTGAA CATATTGTC 2280
TGGTTAGATC CGGCAGCTTT TGTCCAAATG ATTCATGGAG AATCCTCCA AAAAGACAAC 2340
ATCAATAGAG GAACAGTTC TAAAGACATT TTTGAATGCA AACTGCATA TCTAAGTTCC 2400
GGAAGTATAT TTGAGAAGA TCGCCAAAT GGTAAATGA TCTTGCACT ATTTATGGAA 2460
GAGCTGATCG TATATGAAGA TAAGGACTGC TATGTGATAC CGGCTATCT CCGTTTGATC 2520
TCCGATGACG AAGCCTATA ATGGCTTACT TTGGGATTCG AGAGGCCCAA TTTTGTCTC 2580
AAATTCGAAC GTTTTATCCC CTTTGGCCTG ATCAACCAGA TTATAGCTTA CTATGGCCCG 2640
GAAGAAGGTG CTCTAAAGCG GTATTGGCGA GATCAGGTCA TCTTCACAGC AGGCCGTGAG 2700
ATGGATAGGC AAACGCTTGA GCAAGAGAA GAGAAAGAGG GTTTGCCCAA GACCAATGCC 2760
GAGGATTATC AGATCTGAT CAAGCTCGAC TTTACCGACT TGGCCATATC CGTATTATC 2820
AAAGAGCAGA GAAAGACATC AGCTAAGGAT ATGCAGCGGA AAGAGGCTAC TATCCTCAGT 2880
GATATGTTGG ATATSTATTG GAACAATATC CCTCCGAGG AGCAAAATAGG AGATAAGGAT 2940
ACGAGACAAA CGAGAAGCAC TATTCGTGAA ACNACAGAA AGAAGAGACC CATCCAGGAT 3000
CTCTACCTCT CCTGTGCCCA AGCGGATAAA GATTGACGG AGTCTCATT TATCCATTG 3060
GGCAGCTGG ACGATGAAAG CAAGACTACG GCGAGGATTG CAGCCTATCC GTTGAAGAAC 3120
GGCGTTATCG ATAAAGAGCG GGTGCGAGAA GTATCGACTC GTCCCTACAA ACATCTTTCC 3180
GTCAATAAAA ATCTGGCTAC TGCAAAACAG ATCTTTATTT CCTATTCCAA AGAGGATCAG 3240
ACTGAACCTGG AGACCTGTCT GCAATTTTTC AAACCTTGG AGAAGAATGS TCAGATCGAG 3300
ATCTACTATG ATAAGTTGAC TAAGTTTGAA ACACCTATTC ACCCTGAAAT AAGAAAGCGT 3360
ATTGTGGAAG CCGACTGTAT AATCGCTTTG ATCAGCCAAC GCTATCTGGC CACGGATTAC 3420
ATCTGGATC ATGAGTTGCC TGTATTTCGG GAGTATAACA AGACCATAGT GCCGATATTG 3480
ATCAAGCCTT GTACATTCGA AGACGATGAG TTCCTTGGGG AGAAATATTT TGCTCAGAAA 3540
GCTCAATAA TCAATCTTGG AAAAGAGGGA AAAACCATTA AAGCTTATGA TAGTATTACG 3600
GCATCAGCCC ATCGTATGA AATTTGGGTG GCAGTAGTCA GAGAGTTCAA AGAGAAGATA 3660
TTAAGAATAA CAAAACAGGA GGTAAATACA GATCAA 3696

(2) INFORMATION FOR SEQ ID NO:253

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3525 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 60 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 65 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 70 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3525
- 75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

173/ 490

	ATGACTTGGC	TTATTGATT	TCCTGCTCTA	AAAAAGCTTG	ATCTATCGTA	TAACCAATC	60
	AGTAAGCTAG	AGGGTCTAGA	ACGTCTTACT	TCGTAAACAA	AACCTCGTCT	AAGAAGTAAC	120
	CAAAATCCGTA	AACTAGAGGG	CCTGGATAGT	CTCACCTCGC	TAACAAAAC	TTCTCTCTCC	180
	GATAACCAAA	TCAGTAAGCT	AGAGGGCTCTG	GAACGTCTCA	CCTCGTTAGC	GGAGCTTTAT	240
5	CTTTTGGATA	ACCAATCAG	TAAACTAGAG	GGTCTGGAAC	GTCTCAGTCT	CTTAGCAACG	300
	CTTGAACAT	CGGGTAACCA	AATCCGTAA	CTGGAGGGTC	TGGAACGTCT	CACGTCTCTA	360
	GCAACGCTTG	AACTATCGGG	TAACCAAAATC	CGTAAGCTAG	AGGGTCTGGA	ACCTCTCACT	420
	TCGTAAACAA	AGCTTCGTCT	AAGAAGTAAC	CAAATCAGTA	AGCTAGAGGG	TCTGGAACGT	480
	CTCACGTCTCT	TAGCAACGCT	TGAACTATCG	GGTAACCAAA	TCCGTAAGCT	GGAGGGTCTG	540
10	GAACGTCTCA	CGTCTTAGC	AACGCTTGAA	CTGCGGGTA	ACCAATCAG	TAAGCTAGAG	600
	GGTCTGGAAC	GTCTCTCTC	GTTAACAAAG	CTTCGTCTAA	GAAGTAACCA	GATCAGTAAA	660
	CTAGAGGGCC	TGGAACGTCT	CACCTCGCTA	ACAAAACCTT	CTCTCTCGA	TAACCAAAATC	720
	AGTAAGCTAG	AGGGTCTGGA	ACGTCTCACC	TCGTAGCGG	AGCTTTATCT	TTTGGATAAC	780
	CAAAATCCGTA	AGCTGGAGGG	CCTGGAACGT	CTCACCTCGT	TAACAAAGCT	TCGTCTAAGA	840
15	AGTAACCAAA	TCAGTAACT	AGAGGGCCTG	GATAGTCTCA	CCTCGCTAAC	AAAACCTTCT	900
	CTCTCCGATA	ACCAATCAG	TAAACTAGAG	GGCCTGGAAC	GTCTCAGTCT	CTTAGCGGAG	960
	CTTTATCTTT	TGGATAACCA	AATCCGTAA	CTGGAGGGTC	TTGATGGTCT	TGCTTCTCTA	1020
	ACAAGGCTTA	GTCTAAGGCG	CAACCAAAATC	AGTAAGCTGG	AAGGACTAGA	CAGACTAAAG	1080
20	GTTTGGAGAA	AACTTGATGT	TTGCGGCAAT	GATATTCAAT	CTATTGATGA	TATTAAGCTA	1140
	TTGCTCCGTA	TTCTGGAGCA	AACTTTAGAA	AAACTGAGAA	TCCATGACAA	TCCATTGTGT	1200
	GCATCATCAG	CTTGATACT	CTCTCTTTAT	GATAATCATT	TGCCGGAGAT	TAAAGCTCTT	1260
	CTTGAAGGAA	AAAAAGAAAA	ACAGAAAAAG	ACTTCAGTTG	AATATCACCC	ATTTTGCAAA	1320
	GTAATGCTAT	TGGGAAATCA	TTCTTGGGT	AAAACAACAT	TTCTTAGTCA	ATACGATACA	1380
25	AATATACGT	ATCAGAAAAA	TACACATGTG	TTGTGATAC	ATCGAAGCAA	TAACCTAAT	1440
	GCATCTTTT	ACGACTTTGG	GGGACAGGAC	TATTATCATG	GGATTACCA	AGCCTTTTTT	1500
	ACCACCAAT	CGTTATACCT	TCTCTTTTGG	GATGCTAAGA	AGGATCGAAA	CTTTGTGAGC	1560
	GTAGATGATA	AAGAATATCA	GACTCTTAAT	TTCAATCGCT	CCTATTGGTT	AGGACAGATA	1620
	GCCTATGCCT	GCAATCGTTG	TATGTCCGTT	GGAGGAAATC	CTGATGGCAA	GGACACACCA	1680
	CAGACCCAG	ACGATACAAT	TATCATTCAG	ACTCATGCCG	ATGAACGGGG	CCCTAAGCAG	1740
30	CAAACTTAG	GCTGTGCAGC	CGAGAAATGA	GTATTGGAAG	AAATCTATGT	ATCCTTAGAG	1800
	CCCAGGCSA	ATAGTCCCT	ACATGCCGCT	AACTATCTGA	ATGAGCGGGT	GCGAGAAGTT	1860
	GTCCGAAGCA	GGAGTAAATC	AATTCAGATC	ACAGAAAAAG	ATAAGGGATT	GTACGAAGCT	1920
	CTTCCCAAA	TCCCGGTGA	TAATAAACAC	ATCCCTATCT	CTCTCGAAGC	TCTTGCGGCT	1980
35	CAATTGAATA	AGGGAAGAGC	TGAAAAATGAT	CTTACACCA	TAGAGTATCT	ACAGACCGAA	2040
	TTGAACGAGC	TTAGTCTGCG	AGGGGAGGTG	CTTACTATC	GTGAGATGA	GAAGCTGAAC	2100
	AATATGTCT	GGTTAGATCC	GGCAGCTTTT	GTCCAAATGA	TTGATGGAGA	AATCTTCCAA	2160
	AAGACAACA	TCAATAGAGG	AACAGTTCTT	AAAGACATTT	TTGAATGCAA	ACTGCATAT	2220
	CTAAGTCCG	CAAGTATATT	TGAAGAAGAT	GGCCAAAATG	GTAATATGAT	CTTGAGCTA	2280
40	TTATTGGAAG	AGCTGATCGT	ATATGAAGAT	AAGGACTGCT	ATGTGATACC	GGGCTATCTC	2340
	CCTTTGCTAT	CCGATGACGA	AGCCTATAAA	TGGCTTACTT	TGGGATTGGA	GAGGCCCAAT	2400
	TTTGTCTCTA	AATTGGAACG	TTTTATCCCC	TTTGGCTGTA	TCAACAGAT	TATAGCCTAC	2460
	TATGGCCGGG	AAGAAGGTGC	TCTAAAGCGG	TATTGGCGAG	ATCAGGTCTAT	CTTCACAGCA	2520
	GGCCGTGAGA	TGGATAGGCA	AACGCTTGAG	CAAGAAGAG	AGAAAGAGGG	TTTGCCCAAG	2580
45	ACGAATGCCG	AGGATTATCA	GATCTGGATC	AAGCTCGACT	TTACCGACTT	GGCCATATCC	2640
	GTATTCATCA	AAGAGCAGAG	AAAGACATCA	GCTAAGGATA	TGCAGCGGAA	AGAGGCTACT	2700
	ATCCTCAGTG	ATATGTTGGA	TATGTATTTG	AACAATATCC	CTCCGAGGGA	GCAATAGGA	2760
	GATAAGGATA	CGGAGCAAA	GAGAAGCACT	ATTCTGTAAA	CAAAACAGAA	GAAGAGACCC	2820
	ATCCAGGATC	TCTACCTCTC	CTGTGCCCAA	GCGGATAAAG	ATTTGACGGA	GTCTCATTTAT	2880
50	ATCCATTGG	GCACGCTTGA	CGATGAAAGC	AAGACTACGG	CGAGGATTGC	AGCCTATCCG	2940
	TTGAAGAACG	GGGTTATCGA	TAAAGAGCGG	GTGCGAGAG	TATCGACTCG	TCCCTACAAA	3000
	CATCTTTCCG	TCAATAAAAA	TCTGGCTACT	GCAAAACAGA	TCCTTATTTG	CTATTCCAAA	3060
	GAGGATCAGA	CTGAACCTGA	GACCTGTCTG	CAATTTTTC	AACCTTTGGA	GAAGAATGGT	3120
	CAGATCGAGA	TCTACTATGA	TAGTTGACT	AAGTTTGAAA	CACCTATTCA	CCCTGAAATA	3180
55	AGAAAGCGTA	TTGTGGAAGC	CGACTGTATA	ATCGCTTTGA	TCAGCCAAAG	CTATCTGGCC	3240
	ACGGATTACA	TCTTGGATCA	TGAGTTGCCT	GTATTTGGGG	AGTATAACAA	GACCATAGTG	3300
	CGGATATTGA	TCAAGCCTTG	TACATTGAAA	GACGATGAGT	TCCTTCGGGA	GAAATATTTT	3360
	GCTCAGAAAG	CTCAAATAAT	CAATCTTGGA	AAAGAGGGAA	AAACCATTAA	AGCTTATGAT	3420
	AGTATTACGG	CATCAGCCCA	TCGTGATGAA	AATTGGGTGG	CAGTAGTCTAG	AGAGTTCAAA	3480
60	GAGAAGATAT	TAAGAAATAC	AAAACAGGAG	GTAATACAG	ATGAA		3525

(2) INFORMATION FOR SEQ ID NO:254

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

174/ 490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

5 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

10 ATGATGAAAA AAGCATTGTG TTTCTACTA CTGGTTTGCC TATTCTCCTC GTTCAGCAGT 60
TCCGCCCAAA CAAGACGAA CAGTAGCCGG AGTTATTTTA CAGGACGAAT CGAGAAGGTG 120
AGTTTGAACT TAGGGGTCCC CCCGTAAGC ACAGAGGTTT GGGGAATGAC CCATGATGCG 180
AACGGTCTCC CTTTCGAAAT ACCATCTCTT TTAGTCTGTT TCAACAGCCA GGGAGATATA 240
15 GCTACCACTT ATTACATAGC GAATAGCGAG GCAACTTTGA ATGAATGGTG CGACTATGCA 300
CACCCGGGCG GCATCGTGAG GGTAGAAGGT CGTTTTTGGA AAATGACTTA CAACATACCA 360
ACCTACAATG CAGTCTGCAC CCGGATTACA TTCGAAAATC AAGAATAGA AGGAACGATC 420
GTCTTGATAC CCAAGCCCAA AGTCTCGCTG CCTCATGTGT CGGAATCGGT GCCTTGCATC 480
CSAACCGAAG CCGGGAGGGA ATTTATCCTT TGCGAAGAAG ACGACACCTT TGTGTCTCAC 540
20 GATGGTAACG AAGTAACGAT AGGCGGTAAA CCTTCTTTCG TCAATACCAA CGTAAAGATT 600
GTGGGGGACG TATCTCAAAA GTATGCCGTG GGGGTAGGAG AAATTCGATT CCTGCAGATT 660
TGTGCCCAAA CAGTATCACA ACAAAAA 687

(2) INFORMATION FOR SEQ ID NO:255

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 684 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

40 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

45 ATGAAAAAAG CATTGTGTTT CGTACTACTG GTTTCCTAT TCTCCTCGTT CAGCAGTTCC 60
GCCCAAAACAA CGACGAACAG TAGCCGGAGT TATTTTACAG GACGAATCGA GAAGGTGAGT 120
50 TTGAACCTAG GGGTCCCCC CGTAAGCACA GAGGTTTGGG GAATGACCCA TGATGCGAAC 180
GGTCTCCCTT TCGAAATACC TATCTCTTTC AGTCGTTTCA ACAGCCAGGG AGATATAGCT 240
ACCACTTATT ACATAGCGAA TAGCGAGGCA ACTTTGAATG AATGGTGCGA CTATGCACAC 300
CCGGGCGGCA TCGTGAGGGT AGAAGGTGCT TTTTGAAAA TGAATTACAA CATACCAACC 360
TACAATGCAG TCTGCACCCG GATTACATTC GAAAATCAAG AATAGAAGG AACGATCGTC 420
55 TTGATACCCA AGCCCAAAGT CTGCTGCCCT CATGTGTCGG AATCGGTGCC TTGCATCCGA 480
ACCGAAGCCG GGAGGGAATT TATCCTTTGC GAAGAAGACG ACACCTTTGT GTCTCAGGAT 540
GGTAACGAAG TAACGATAGG CGGTAAACCT TTCTTGCTCA ATACCAACGT AAAGATTGTG 600
GGGACGATAT CTCAAAGTA TGCCGTGGGG GTAGGAGAAA TTCGATTCTT GCAGATTGTG 660
60 GCCCAACAG TATCACAACA AAAA 684

(2) INFORMATION FOR SEQ ID NO:256

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

70 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

75 (vi) ORIGINAL SOURCE:

175/ 490

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1620

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

10	ATGAAGACAA AAGTTTACG CAAATTCGTG GTGGCGGCTT TCGCCGTCGC AACCCCTCTGT	60
	CCTCTCGCCC AAGCGCAGAC GATGGGAGGA GATGATGTCA AGGTGGTCCA GTACAATCAG	120
	GAAAACTGGG TACAAACGAG GATGAGTGTG GCGGACACCG GATGGATCTA TGTAAATGACC	180
	CACAGTGGAT ACGACACCGG CAATAGCAAT GTGAAGATCT TCGCTCCAA AGACCAAGGT	240
	GCCACATACC AAAAGTTGAG GGATTGGGAT CCATCGGATG ATTATCAGTT TCAAGACTTC	300
15	GATATCGTGG TAACGGGTAA GAATGAATCC GACATCAAGA TTTGGTCCGT AGAGCTCATG	360
	AATAAGCCCG GAGGATATAA CAGTAGAGTT GCGGTCTTCA GTCGCGATGC CAACGCGCAG	420
	AATGCGAAAC TCGTGTATAA GGAAGACTTC TCCAATGTGC AGTTGTACGA TGTGGATATA	480
	GCCTCCAACT ATCGTTCCGC TTCTTCTCTT AACATGGTG GCAACCCCTT TGCTTTGGCT	540
	TTCCGTTACA CCGGCTTCAA CAATACGCAC AAAATAAGTT TGTGGACTA TGTGTTCTCT	600
20	CTGAATGGAG GGCAAAATTT CAATAAAAAC TTACTCTTCA GTCAAGATGG AGAGAAGAAA	660
	ATTGACAAGG TGGATCTCTC ATTGGGTAGC ACCTCTGAAT CCATGGGTCA CAATGCCTGG	720
	CCGCTAATGG GTGTGGTATT CGAAATGAAT AAACAAGGGG GAAAAAGCGA TATCGGTTTC	780
	TTGTCCGAAT TTGTGACAAA TGATCCCGAA TTTCAGTGGT CAGGCCCTAT AAAAGTGAGT	840
	GAAAGCGACA TCTCGTTCAG CCCCAAAATC CAAATGTGTC TGGACGAGGA TAACAAATACG	900
25	ATCAATGGGG AGAGTTGCCA CAACTTCATG ATTACGTACA GCGATTATGA TTCTGAATAT	960
	TCCGATTGGG ACATTCGGTA TGTATATCCC AAGAAATCCT TCAAGTATGA AAAAGGAAAA	1020
	ACTCCGACTA TGGATGATCT GGTGGAAGCT TTCCTTACAG CTTCGTACCA GAGTGAGACC	1080
	AATCCGGGCG TGGGGTATGA CAAGAAAGCTT AATCACTACC TGATTACATA TGCCAAAAAA	1140
	GAAGAGAACG GTACGAACAC GCTGAAATAC CGCTGGGCCA ATTATGACAA GATTCAATAC	1200
30	AAAGATTGGT GGAAGCGACAC ATTTACGTAT ACATCATCTG CCAATGCTCT CTACACACCT	1260
	CAAGTAGACA TCAATCCGAC CAAGGGTCTC GTGTGCTGGT CATGGGTGGA ATATCTGCCG	1320
	GGCAAAACGGA TCGTTTGGTC TGATACGCAG TGGACCCATG CCAACGGTGT AGAAGACATC	1380
	GTATATGAAG AAGGCAGCAT GAAGCTCTAC CCGAATCCGG CTCAGAATA TGCTGTGATT	1440
	AGCTGCGCGA CGGCAGCAAA CTGCAAGGCT GTTGTTTACG ATATGCAAGG CAGAGTAGTC	1500
35	GCTGAGGCTT CTTTCTCCGG CAACGAATAC AGGCTGAACG TGCAGCACTT GGCTAAGGGT	1560
	ACGTACATAC TCAAGGTCGT ATCCGATACG GAGCGTTTCG TAGAGAAGCT CATCGTGGAA	1620

(2) INFORMATION FOR SEQ ID NO:257

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 2313 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
45	(D) TOPOLOGY: circular
	(ii) MOLECULE TYPE: DNA (genomic)
	(iii) HYPOTHETICAL: NO
50	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
55	(ix) FEATURE:
	(A) NAME/KEY: misc_feature
	(B) LOCATION 1...2313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

60	ATGCTGACGA TCCGAAACTT CCTCCTCTTT TGTGTCTGT CGCTGATAGC GTTTGCTGCC	60
	GATGCACAAA GCTCTGTCTC TTCGGGTAGA CGACTGACAG AATATGTCAA TCCCTTTATC	120
	GGAAACGGCA ATTACGGTAC CACGAATCCG GAGGAGTAT TGCCCAATGG GTTGATGAGC	180
65	GTTACCCCTT TCAATGTCTG CGGATCGACA GAGAATCGCT TCGACAAAGA TTCCGCTTGG	240
	TGGAGTGGCC CTATTCCGGC CGACAATAGT TACTGCATCG GTTTCAGCCA TGTGAATCTG	300
	AGTGGAGTAG GCTGTCCCGA ACTGAGTGGG ATACTGTGTA TGGCCACTTC CGGCACATTC	360
	GATCCTGATT ACTGCTGCTA TGGCTCTTCG CTCAGTCCAG AATATGCCGG CCCGGGAGAA	420
	TACAGGCTGT TATTGGACAA ATACGGTATA GATGAGCCG TGACCGTAAC CGAGCGGACT	480
	GCTTTGACCG AATTGTCTTT TCCCGAAGGA GAAGGCCATA TCCTGCTGAA CCTGGGACAG	540
70	GCCCTAAGCA ATGAATCGGG AGCCTCTGTT CGATTCTTAA ACGACTCCAC AGTCGTGGGC	600
	AGCAGGCTGA TGGGGACGTT CTGCTACAA CCGCAAGCAG TTTTGTGCA GTATTTCTGA	660
	CTTCAGGTGA GTCCGCGACC GATCTCTGCC GGCTATTGGA AGAAGCAGCC TCCTATGACA	720
	GTGGAAGCCG AATGGGATTC GACTGCAGGG AATATAAGC AGTACGACGG CTACAAGCGT	780
75	AGATGAGCG GTGATGACAT CGGTGTCCGA TTCTCGTTCA ACTGCGATCA GGGGAAAAAG	840
	ATCTATGTAC GATCGGCCGT TTCATTCGTC AGCGAAGCCA ATGGGCTCTA TAACTGGA	900

176/ 490

5 GCGGAGCAAG AAGAGGTGTT CAAAGTGTG GGAGGGAATC CGGCCAAGGC TTTCTCCGCT 960
ATACGCTCTC GCGCTATAGA GCGTTGGGAG GAAGCCCTCG GTACGGTGGG AGTGGGAAGGA 1020
GGCACACCGG ATGAAAAGAC GATATTCTAT ACUGCACTCT ATCACCTGCT GATACATCCG 1080
AATATCCTAC AAGATGCCAA TGGAGAATAT CCTATGATGG GCAGTGGCAA AACGGGTAAT 1140
ACGGCTCACC ACCGCTACAC CGTGTCTCT CTTTGGGACA CGTACGCCAA TGTACACCGG 1200
CTGCTCTGCC TCCTCTATCC GGAGAAGCAG TTGGATATGG TACGGACACT GATCGACATG 1260
TACCGAGAGA GCGGGTGGCT GCCGAGATGG GAGCTGTACG GACAGGAGAC CCTGACGATG 1320
GAGGCGCACC CCTCGCTTAT CSTCATCMY SACTTGGC AAAGGGCCT TCGTCTTTC 1380
GATACGGCAA CGGCTATGA AGCCATGAAA AAAAATGCTT CTTCGGCAGG AGCGACCCAT 1440
CCGATCCGTC CTGACAACGA CGACTATCTC ACCCTCGGCT TCGTACCGCT TCGCGAACAG 1500
TACGACAATT CGGTATCGCA TCGCTGGAA TACTATCTG CCGACTGGAA TCTGTCCCG 1560
TTTGCCACG CACTTGGGCA TAAAGAAGAC GCAGCTCTAT TCGGAAAACG CTGTTGGGC 1620
TACGACACT ATTATAATAA GGAGTATGGT ATGCTGTGTC CATTGCTGCC GGATGGATCA 1680
TTCTCTACTC CTTTCGATCC CAAACAGGGT GAAAACCTCG AGCCTAATCC CGGTTTCCAC 1740
15 GAGGGCAGTG CTTATACTA TGCCTTTTTC GTTCCCGACG ATATACAAGG GCTTGGCCGG 1800
CTGATGGGAG GAGCAAGGT TTTTTCGGAA AGGTTSCAGA AAGTCTTGA TGAAGGATAT 1860
TATGATCGGA CCAACGAGCC GGACATCGCC TATCCTTACC TCTTCTCTA TTTCCCAAG 1920
GAAGCATGGC GAACGCAGAA ATTGACCCGG GAGTTGATAG ACAACATTT TTGCAATGCT 1980
CCTAACGGCT TGCCCGGTAA TGACGATGCC GGTACGATGA GTGCTTGGCT TGTCTATTCC 2040
20 ATGCTGGGAT TCTACCTGA CTGTCGGGC AGCCCCACCT ATACACTGAC CTGCGCGGTA 2100
TTCCCGGAG TTAGGATTCG GCTCAATCCG CAGTATTATC CTCAGGGGGA GTTGATCATT 2160
ACGACCMNTA CAGAGAATCA ACCGACAGAT TCCATTACA TCCATACGGT TTCTCTTGGC 2220
AATAAAACAC TTCGCGCATG AACAAGGCAT ATCAGCCATG CCGATTGGT GCGCTCGGCT 2280
CACCTCCGTT ACGAACTAAG CAATCGTCT CGA 2313

(2) INFORMATION FOR SEQ ID NO:258

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- 45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...2328
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

50 ATGTGCAAAA TAAGATTCAG CCTCTTCAG GCTCTGTG TCTGCTTATT GTTCACCTCT 60
TTTTCTCTCC AAGCTCAAGA GGAAGGTATT TGGAAATACC TCTTGGCTAT CCACAAGAGG 120
GAAAAAGCCG TAGAAGCCGC CAAGAAAGTC TTTGCCGTAG CCNACGGAGT ACTTTACTCG 180
GTGGGCAAGG AAGCTCCCCA TGAGGCAAGG ATCTTCGACC GTATCAGCGG ATCAGCGAT 240
ACATCGGTAA GCAGCATAGC CTACTCCGAG CAACTAAAAT CTTGGTCAAT ATACTATGCA 300
55 TCAGGCAATA TCGACATCTT GGACGAGCA GCGCGTGTGA CCAACGTACC TGCATTGAAA 360
GACAATATCG ATCTGATAGA CAAAACGCTC AATCGCCTTT TGATCGTAGG CAACAGGGCT 420
TATTTGSCAG GAGGATTCGG CCTCTCCGTT CTGGATGTG CCGAAGCTCG CATACCGGCT 480
ACCTAGGCCA AGGGAAGTAA GGTGACCGAT GTGGCTAAGT TGGACAATGA TCGCTTGTG 540
ATGCTGAAGG AAGGSCAGCT CTTCATCGGA AAAGAGACCG ATAACCTGCA AGATCCGGCC 600
60 GCATGGACAG CCTTGTCTTT GAATTTGCCG ATGGGCTCGG TCACCGGTCT GGGCATTGTC 660
GGGGAAGACA TCTGTTTCCT GCTGGCCGAT GGCCGTGTAT ATGTGCTGTC AAACCAATCG 720
TTTGAGCCGG AGCTATTGCT CTCTCTCTCC GCGATTAC GACTGTATGT GACGGATCGT 780
GGTCTGTTC TCTGTGCCGA GAATCGAATT TATTTCAATG AAAAAGGTCT CAAAACGACA 840
CAATTTCTTA TAGCCGAGCT CTTTGGGTGCT GGTGCCATGA ACGAAAGCAA TACGGCATA 900
65 ATAGCATTTG GAGAAGAAGG TTTGGCTTCA CTCTTCTCG CAGAGGGGAG TACGGCCGAA 960
GCCATGCCCT TAGCATTCGA CGGACCGGGG GACAATGATT TCTACGAGAT GCGGTTTGT 1020
CACGGACGTC TGTATGACGC CAGCGGACTC TGGGGAACAA ACCTGATGG ACATGCCGCT 1080
ATGGTGAAGC TATACGACGG CAACCGATGG ACTAATCTG ACAAGAAGAC CGTACAGGAA 1140
CAGTTGGGCG GCGGATTCAG TTTCATGAT GCTATCGATA TAGCTGTTTC CAACGGAGAC 1200
70 CCCGATCACT TTTTGTGCG TACATGGGGA AACGGTCTGT TCGAATTCAA GGATGGCAA 1260
GCCATAGCTC GCTATTCGGG AAACGAAACT GCTATCGCAG AATGTAATCC CGGAGATGCC 1320
CGTGTGAAGG CGATTGCTT TGACAATAAG GSCAACCTCT GGGGGACGCT CGGTGCCGTA 1380
GGCAAGACA TCTTCATGTA CGATCCGCG AGTAGCACAT GGCATTCTTT CAGCTATCCG 1440
GATSTAGCCA ATCTGGCCTC CTTCGGCAAT ATGATTATTC TACCAACCGG AGACAAATCG 1500
75 GTAATATACC TTCAACGTAG TGGCGGATCC ACSCGCAAG GTGTCTTGAT CTTCAACGAT 1560

177/ 490

5 CGGGGTACAC CGGAAACGAC TTCGGACGAC AGCCATCTTT ACGTCGAGCA GTTTGTCAAT 1620
CGCCTCGGG CAGCCATAGG ACATAAGACT ATCTATGCAA TGGCCGTCGA TCATAACGGC 1680
TCTGTCTGGA TGGGATCGGA TATAGGCATT TTCGGCGTCT ACAATGCAGC CGGAGTATTG 1740
TCCTCGACTT CTACCCCTAT CGCTGTTCCG CCGGTCCGAG GAGAAGAACC CAATTTGTAC 1800
TATGTGCTGG ACAAGGTGAC GGTGACAGAC ATCGTCTGGG ACAAACCTCA TCACAAATGG 1860
GTTGCCACCC AAGGGACAGG ACTCTATCTC CTTTCGGAG ATTGCAGTAA GATCCTCGCG 1920
CAATTTACCG TAGAAACAG CCCTTTGCTT TCTAACAACA TACTATCCCT GGCCTTAAAT 1980
GACGATAACG GACTGCTGTA CATCGGTACG GCGGACGGAC TGATGACGTT CCAACCGGT 2040
ACGGGGAGTG GATCAGCTTC CGAACTGGAC GCGGTCTATG TATACCCCAA TCCGCTAAGG 2100
10 CCGGAATATC CCGATGGCGT CACCATTTGCC GGAAGTCAAG CCGGCTGTAG TGTCAAAATC 2160
ACCGATACCA CCGGCAGACT GCTATACCAG ACTGAGAGCG TAACCAACGA AGTCAAAATG 2220
AATGCTCGAG GTGCCGATGG CAATAGGTA GCTTCGGGCG TATATGCCGT TGCAGTGTAC 2280
GATCGGSTAT CGAAAAAGTC CAACTAATT CGCTTCGCAG TGATTTCG 2328

15

(2) INFORMATION FOR SEQ ID NO:259

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 3474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

25

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(v) ORIGINAL SOURCE:

(A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

35

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...3474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

40 ATGAACGAA TACTTCCAAT AGTCGCATTC CTTTCTCTCT TCCTTGCCCT TGCTTTGCCT 60
GCGAAAGCGC AACGAGCTAT GGGGAAGACG GCGGACCGTT CGCTAATGGC TTCGGGACAT 120
TGGGTCAAGA TACGTGTGGA TGCAAGTGGG GTGTATCGCC TTACGGACGA ACAGCTCCGT 180
GCCAATGGCT TCTCCGATCC GTCCAAGGTA GGTGTGTTCG GTTATGGTGG AGGGGTGCTT 240
CCCGAAGATC TGAGCCGGAT CACGACAGAC GATTTCGCTC CGGTACCGGT ACTCCGTCAG 300
GGCAATGCGC TGTATTTCTA TGCCGTGGGG CCGGTGACAT GGTTCCTACAA TCCGGCCAAA 360
45 ACCACCATGG AGCATACGGT GAATACATAC AGTACGCGATG GCTACTACTT CCGTCTCGAT 420
GCTSCCGGAG CACCTTTGCA GATGTCCCAA TATACGGGTG GAGGTGCGTC GGCCGAGGCT 480
TTGATCGACT ACTACGATGA GCTGATGCTC CATGAACAGG AATTGTATTG GCCCAAAGAA 540
TCGGGACGAG ATCTGTATGG CGAGTCTTTC AGTGCAGTCA ATACGGGTAC GGTCAAGTTC 600
CCTTTGAGGG GCAACACCCG CTGCTCTGGC GAACTCGGTA CCGTATTCTC ATACATAGCC 660
50 AAGGCCAGAT CCGCCCGTGG CCGCCGTGAG ATGTCGCTCT CCGCGAATGG CATTCTGATC 720
TTCAGCGATC CTTTTCCAT GACATCGAAT GAAGTCTCCA ATTCTATTG GGCCGGCAAG 780
AAGCGTCGTC TCTATCACAG TACGCCGATG AACAGCTTGG TCAATGAGTT GCGCTTGGAC 840
GCCAATATA GCATGACAGG AGATGCGGTC AATCTGGATT TCATAGAGGT GGCTACACAG 900
AAGCACTCC GGTACGATGG CGCACCCATG CATATCAGGC GGTTCCTCAA TTGCCCCGTT 960
55 TTGGGGGGCG AGTCCGTGCG GTTCGTTATC AGTGAGGTGC CCGAGTCTCT GGTGGTTTTG 1020
CAGGCCAATT CTTCCCTGAC AGCATCGCTT GTTCCCGTTA AGACTCTCGG GGATAAGACC 1080
ATTGAGTTTG TGCTCCGCCG GAAGGGTCAG GATCGTAGGA CTATCAATAC GTTTTATGCC 1140
GTGGACTTGT CACAGGCTTC TGCTCCGGAG ATCCTCGGAG CCGTACCCAA TCAAAACCTG 1200
CATGGAGAGG AATCCCTGA TCTGATCATT GTCTCTACTC AGGCGCTCCT CTTGAGGCT 1260
60 GATCGACTGG CCACCTATCG TAGAGAGAAA AACGGGCTGA AGGTTTGGT CGTGTTCGAT 1320
GAACAGGTGT TCAACGAGTT TTCGGGTGGA ACTCCCGATG CTACAGCATA CCGCCTCTTT 1380
GCCAAATGT TCTACGACAG ATGGAAGGCA AATGCACCTG TGGGAGAGAC CTTCCCGATG 1440
CAATGCTTC TCTTCGTTGA TCGGGCTCAT GACAACAGGA AGGTCTCCGT AGCTTGGCAG 1500
65 AAACCGTATC TCCAACAAAC GGAGTTCTTG CTGACATTCC AAGCGTCAA TTCGACGAAC 1560
GTAAACAGTT ATGTGACGGA TGATTACTTC GGTTCGCTCG ATGATCAGCC GGCCTCGGTC 1620
AATATCGSTT GCGCAATTA TAATATGGCT GTAGGGCGAT TCCCGTAGC TACTCCGGCC 1680
GAAGCTCGCA TCGCAGTGGG CAAGACCATC CGATATGAGG AGGATCGAGA GAGTGGTGCC 1740
TGCGGTATTG GTGCTGTTT TCGGGCAGAC AACGGGGAAC AGCACGCAAC CGAGACTTCC 1800
CGTTTGATCG ATACCGTCAA GCGTTATGCT CCGTCCATCA TGCCGGTACG CGCCTTTCAG 1860
70 GAGTATATC CCGATGTCT CGAGAACGGG TTGCACAGCA TTCGGGTGCG AAAGAAAAAG 1920
ATGCTGGAAA CCCTTCAGTC GGTATATATC CTGCTTAAT ATGCTGGTCA TGGCGGTCCT 1980
CCGGATGCT CCGACGAGCA TTTGCTGACG CTCAACGATA TACACAAATT CAATATATAG 2040
CATATGCTCA TTTGATTAC TGCCACGTGC GACTTTGCCA ACTATGACAG TCAGACGACC 2100
TCGGCAGGGG AGGAGGTTT CCTCCATGAG AAGAGTGGCA CTCGATCAT GTTCTCGACT 2160
75 ACCCGTGTG TTTACAATAC GCAGAATGAG AAGATCAATG GTTTATGCT TCGCGGTATG 2220

5 TCCGAGAAAG CTAAGGATGG GCGTTATCGT ACGATGGGCG AGATTATCCG ATCGGCCAAA 2280
CAGGGGATGC TCAGTACTGT TTTCCCGGAT TCGATCAACC AGTTGAGTTT CTTCCTGATG 2340
GGTGATCCGT CCGTGGGTAT GAATCTTCTT ACCCACAAGG TGCAATTGAC CGCAATCAAC 2400
GGGCAGGATC CCGAAGGGCA GTATGGAAGT ATTATGCTCA AGTCTTTGGA ACGGGTAGCT 2460
C'GAAGGGTA AGGTAACCGA TGAAAAGGGG ACATTGACG AGACATTGAG TGGCAAGGTT 2520
TTCTGACCG TCTTCGATGG CAGAAAGAAA ATGACAGCTT TGGAGAGGA GGGAAACGAT 2580
CTCTCTCTTG TATATTATGA CTATCCTAAC GTGATGTATG CCGGTATTGC CGAGGTGAAA 2640
GACGGACTCT TCGAACTTC GTTATCGTA CCCAAGGATG TGAATATTG CGAGCACGAA 2700
GGCCGGATCA ATCTTTATCC TTATAACGAG AGCACAAGG CGGAAGCCAT GGGGGTAGAC 2760
10 TTCTCCATCA GAGTCCAACC GGGTATTCTT GATGAGGTAA CGGAAGATAA TACACCGCCT 2820
GAAATCATAA GCTGCTTCTT CAATGACAGT ACATTCCGAT CGGAGATGA GGTAAATCCT 2880
ACTCCTCTGT TTATGGCCGA AGTATTGAC TTGAATGGAA TCAATATCAC GGGTAGCGGA 2940
GTAGGGCATG ATATTACGCT TTGTATCGAT GGGCGTGCCG ACCTGACCTA CAACCTCAAT 3000
GCATATTICA CAAGTTGGGC TACGGATGCA GGTGTGGGCA CTATTCTCTT CATGATACCG 3060
15 GCTTTGGCCG AAGGAGATCA TACTGCCCGA CTGACGGTTT GGGACATTTT CAATAATGCC 3120
GTCCATCATG ACTTTTCATT CAGAGTGGTA GATGGCATTT CTCCGGATGT GGTGATGTG 3180
ATTCTATCC CGAATCCGGT ACGCGAGAGT GCTACGTTCC GAATCTTCCA CAATCCCCCC 3240
GGAAGCGATT TGAACGTGGC CGTGGAGATC TATGACTTCA CCGGTCGTCT TGTGAACAGT 3300
20 TTGCCAGTCA AGACCTATTG GTCTTCCTAC GGAGAACCIA TAGAGATCAA GTGGGATCTG 3360
ACCTCCAAAT ACGGAGTGAA GATCGGAAC GATTCTACC TCTATCGTIG TGTGGTGAAC 3420
TCTCCCGGAG GACAGACGGC CTCCATGGCC AAGAAAATGA TCGTGGTAGG ACAA 3474

(2) INFORMATION FOR SEQ ID NO:260

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2883 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
40 (A) ORGANISM: PORPHYROMONAS GINGIVALIS
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2883
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

ATGAAGAAAC TTTTCCCAT ATTATTACT ATAT'GTGCGA TTTTGGTCGG ATGTGGAAAA 60
AAAGAAAAC ACTCTGTAACT TGAATCCGCC CGAGAGAAAA AGCTATTAC TGCATTGCTG 120
TACGAAAAAG AACTCCCCAC TGATTCTGTT AVACAGCTTT ACGAGAACAG CGTACAGAAC 180
AAGAACCCTTG TGGGACAAAT GTTATTCCGG ATCGAGGTCC GCAACCGGAT GCGTAATATG 240
TCCCAATACA CAGATGCCAT GCTATATCAC CAAAAGGGT TGAACCGTGC ATTGAATCTA 300
AGGGACACCA TCGTAGCCGC ACAAGCATGG AATCATCTCG GAACGGATAG CCGTCGTATC 360
GGTGCTTTGG CAGAAGCTTC GGATTATCAT TACAAGGCTC TTTCTTGTAT AGAATCTTTT 420
AGCGGAAAAC AGAATAGGCC TCGATCAAAA GCCAGATCGG CGGCCCTGAA CGGCATCGGC 480
55 AACATCAATC TTGAGTTAGG ATACCATGAT GAGGCCGAAA AGAATTTCTT GAAAGCACTG 540
CAAGGTGAGA AAGAACTCGA CAGTCCCTCC GGGCAAGCTA TCAACTATGC GAACCTCGGA 600
CGTATCTATC GACAACGCAA AGAATACGAC AAGGCTCGTA CCTACTTCCT CTGTCTCTG 660
GAGCAGAAAC ATATGGCAGA GAATCTGATG GGTATCGGAC TCTGTAGCAT CAATCTCGGA 720
GAAGTAGACG AAGAAAAGG GGATTATCAA AAGGCTTTGC AAGAGTATGC CACGGCATAAC 780
60 AAACCTGATG AACAGTTGTC CGATCGATGG CACTGGCTGA ATTCTGTAT CCGGATGGCA 840
CGTATCAATC TCAACAAGG TAACGAAAGG CTCTACCAAC ATTTCAITTC TTTGGCCGAA 900
GGGACTCGCA AAGAAATTA TCCGACTTCA CATCTGATAG AATATACAA TCTTCAATAC 960
GAGAATCTCG AGCGTAAAAA AGAATACAAA CAAGCCCTCG AAGCATTCTG TCTGAGCAAG 1020
ACGTTGAGCG ACAGCATGTC CATTCGCGAC AAGGTGAGCA GCATACAAGA AACCGGATTG 1080
65 AACTACGAAC GAACAAGTC CCAAAAAGAG CTTGAAGAAA TACAGCAAGT AAGCAAGGCA 1140
AAACAAGAGA AATCGAAGTT TATCCTCTTG AGCACTCTTT TTGCCCTTTT CATCTCGATT 1200
CTTTTGATTT CTGTTCTGAC ATATGCATAC CGTCAGGGCA AGAAGCATAA CAAGCTGATC 1260
AAAGAGACGG ATAAACTTCG CTCGGGCTTT TTCAACGGTA TTACACAGCA ATTTCTGATG 1320
70 CCTATCACCG TCATACAAAG TTTGAATGAG AAAATGAGTI CAAGTCTGTA TCTCCAAGCA 1380
TCGGACAGAA CCGAGCTGCA CAAGATAATA GACAGACAGA GTAGCCATAT GCTGAATTTG 1440
GTGAACCAGC TGTGATATG TTGCAAGATC AGAAGCGGAG TATCCACGCC CGAATGGGCG 1500
AATGGCGACA TCGTCTCCTT CGTACAGATT CTCTATCGATT CGTTTGCACC ATACGCACAG 1560
GCTCAAGACA TAACCTTGA GCTACAACCC GAGAGCAAAC CTATTGTCGT GCACCTCGTC 1620
75 CCCTCCTACT TGCAAAAAAT CATATCCAAT CTTTGTGTTA ATGCCATCAA GTATTCTTTA 1680
GCCGGAGGGA GAGTGGTCAT ATCTCTGGCA AAAACCAAGA ATGAAAAAAA TCTGATCATA 1740

179/490

CGGGTTGCGAG ACAATGGCAT AGGAATAGAT AAAACTGATC AGGCTCATAT CTTCGACATC 1800
TTCTATCGAG GACAGTCCGC TACCGAAAAG CATGGATCAG GCGTCGGACT CTCGTTTACC 1860
AATATACTGG TCGAAAACCT TCGAGGTACG ATCAAAGTGG AAAGCCAGCC GGGGAAAGGA 1920
AGTGCCTTCA CCATCAGTAT TCCTACACAA AACCAGTCTT CTTCGGCAGA GATTCTTCCT 1980
5 TGGCTACCCCT COTCCGATGA CATTGTCTAG COTGTCCACA TCGCGCCCGA TGAATTCACG 2040
ACATCTCCGA TGGTAGCAGC TCTGAATCAT CGCTTCGAGG ACGAAGCTCC GACCATATCG 2100
CTCCTCGAGG ACAATAAGGA TATCAACCTG CTCGTCAAAC TACTCCTTTG CGATCGCTAC 2160
AATGTCTAT CCGCCGCAAA CGGAAAAGAG GGTATAGCCC TCGTACCGA GCATATTCOC 2220
10 GACATTATCA TTACGGATAT TATGATGCCG ATAATGGATG GGATAGAAAT GACATCCOGG 2280
ATGAAGCAAT CGCCTCTGCT CTGTCACTT CCCATGTCTG CTTTGACGGC CAAGAGTACC 2340
GAACAGGACA GATTGGAAGG AATCAAAAGC GGTGTAGTCT CTTATCTATG CAAGCCATTG 2400
TCTCCGGAGG AGCTTTTGAT GCGGATCGAG CAGCTTCTGA AAGACCGTGA GTTGCTCAAG 2460
AAGTTCTATA TGCAAAACCT CATGCTGGAT CGGAAGCCGG AGGAGGAGCC TCAACCGATA 2520
GATGACAGCA GTATGCAGTT TCTCCTTGCT GCCAAAGATG CAGTGTCCGG TGGAAATCAA 2580
15 CAAAATCCGG ATTTTTCGCG TCAAGACTTG GCCGAAAAA TGTGCATGAG TCCATCCCAA 2640
CTCAACAGAA AGCTCACGAG TGTCTAGGT TGCTCCACCA TCGGCTACAT ACAGCAGATC 2700
AAGATAAAAT TGGCCTGCAA GCTCCTTGCC GATGAGAGCA AAAACATCTC CGACATTAGC 2760
ATTGAGGCAG GCTTTTCGGA TCCGGCTTAC TTCTCTCGCA CCTTCAACG CTACATGAAC 2820
20 TGCTCTCCCT CCCAATATCG GCAAAAACCT CTTGCCATGC CGGGGAGCGA CAAGGAGACA 2880
GTT 2903

(2) INFORMATION FOR SEQ ID NO:261

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1668 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
30 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
35 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
40 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

45 ATGAAAAAGC TTTTACAGGC TAAAGCCTTG ATTCTGGCAT TGGGACTCTT CCAACTGCCC 60
GCAATCGCCG AAACGCAAAAT GCAAGCAGAC CGAACAACCG GTCAATTTCG AACAGAAGAG 120
ATGCAACGAG CATTCAGGGA AACGAATCCC CCTGCAGGTC CTGTGCGTGC TATCGCTGAG 180
TACGAACGCT CTGCAGCCGT TTTGGTACGC TACCCGTTGG GTATCCGAT GGAATTGATC 240
50 AAAGAGCTGG CCAAGAACGA CAAGGTGATT ACCATTGTGG CGAGTGAAAG CCAAAAAAAC 300
ACCGTTATAA CCCAGTACAC CCAAGCGGT GTGAATCTCT CTAATTGCGA TTTCATCAT 360
GCGAAAACAG ACTCTTACTG GACACGCGAC TATACCGGTT GGTTCCGAAT GTACGATACG 420
AACAAAGTAG GTCTCGTGGG CTTTATTAT AACCCGCTC GTCTTAACGA TGATGAATTC 480
55 CCCAAATACG AAGCACAATA TCTGGGCATC GAGATGTTCG GGATGAAGCT CAAGCAGACC 540
GGTGGCAACT ACATGACGGA CGGATATGGA TCCGCTGTGC AGTCACATAT CGCATATACG 600
GAGAACTCCT CTCTGTCTCA AGCTCAAGTA AATCAAAAGA TGAAAGACTA TCTCGGCATC 660
ACACATCATG ATGTGGTACA AGATCCGAAC GCGGAATATA TCAACCATGT GGACTGTTGG 720
GGCAAGTATT TGGCAGCGAA CAAAATCCTC ATCAGGAAAG TGCCTGACAA TCACCTCAG 780
60 CACCAAGCCC TGAAGATAT GGCAGCCTAC TTGCGAGCAC AGACCTGCGC ATGGGGAACG 840
AAGTACGAGG TATATCGCGC TTTGGCCACC AATGAACAAC CGTACACGAA CTCTCTGATT 900
CTGAACAACA GGGTATTGT TCTGTCAAT GGCCCGGCT CCGTGGACAA CGATGCTCTG 960
AACGTCTATA AGACGGCAAT GCCCGGTTAC GAAATTATAG GTGTCAAAGG GGCTTCAGGA 1020
ACACCTTGGT TAGGAACAGA TGCCCTGCAT TGTCTACTC ACGAGGTAGC GGATAAGGGC 1080
65 TATCTCTATA TCAAGCACTA CCCGATACTG GCGGAACAGG CAGGCCCTGA TTATAAGATC 1140
GAAGCAGATG TCGTCTCATG CGCCAATGCT ACTATCTGCG CGGTACAATG TTAATATCGT 1200
ATCAATGGTT CCGGTAGCTT TAAGGCTGCT GATATGACGA TGGAAATCAAC AGGTCACTAT 1260
ACTTATAGCT TTACAGGTCT TAACAAGAAT GATAAGGTAG AATACTATAT CTCTGCCGCT 1320
GACAATAGTG TTCGCAAAAG GACTTATCCC TTTATCGGCG AACCTGATCC TTTCAAGTTT 1380
70 ACGTGTATGA ACGAAACCAA TACATGTAAT GTGACCGGAG CTGCCAAAGC TCTTCGTGCA 1440
TGGTTCAAGC CCGGTCGTTT AGAACTGGCT GTTTCGGTAA GTTTGAATAT TGCCGGCACA 1500
TATCGGATAA AGCTTTATAA CACCCGAGGA GAAGAAGTCG CTGCAATGAC CAAGGAATTA 1560
GTAGCAGGGA CGAGTGTCTT CAGTATGGAT GTGTATTCTC AGGCTCCGGG CACATATGTT 1620
CTGGTTGTTG AAGGAAATGG AATCCGTGAG ACAATGAAAA TTCTCAAA 1668

75

(2) INFORMATION FOR SEQ ID NO:262

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRAINEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

25 ATGAACTTT CATCTAAGAA AATCTTAGCA ATCATTGCAT TSCGTACGAT GGGACATGCT 60
GTGCAGGCAC AGTTTGTTC GGCCTCCACC ACAGGGATTC GCATGTCTGT CACTACCAACC 120
AAGGCCGTAG GCGAAAAAT CGAATTGTGT GTTCATTCCA TAGAGAGAA AGGCATCTGG 180
ATCGATCTCA ATGGGATGC CACTTACCA CAAGGAGAGG AATAACCGT ATTCGATGAG 240
GCATACCAAG AATACACGAT CCGGACGCAA ACCCTCACTA TCTATGGTAA TACGACCCGA 300
TTGGGCTGTC GATCTACCGG TGCAACGGCT GTCGATGTAA CGAAAAACCC TAATCTGACC 360
TATCTCGCAT GCCCGAAAAA TAACTCTGAA TCATTGGACT TGACGCAAAA CCCAAAGCTG 420
CTGCGAGTTT GGTGCGACTC TAACGAATA GAAAGTTGG ACCTGAGTGG CAATCCGGCT 480
TTGATCATCC TCGGCTGTA CAGGAATAAG CTGACTGAGC TGAAGACCGA TAACAACCCC 540
AAGTTGGCCT CTCTTTGGTG TTCTGATAAT AACCTGACGG AGTTGGAAT CAGTGCCCAT 600
CCTGCTCTCA ATGATCTTTG GTGCTTCGGT AATCGGATCA CGAAACTCGA TCTGAGTGCC 660
AAGAATTGGG ACGTTGCTTA CCTTTGGTGT TCATCGAACA AACTTACATC CTTGATCTG 720
TCGGGGGTGA AGGGAAGTGA TGTTTGGTGT TGTCTATCCA ATCAGATCGC AGGTGAAGAA 780
ATGACGAAAG TGGTGAATGC TTTGCCACCA CTATCTCCCG GCGCAGGCGC TCAGAGCAAG 840
TTCTGCTGTG TAGACCTCAA GGACACTGAT GAGAAGAATA TCTGTACCGT AAGGATGTG 900
GAAAAAGCTA AAAGTAAGAA CTGGCGAGTA TTTGACTTCA ACGGTGATTC TGACAATATG 960
CTTCCATACG AAGGAAGTCC GACATCGAAC TTGGCAGTAG ATGCTCCCAC TGTACGGATA 1020
TATCCCAATC CGGTAGGAAG ATATGCGCTC GTCGAGATCC CCGAGTCTCT TTTAGGGCAG 1080
GAAGCTGCTT TATACGATAT GAATGGGGA AAAGTCTATA GTTTCGGGCT AGAGTCTCTT 1140
CGTCAGAAAC TTGACCTGAC ACATCTTCCC GACGGCACTT ATTTCTTCCG TCTCGATAAC 1200
45 TATACCACTA AGTCATCAA ACAG 1260
1284

(2) INFORMATION FOR SEQ ID NO:263

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRAINEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

70 ATGAGAAAA CAATAATTT CTGCTTGTG CTGCCCCTAT TTGCTGTTT TTGGGCACAA 60
GAAAGAGTCG ATGAAAAAGT ATTCTCCGCA GGAACAAGTA TTTTATGGG CATCCTTGAA 120
AAGGTGAAGT CACCGCTTAT GTATGGAGAT CGTGAGGTAT GGGGTATGGC TCGTGCGAGC 180
75 GAGGATTTCT TTTTATACT TCCGTTACG GATGACCTCA CTCCCGTGT TTTCTATAAC 240
CGTCTTACAA ACGAACCTG CTTTGTGTCA GACCAAGGAA TAACTGAGTA TTTCAAATTC 300

181/490

5 GCTCAAGAAG GTGATTACAT TGAAGTCGAA GGAAGCTCTG TATTCATGGC GAATCTTTTC 360
TACTATCGTT TTTTCCCGAC AAGAATTACC TCCTATAATG CTCCCATTGA AGGTGTTGTG 420
AGCAAGACGG GAAATCTGTC TTTTACAATC CCGATGCTCC CCGGGGTTTC TGATTGCATA 480
GAAATCTCAA ACAACCGCAA AGTCTTTCTG ACCAATCAAT TACGGGTTGT AAACATCACT 540
GACGGGATGG AACCTCCGAT TATTGCCGGA GTCTCTGCTT CCTATGGATC TTCCGTCCGG 600
GTGTATGGTC ATGTCTCACA GCGGTGGGAC ATCATAGGCC ATTGCTATTT GGATATCTAC 660
CCRAACCAATT GCTATCCGCT CAGCACGAAA CCCGTTGCAG GAGACGATGA GGTTTTTGTC 720
AAACAAAGAG GCAGGCAAAAT AGAGATCGAT AGCAACAGCC CCATAGTCCA AGTGGTCGTA 780
TACGATCTTG AGGGGAAAAG TGTTTTTCGC AAAAGAATGA CCGAAACGC TTATACCCTA 840
10 TCCTTTAGAG CACCCATGCT CGGCTTTATG ACCATCATGA TCGAAACACA AAATTCGATT 900
ATCAATAAAA AACTTAATGT TACACAGCTA 930

(2) INFORMATION FOR SEQ ID NO:264

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1215 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
25 (iv) ANTI-SENSE: NO
(v) ORIGINAL SOURCE:
(A) ORGANISM: PORPHYROMONAS GINGIVALIS
30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

35 ATGAAAAAAA CAACCATAT TTCTTTGATT GTCTTCGGTG CTTTCTTTGC AGCCGTGGGC 60
CAACCAAGG ACAATTCTTC TTACAAACCT TTTTCGAAAG AAGATATTGC CGGAGGAGTT 120
TACTCTCTCC CGACTCAAAA TCGTGCGCAG AAGGACAATG CCGAGTGGCT TCTTACAGCG 180
40 ACCGTCTCCA CAACCCAGTC TGCAGATACT CACTTTATCT TCGATGAGAA CAACCGCTAT 240
ATCGCTCGTG ACATAAAAGC CAATGGGGTA AGAAAAATCCA CGGACTCCAT TTACTACGAT 300
GCCAACGGGC GAATATCGCA TGTGGATCTT TATATCTCGT TCAGTGGCGG AGAGCCTGCA 360
CTCGACACCC GATTCAGTA CACCTATGAT GACGAGGGA AGATGACCGT GAGGGAAGTA 420
TTATGCTGG TAATGGATCC GAATACACCT ATCTCAGGCT TGAATATCA TTATGATGCA 480
45 CAGGSCAGAG TGACCCACTG GATTTCTTTT GCTTTCGGGG CAGAATCCCA AAAGAATACG 540
TATCACTATA ATGAAAAAGG TCTGTTGGTC AGCGAAGTGC TGAGCAATGC AATGGGGACA 600
ACCTATTACG ACACCGGCAA AACGGAAATAC AGCTATGACG ATGCAGATAA TATGGTGAAG 660
GCCGAGTACT TCGTGGTCCA GCAAGGAAG GCATGGCAAG TACTCAAAAG AGAGGAATAC 720
ACCTATGAGG ACAATATCTG CATACAAATAT TTGGCTATTA ACGGTACCGA CACAAAGGTG 780
50 TACAAGCGAG ACATCGAGAG CGATAAGTCC ATCTCCGCAA ATCTCATTGA CATTCCGTCA 840
ATGCCGGAAC AGACCTGGCC TAATATGTAC GGATTCAAAG CAAAGCGACT GAAAGAGACT 900
TATTCCTCCT ACGAAGGAGA TGTGGCTACT CCTATATTGG ACTATATCTA TACGTACAG 960
GCTCTTACCT CAATGGCAAC ACCTTCGACA GAAGCTCAGG TAGCAGTCTA TCTCAATCCG 1020
TCACCGGACC GGTAGTGTAT TCTGGCCAAC GGCATCACAC ATCTGAGCAT GTACGACTTG 1080
55 CAGGGTAAGC TTATCCGTGA TTGTGCCTTG AGCGGCGATA AGGTGGAAAT GGGGTGCGGA 1140
TCTTTGACCA AAGGACATA CTTGCTTAAA GTGAATACGG ATCAGGGAGC CTTTGTGAGA 1200
AAAGTCGTGA TTCGA 1215

(2) INFORMATION FOR SEQ ID NO:265

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 amino acids
(B) TYPE: amino acid
65 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
70 (v) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
75 (A) NAME/KEY: misc_feature

(B) LOCATION 1...454

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:265

5 Phe Cys Val Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu
1 5 10 15
Acn Leu Lys Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln
20 25 30
10 Ser Pro Thr Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro
35 40 45
Lys Val Thr Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu
50 55 60
Met His His Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser
65 70 75 80
15 Gly Glu Val Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser
85 90 95
Ile Glu Val Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val
100 105 110
20 Gly Asp Pro Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu
115 120 125
Ser Ser Gly Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val
130 135 140
Ala Thr Pro Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe
145 150 155 160
25 Thr Ala Pro Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu
165 170 175
Arg Ala Leu Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly
180 185 190
30 Lys Val Tyr Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn
195 200 205
Ala Glu Ile Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly
210 215 220
Val Leu Ile Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp
225 230 235 240
35 Thr Leu Lys Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr
245 250 255
Gly Lys Ala Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala
260 265 270
40 Ala Ala His Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala
275 280 285
Ser Phe Pro Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile
290 295 300
Asp Gly Asn Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe
305 310 315 320
45 Leu Ser Ala Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp
325 330 335
Val Asp Glu Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser
340 345 350
50 Met Ser Arg Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr
355 360 365
Val Leu Asp Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser
370 375 380
Asn Glu Tyr Asp Arg Val Phe Pro Met Asp Ile Tyr Pro Glu Tyr Leu
385 390 395 400
55 Leu Lys Ala Ile Ile Ala Phe Asp Ile Asp Lys Met Glu Asp Leu Gly
405 410 415
Ile Tyr Glu Val Ala Pro Glu Asp Phe Ala Thr Cys Glu Phe Val Asp
420 425 430
60 Thr Ser Lys Ile Glu Leu Gln Arg Ile Val Arg Glu Gly Leu Asp Met
435 440 445
Leu Tyr Lys Glu Met Asn
450

(2) INFORMATION FOR SEQ ID NO:266

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(111) ORIGINAL SOURCE:

183/490

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

5

(A) NAME/KEY: misc_feature
(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

10 Glu Leu Ser Lys Cys Tyr Met Asp Lys Val Ser Tyr Ala Leu Gly Leu
1 5 10 15
Ser Ile Gly Asn Asn Phe Lys Ser Ser Gly Ile Asp Ser Val Val Met
20 25 30
Asp Asp Phe Met Gln Gly Leu Ser Asp Val Leu Glu Lys Ala Pro
35 40 45
15 Gln Leu Ser Tyr Asp Glu Ala Lys Arg Glu Ile Glu Ala Tyr Phe Met
50 55 60
Asp Leu Gln Gln Lys Ala Val Lys Leu Asn Lys Glu Ala Gly Glu Glu
65 70 75 80
Phe Leu Lys Ile Asn Ala His Lys Glu Gly Val Thr Thr Leu Pro Ser
85 90 95
20 Gly Leu Gln Tyr Glu Val Ile Lys Met Gly Glu Gly Pro Lys Pro Thr
100 105 110
Leu Ser Asp Thr Val Thr Cys His Tyr His Gly Thr Leu Ile Asn Gly
115 120 125
25 Ile Val Phe Asp Ser Ser Met Asp Arg Gly Glu Pro Ala Ser Phe Pro
130 135 140
Leu Arg Gly Val Ile Ala Gly Trp Thr Glu Ile Leu Gln Leu Met Pro
145 150 155 160
30 Val Gly Ser Lys Trp Lys Val Thr Ile Pro Ser Asp Leu Ala Tyr Gly
165 170 175
Asp Arg Gly Ala Gly Glu His Ile Lys Pro Gly Ser Thr Leu Ile Phe
180 185 190
Ile Ile Glu Leu Leu Ser Ile Asn Lys
195 200

35

(2) INFORMATION FOR SEQ ID NO:267

(1) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 279 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

50

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

55

60 Gln Lys Asn Lys Arg Lys Met Lys Lys Ala Leu Leu Ile Gly Ala Ala
1 5 10 15
Leu Leu Gly Ala Val Ser Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile
20 25 30
Lys Val Gln Asn Asn Ser Val Gln Gln Pro Arg Glu Glu Ala Thr Ile
35 40 45
Gln Val Cys Gly Glu Leu Ala Glu Gln Val Asp Cys Ile Gly Thr Gly
50 55 60
65 Asn Ser Ala Ile Ile Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu
65 70 75 80
Glu Ser Tyr Val Gly Trp Glu Ile Met Ser Val Asp Phe Phe Pro Gly
85 90 95
Tyr Lys Ala Cys Lys Tyr Thr Ser Ala Val Trp Ala Asp Asp Met Thr
100 105 110
70 Ile Leu Gly Gln Ser Glu Asp Ser Asp Pro Glu Met Gln Thr Ile Asn
115 120 125
Asn Leu Ala Leu Lys Thr Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr
130 135 140
75 Ile Val Gly Tyr Ile Ala Asn Thr Ala Gly Gly His Pro Ile Gly Cys
145 150 155 160

184/ 490

Asp Gln Gly Pro Ala Val Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser
 165 170 175
 Glu Asp Gly Gly Ala Thr Phe Pro Pro Phe Glu Ser Leu His Gln Ala
 180 185 190
 5 Val Pro Thr Leu Asn Tyr Asn Ile Tyr Val Val Val His Leu Lys Lys
 195 200 205
 Gly Glu Gly Val Glu Ala Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr
 210 215 220
 10 Val Gln Asn Gly Val Ile Tyr Val Ala Gly Ala Asn Gly Arg Gln Val
 225 230 235 240
 Ser Leu Phe Asp Met Asn Gly Lys Val Val Tyr Thr Gly Val Ser Glu
 245 250 255
 Thr Ile Ala Ala Pro Gln Lys Gly Met Tyr Ile Leu Arg Val Gly Ala
 260 265 270
 15 Lys Ser Ile Lys Leu Ala Ile
 275

(2) INFORMATION FOR SEQ ID NO:268

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...157
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

Arg Unk Phe Leu Pro Glu Lys Ala Leu Tyr Ile Gly Cys Arg Val Glu
 1 5 10 15
 40 Thr Gln Glu Gly His Ala Val Gly Phe Gly Leu Asp Asp Gly Pro Ala
 20 25 30
 Met Lys Gly Lys Gly Asp Leu Val Gly Ser Tyr Leu Pro Gly Ala Ala
 35 40 45
 45 Pro Met Pro Phe Val Pro Leu Ser Asp Ile Pro Ala Arg Ser Met Asp
 50 55 60
 Ala Asn Phe Tyr Ile Tyr Ser Arg Ile Ser Leu Gly Ser Gly Thr Gln
 65 70 75 80
 Asp Val Leu Gln His Arg Met Lys Val Tyr Pro Asn Pro Ala Thr Thr
 85 90 95
 50 Glu Leu His Val Glu Ala Leu Ser Ala Trp Val Gly Glu Gln Ala Ala
 100 105 110
 Val Tyr Asp Met Arg Gly Arg Val Ser Ala Arg Thr Val Asp Ser
 115 120 125
 55 Glu Lys Leu Cys Ile Asp Ile Ala Ser Leu Pro Val Gly Val Tyr Met
 130 135 140
 Leu Arg Ile Gly Ser Tyr Ser Ala Lys Phe Glu Lys Arg
 145 150 155

(2) INFORMATION FOR SEQ ID NO:269

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 562 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 65 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 70 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...562
 75

185/490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

5	Thr Arg Asn Val Ser Leu Ile Lys Met Pro Arg Ile Met Lys Leu Lys	1	5	10	15
	Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile Val Leu Phe Ser	20	25	30	
	Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp Asp Val Leu Ile	35	40	45	
10	Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp Phe Tyr Tyr Lys	50	55	60	
	Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met Leu Asp Phe Ser	65	70	75	80
	Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser Lys Asp Gly Gly	85	90	95	
15	Ala Thr Tyr Gln Lys Leu Gly Ser Leu Gly Ser Leu Val Pro Tyr Asp	100	105	110	
	Phe Asp Val Ser His Cys Asp Phe Ile Val Thr Gly Lys Asp Glu Asp	115	120	125	
20	Asp Ile Asn Val Trp Thr Val Met Thr Ala Phe Glu Tyr Val Gly Gly	130	135	140	
	Thr Ile Gly Asn Gly Val Leu Leu Met His Arg His Asp Ala Asp Ile	145	150	155	160
	Asn Asn Thr Glu Cys Val Tyr Lys Lys Asp Phe Pro Asn Asn Arg Leu	165	170	175	
25	Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro Ser Pro Tyr Gly	180	185	190	
	Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val Ser Gly Ser Gly	195	200	205	
30	Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu Asp Gly Gly Val	210	215	220	
	His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln Lys Leu Thr Ile	225	230	235	240
	Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro Ser Leu Gly Phe	245	250	255	
35	Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Asn Leu	260	265	270	
	Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val Asp Tyr Asp Pro	275	280	285	
40	Arg Tyr Ala Trp Ser Glu Pro Ile Ile Ile Glu Glu Asp Cys Gly Trp	290	295	300	
	Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu Ile Gln Met Met	305	310	315	320
	Leu Asp Asp Asn Ser Asp Asn Thr Val Gly Gly Glu Arg Ser His Asn	325	330	335	
45	Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro Lys Gln Ser Phe	340	345	350	
	Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp Leu Val Phe Lys	355	360	365	
50	His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys Glu Gly Asp Arg	370	375	380	
	Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg Tyr Arg Trp Ile	385	390	395	400
	Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser Trp Pro Tyr Val	405	410	415	
55	Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg Pro Gln Val Ala	420	425	430	
	Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp His Thr Arg Lys	435	440	445	
60	Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro Val Ile Ile Lys	450	455	460	
	His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala Leu Asp Val Gly	465	470	475	480
	Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala	485	490	495	
65	Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly Gly His Glu Ala	500	505	510	
	Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys Val Ser Phe Ser	515	520	525	
70	Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser Lys Gly Thr Tyr	530	535	540	
	Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val Glu Lys Ile Ile	545	550	555	560
75	Val Glu				

(2) INFORMATION FOR SEQ ID NO:270

5 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...391

20 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:270

Gln Met Lys Arg Leu Leu Pro Phe Leu Leu Leu Ala Gly Leu Val Ala
 1 5 10 15
 Val Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val
 20 25 30
 His Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser
 35 40 45
 Val Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr
 50 55 60
 Ile Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile
 65 70 75 80
 Asp Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe
 85 90 95
 Asp Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly
 100 105 110
 Ser Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr
 115 120 125
 Pro Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro
 130 135 140
 Phe Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr
 145 150 155 160
 Leu Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln
 165 170 175
 Gln Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu
 180 185 190
 Phe Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu
 195 200 205
 Pro Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr
 210 215 220
 Asp Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr
 225 230 235 240
 Leu Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser
 245 250 255
 Ser Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro
 260 265 270
 Asn Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser
 275 280 285
 Gly Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp
 290 295 300
 Met Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys
 305 310 315 320
 Ile Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln
 325 330 335
 Leu Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala
 340 345 350
 Thr Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro
 355 360 365
 Arg Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile
 370 375 380
 Arg Ala Lys Val Ser Leu Arg
 385 390

(2) INFORMATION FOR SEQ ID NO:271

75 (1) SEQUENCE CHARACTERISTICS:

187/ 490

(A) LENGTH: 428 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...428

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

1 Lys Arg Asn Pro Leu Pro Leu Thr Ala Ser Asn Arg Lys Ile Phe Ile
 5 10 15
 20 Lys Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu
 20 25 30
 Leu Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys
 35 40 45
 25 Gln Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro
 50 60
 Asp Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln
 65 70 75 80
 Glu Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe
 85 90 95
 30 Pro Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly
 100 105 110
 Ile Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile
 115 120 125
 35 Ser Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro
 130 135 140
 Val Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe
 145 150 155 160
 Trp Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp
 165 170 175
 40 Lys Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val
 180 185 190
 Ile Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met
 195 200 205
 45 Trp Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu
 210 215 220
 Ser Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly
 225 230 235 240
 Tyr Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp
 245 250 255
 50 Phe Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys
 260 265 270
 Cys Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met
 275 280 285
 55 Ala Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu
 290 295 300
 Arg Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg
 305 310 315 320
 Lys Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu
 325 330 335
 60 Gly Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala
 340 345 350
 Ile Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln
 355 360 365
 65 Ala Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg
 370 375 380
 Pro Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu
 385 390 395 400
 Ile Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu
 405 410 415
 70 Thr Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro
 420 425

(2) INFORMATION FOR SEQ ID NO:272

75 (i) SEQUENCE CHARACTERISTICS:

188/ 490

- (A) LENGTH: 282 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...282
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272
- 20 Leu Ser Arg Gly Val Phe Pro Leu Met Tyr Gly Arg Arg Gly Ser Ile
1 5 10 15
Arg Ala Ser Ser Gly His Arg Asp Lys Ile Phe Lys Asn Thr Ile Ile
20 25 30
Arg Phe Ile Thr Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn
35 40 45
25 Ala Val Tyr Pro Glu Val Gly Ile Ala Thr Tyr Lys Leu Leu Lys Ser
50 55 60
Leu Asp Ile Asp Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln
65 70 75 80
Pro Met Ala Asn Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu
85 90 95
30 Arg Phe Glu Glu Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser
100 105 110
Ala Ser Cys Val Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg
115 120 125
35 Pro Thr Gly His Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys
130 135 140
Glu Phe Leu His Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe
145 150 155 160
Ala His Lys Val Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu
165 170 175
40 His Leu Ser Thr Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val
180 185 190
Arg Arg Leu Leu Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys
195 200 205
45 Arg Ile Asp Glu Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu
210 215 220
Pro Glu Val Ser Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile
225 230 235 240
Ser Thr Gly Ala Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met
245 250 255
50 His Met Gln Gly Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile
260 265 270
His Ala Val Glu Ile Leu Ala Ala Asn Leu
275 280
- 55 (2) INFORMATION FOR SEQ ID NO:273
- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 65 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...251
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273
- 75 Pro Leu Lys Lys Arg Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu

189/490

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1      5      10      15
Val Val Glu Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile
20      25      30
5 Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu
35      40      45
Ile Gly Ser Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr
50      55      60
Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp
65      70      75      80
10 Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu
85      90      95
Gly Ile Val Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala
100      105      110
15 Glu Asn Leu Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala
115      120      125
Asp Arg Glu Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser
130      135      140
Arg Lys Ala Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln
145      150      155      160
20 Arg Val Gly Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu
165      170      175
Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile
180      185      190
25 Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met
195      200      205
Ser Thr His Asn Ser Ser Leu Ser His Leu Pro Ala Arg Thr Leu
210      215      220
Ala Val Arg Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala
225      230      235      240
30 Asp Ala Val Ser Arg Lys Asn Thr Glu Ile Asp
245

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(2) INFORMATION FOR SEQ ID NO:274

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...238
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

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1      5      10      15
Thr Arg His Cys Pro Ala Cys Arg Ser Ser Phe His Leu Ile Lys Thr
20      25      30
55 Ser Lys Thr Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr
35      40      45
Glu Glu Ile Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp
50      55      60
60 Lys Gly Glu Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser
65 Thr Leu Leu Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile
70 Tyr Lys Leu Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg
85      90      95
Thr Ala Val Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn
100      105      110
Leu Ile Glu Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val
115      120      125
75 Tyr Leu Gly Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala
130      135      140
Leu Arg Lys Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln
145      150      155      160
Leu Ser Gly Gly Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val
165      170      175
Ala Asn Pro Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp

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190/ 490

180 185 190
 Ser Lys Asn Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg
 195 200 205
 Glu Gly Ala Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg
 210 215 220
 Ser Ala Gly Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg
 225 230 235

(2) INFORMATION FOR SEQ ID NO:275
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 604 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...604
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

Ser Thr Glu Thr Asn Ser Lys Ser Glu Met Lys Glu Phe Phe Lys Met
 1 5 10 15
 Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu Phe
 20 25 30
 Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala Ser
 35 40 45
 Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile Leu
 50 55 60
 His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro Trp
 65 70 75 80
 Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala Val
 85 90 95
 Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile Phe
 100 105 110
 Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu Leu
 115 120 125
 Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val Ser
 130 135 140
 Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile Ala
 145 150 155 160
 Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly Ile
 165 170 175
 Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly Val
 180 185 190
 Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu Pro
 195 200 205
 Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr Thr
 210 215 220
 Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu Ser
 225 230 235 240
 Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly Glu
 245 250 255
 Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp Glu
 260 265 270
 Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser Gln
 275 280 285
 Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val Leu
 290 295 300
 Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val Leu
 305 310 315 320
 Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe Asp
 325 330 335
 Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys Ala
 340 345 350
 Ala Ala Asp Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn Ser
 355 360 365
 Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val Ala

191/ 490

370 375 380
 Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val Ala
 385 390 395 400
 5 Ala Ser Gly Gly Tyr Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val Ala
 405 410 415
 Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe Pro
 420 425 430
 Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val Val
 435 440 445
 10 Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met Thr
 450 455 460
 Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr Asp
 465 470 475 480
 15 Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala Gln
 485 490 495
 Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala Leu
 500 505 510
 Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile Lys
 515 520 525
 20 Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu Tyr
 530 535 540
 Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Leu Ser Ser Ser Ala
 545 550 555 560
 25 Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro Glu
 565 570 575
 Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser Gly
 580 585 590
 30 Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr
 595 600
 (2) INFORMATION FOR SEQ ID NO:276
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...324
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276
 Leu Thr Leu Phe Cys Cys Asn Tyr Phe Lys Gln Met Arg Ala Asn Ile
 1 5 10 15
 Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe Gly Thr Ala Ile
 20 25 30
 55 Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu Ala Tyr Val Lys Gln
 35 40 45
 Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg Tyr Asn Ile Pro Ala
 50 55 60
 60 Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr Gly Ala Gly Ala Ser
 65 70 75 80
 Thr Leu Ala Ser Val His Asn Asn His Phe Gly Ile Lys Cys His Lys
 85 90 95
 Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp Asp Ala Pro Asn Glu
 100 105 110
 65 Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser Tyr Glu Asp His Ser
 115 120 125
 Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu Phe Lys Leu Asp Arg
 130 135 140
 70 Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln Arg Cys Gly Tyr Ala
 145 150 155 160
 Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys Met Val Glu Leu Tyr
 165 170 175
 Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro Ser Trp Phe His Lys
 180 185 190
 75 Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln Thr Thr Lys Gln Lys

192/490

195 200 205
 Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser Tyr Gly Leu Leu Tyr
 210 215 220
 5 Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser Leu Ala Glu Glu Phe
 225 230 235 240
 Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn Asp Ala Pro Val Asp
 245 250 255
 Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu Glu Lys Lys His Ala
 260 265 270
 10 Cys Ser Ile Ser Lys His Thr Gln His Val Val Arg Val Gly Asp Ser
 275 280 285
 Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg Met Lys Asn Leu Tyr
 290 295 300
 15 Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro Gln Glu Gly Asp Ile
 305 310 315 320
 Leu Arg Leu Arg

20 (2) INFORMATION FOR SEQ ID NO:277

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 533 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

40 Arg Ile Pro Asp Glu Gln Thr Gly Arg Ile Met Asp Gly Arg Arg Tyr
 1 5 10 15
 Ser Asp Gly Leu His Gln Ala Ile Glu Ala Lys Glu His Val Lys Val
 20 25 30
 Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile Thr Leu Gln Asn Tyr Phe
 35 40 45
 45 Arg Met Tyr His Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr Glu
 50 55 60
 Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu Asp Val Val Ile Pro
 65 70 75 80
 50 Thr Asn Lys Pro Ile Ala Arg Lys Asp Met Asn Asp Arg Ile Tyr Lys
 85 90 95
 Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile Glu Glu Ile Val Arg Leu
 100 105 110
 Val Glu Glu Gly Arg Pro Val Leu Val Gly Thr Thr Ser Val Glu Ile
 115 120 125
 55 Ser Glu Leu Leu Ser Arg Met Leu Arg Leu Arg Gly Ile Gln His Asn
 130 135 140
 Val Leu Asn Ala Lys Leu His Gln Lys Glu Ala Glu Ile Val Ala Gln
 145 150 155 160
 60 Ala Gly Gln Lys Gly Thr Val Thr Ile Ala Thr Asn Met Ala Gly Arg
 165 170 175
 Gly Thr Asp Ile Lys Leu Ser Ala Glu Val Lys Lys Ala Gly Gly Leu
 180 185 190
 Ala Ile Ile Gly Thr Glu Arg His Glu Ser Arg Arg Val Asp Arg Gln
 195 200 205
 65 Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Ser Ser Ile Phe
 210 215 220
 Tyr Val Ser Leu Glu Asp His Leu Met Arg Leu Phe Ala Thr Glu Lys
 225 230 235 240
 70 Ile Ala Ser Leu Met Asp Arg Leu Gly Phe Lys Glu Gly Glu Val Leu
 245 250 255
 Glu Asn Asn Met Leu Ser Lys Ser Val Glu Arg Ala Gln Lys Lys Val
 260 265 270
 Glu Glu Asn Asn Phe Gly Ile Arg Lys His Leu Leu Glu Tyr Asp Asp
 275 280 285
 75 Val Met Asn Ser Gln Arg Glu Val Ile Tyr Thr Arg Arg Arg His Ala

193/490

290 295 300
 Leu Met Gly Glu Arg Ile Gly Met Asp Val Leu Asn Thr Ile Tyr Asp
 305 310 315 320
 Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala Glu Ala Asn Asp Phe Glu
 325 330 335
 Gly Phe Lys Glu Asp Leu Met Arg Ala Leu Ala Ile Glu Ser Pro Ile
 340 345 350
 Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala Glu Glu Leu Thr Asp Met
 355 360 365
 10 Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln Arg Lys Met Asp Leu Ile
 370 375 380
 Ala Glu Val Ala His Pro Val Val His Gln Val Phe Glu Thr Gln Ala
 385 390 395 400
 15 Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile Thr Asp Gly Lys Arg Val
 405 410 415
 Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala Asp Glu Thr Gln Gly Lys
 420 425 430
 Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile Val Leu His Thr Ile Asp
 435 440 445
 20 Glu Ser Trp Lys Glu His Leu Arg Glu Met Asp Glu Leu Arg Asn Ser
 450 455 460
 Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp Pro Leu Leu Ile Tyr Lys
 465 470 475 480
 25 Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met Val Glu Ala Met Asn Arg
 485 490 495
 Lys Thr Val Ala Ile Leu Met Arg Ala Arg Ile Pro Val Pro Glu Ala
 500 505 510
 Pro Ser Gln Glu Glu Leu Glu His Arg Arg Gln Ile Glu Ile Arg His
 515 520 525
 30 Ala Thr Gln Gln Arg
 530

(2) INFORMATION FOR SEQ ID NO:278

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 720 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 45 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...720
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

Lys Ser Cys Arg Val Ile Gly Gln Thr Arg Arg Tyr Gly Cys Cys Pro
 1 5 10 15
 55 Val Gly Leu Arg Pro Cys His Gln Ser Leu Ser Gly Val Cys Arg Cys
 20 25 30
 Leu Phe Gln Ser Arg Pro Ala Val Ala Phe Ala Arg Lys Gly Gln Arg
 35 40 45
 60 Arg His Arg Arg Ser Glu Ser Gly Arg Arg Ile Arg Ala Leu Gln Gly
 50 55 60
 Val Gln His His Gln Thr Asn Glu His Glu Val Met Ile Ser Val Asn
 65 70 75 80
 Asn Leu Thr Val Asp Phe Gly Thr Arg Leu Leu Phe Asp Gln Val Ser
 85 90 95
 65 Phe Val Ile Asn Arg Arg Asp Arg Ile Ala Leu Val Gly Lys Asn Gly
 100 105 110
 Ala Gly Lys Ser Thr Leu Leu Lys Leu Ile Ala Gly Met Glu Glu Pro
 115 120 125
 70 Thr Ser Gly His Ile Ala Arg Pro Lys Gly Ile Arg Ile Gly Tyr Leu
 130 135 140
 Pro Gln Val Met Arg Leu Gln Asp Gly His Thr Val Tyr Glu Glu Val
 145 150 155 160
 Glu Gln Ala Phe Asn Asp Ile Arg Gln Ile Glu Glu Glu Ile Arg Arg
 165 170 175
 75 Leu Ser Asp Glu Met Ala Gly Arg Thr Asp Tyr Glu Ser Asp Asp Tyr

194/ 490

180 185 190
 Ile Arg Leu Ile Glu His Tyr Thr Asn Met Ser Glu Thr Leu Ser Leu
 195 200 205
 Met Gln Gln Gly Asn Tyr His Ala Ala Ile Glu Gln Thr Leu Ile Gly
 210 215 220
 Leu Gly Phe Gly Arg Glu Asp Phe His Arg Pro Thr Ala Asp Phe Ser
 225 230 235 240
 Gly Gly Trp Arg Met Arg Ile Glu Leu Ala Lys Leu Leu Leu Gln Arg
 245 250 255
 10 Pro Glu Val Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ile Glu
 260 265 270
 Ser Ile Gly Trp Leu Glu Gln Phe Ile Ala Thr Asn Ala Gly Ala Val
 275 280 285
 15 Ile Leu Val Ser His Asp Arg Ala Phe Ile Asp Asn Thr Thr Thr Arg
 290 295 300
 Thr Ile Glu Ile Glu Leu Gly His Ile Tyr Asp Tyr Lys Thr Asn Tyr
 305 310 315 320
 Ser His Tyr Val Glu Leu Arg Glu Glu Arg Leu Arg Gln Gln Met Arg
 325 330 335
 20 Ala Tyr Glu Asn Gln Gln Lys Met Ile Arg Asp Thr Glu Asp Phe Ile
 340 345 350
 Glu Arg Phe Arg Tyr Lys Ala Thr Lys Ser Val Gln Val Gln Ser Arg
 355 360 365
 25 Ile Lys Gln Leu Glu Lys Val Glu Arg Val Glu Ile Asp Glu Arg Asp
 370 375 380
 Arg Ser Ala Phe His Phe Arg Phe Ile Pro Ala Gln Pro Ser Gly Ser
 385 390 395 400
 Tyr Pro Leu Ile Val Asp Asp Leu Ala Lys Ala Tyr Gly Asp His Gln
 405 410 415
 30 Val Phe Ser Gly Ala Thr Tyr Thr Ile Glu Arg Gly Glu Lys Val Ala
 420 425 430
 Phe Val Gly Lys Asn Gly Ala Gly Lys Ser Thr Met Val Lys Cys Ile
 435 440 445
 35 Met Gly Glu Leu Thr Asp Tyr Thr Gly Lys Leu Glu Leu Gly His Asn
 450 455 460
 Val Gln Leu Gly Tyr Phe Ala Gln Asn Glu Ala Gln Glu Leu Arg Gly
 465 470 475 480
 Asp Leu Thr Val Phe Asp Thr Ile Asp Arg Glu Ala Val Gly Asp Ile
 485 490 495
 40 Arg Leu Arg Leu Asn Asp Leu Leu Gly Ala Phe Leu Phe Gly Gly Glu
 500 505 510
 Ala Ser Glu Lys Lys Val Ser Val Leu Ser Gly Gly Glu Arg Ala Arg
 515 520 525
 45 Leu Ala Ile Ile Arg Leu Leu Gln Pro Ala Asn Phe Leu Ile Leu
 530 535 540
 Asp Glu Pro Thr Asn His Leu Asp Met Arg Ser Lys Asp Val Leu Lys
 545 550 555 560
 Glu Ala Ile Lys Asn Phe Asp Gly Thr Val Ile Val Val Ser His Asp
 565 570 575
 50 Arg Glu Phe Leu Asp Gly Leu Val Ser Lys Val Tyr Glu Phe Ala Asp
 580 585 590
 Gly Gln Val Asn Glu His Leu Gly Gly Ile Tyr Asp Tyr Leu Arg Thr
 595 600 605
 55 Arg Arg Met Gln Thr Leu Thr Glu Leu Glu Arg Thr Thr Thr Ile Glu
 610 615 620
 Thr Lys Thr Thr Arg Glu Ala Ile Pro Glu Thr Glu Ala Lys Ala Asp
 625 630 635 640
 Tyr Arg Arg Gln Lys Glu Val Ala Lys Gln Leu Arg Thr Leu Glu Arg
 645 650 655
 60 Thr Val Ala Thr Cys Glu Glu Arg Ile Gly Lys Leu Glu Ser Glu Leu
 660 665 670
 Gln Ala Ile Glu Met Leu Leu Gln Asp Pro Lys His Ala Thr Asp Ala
 675 680 685
 65 Asn Leu Phe Glu Arg Tyr Ala Gly Met Lys Gln Glu Leu Glu Lys Ala
 690 695 700
 Met Glu Asp Trp Glu Gln Ala Ser Glu Ala Leu Ser Glu Ala Gln Gly
 705 710 715 720

(2) INFORMATION FOR SEQ ID NO:279

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

195/ 490

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
10 (A) NAME/KEY: misc feature
(B) LOCATION 1...385
(x) SEQUENCE DESCRIPTION: SEQ ID NO:279
15 Tyr Leu Lys Leu Leu Ile Leu Gln Ile Ala Leu Met Asn Phe Leu Lys
1 5 10 15
Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr Leu Leu Leu Asp Thr
20 20 25 30
Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val Ile Asn Leu Ala Asn
35 40 45
20 Asn Leu His Ala Asn Gly His Arg Val Ser Leu Val Ser Val Cys Thr
50 55 60
Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys Gly Ile Glu Val His
65 70 75 80
25 His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu Ala Arg Lys Thr Val
85 90 95
Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu Tyr Lys Lys Arg Glu
100 105 110
Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile Asn Thr Ile Leu Ser
115 120 125
30 Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile Gly Cys Glu His Ile
130 135 140
Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg Ile Arg Gly Phe Leu
145 150 155 160
35 Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr Lys Arg Asp Gln Gln
165 170 175
Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys Ala Tyr Val Ile Pro
180 185 190
Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp Ala Thr Thr His Lys
195 200 205
40 Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln Lys Gly Phe Glu Phe
210 215 220
Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu Arg Pro Asp Trp Lys
225 230 235 240
45 Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser Met Leu Arg Lys Glu
245 250 255
Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu Ile His Pro Ser Thr
260 265 270
Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala Ile Tyr Leu Met Thr
275 280 285
50 Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu Glu Ala Glu Ala Tyr
290 295 300
Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr Gly Pro Arg Glu Leu
305 310 315 320
55 Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro Met Glu Ala His Glu
325 330 335
Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp Asp Glu Thr Leu Arg
340 345 350
Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val Lys Ser Tyr Ser Pro
355 360 365
60 Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe Val Glu Ile Gly Tyr
370 375 380
Met Asn
385
65 (2) INFORMATION FOR SEQ ID NO:280
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 655 amino acids
70 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
75 (iii) HYPOTHETICAL: YES

196/490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

10 Thr Thr Lys Glu Asn Glu Thr Thr Thr Lys Asn Glu Tyr Arg Ile Met
1 5 10 15
Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val Ser
20 25 30
15 Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly Lys
35 40 45
Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Glu Arg Lys
50 55 60
Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys Thr
65 70 75 80
20 Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val Ser
85 90 95
Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn Asn
100 105 110
25 Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu Ile
115 120 125
Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr Leu
130 135 140
Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe Asn
145 150 155 160
30 Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly Leu
165 170 175
Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala Tyr
180 185 190
35 Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp Leu
195 200 205
Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly Val
210 215 220
Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp Asp
225 230 235 240
40 Phe Asp His Val Ile Ile Asp Trp Leu Ala Glu Glu Phe Lys Ser Gln
245 250 255
Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu Lys
260 265 270
45 Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser Thr
275 280 285
Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys His
290 295 300
Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp Arg
305 310 315 320
50 Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp Ala
325 330 335
Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly Ser
340 345 350
55 Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly Lys
355 360 365
Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala
370 375 380
Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu Leu
385 390 395 400
60 Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly Val
405 410 415
Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys Ser
420 425 430
65 Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile His
435 440 445
Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile Gly
450 455 460
Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro Gln
465 470 475 480
70 Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Thr
485 490 495
Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu Ala
500 505 510
75 Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu Ala
515 520 525

197/490

Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp Lys
 530 535 540
 Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu Lys
 545 550 555 560
 5 Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp Thr
 565 570 575
 Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala Ala
 580 585 590
 10 Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala Gly
 595 600 605
 Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln Pro
 610 615 620
 Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln Pro
 625 630 635 640
 15 Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys
 645 650 655

(2) INFORMATION FOR SEQ ID NO:281

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 467 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...467
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

Lys Trp Ala Arg Thr Thr Leu Arg Ile Ser Asn Ala Thr Ile Tyr
 1 5 10 15
 40 Lys Thr Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly
 20 25 30
 Tyr Thr Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu
 35 40 45
 45 Ile Glu Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile
 50 55 60
 Pro Thr Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala
 65 70 75 80
 Thr Ala Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu
 85 90 95
 50 Gly Lys Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala
 100 105 110
 Gly Ile Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala
 115 120 125
 55 Glu Ala Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr
 130 135 140
 Ala Gly Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Cys Thr Gly
 145 150 155 160
 Ser Glu Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr
 165 170 175
 60 Tip Thr Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu
 180 185 190
 Val Ile Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe
 195 200 205
 65 Asn Gly Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile
 210 215 220
 Leu Asn Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr
 225 230 235 240
 Glu Lys Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val
 245 250 255
 70 Arg Asn Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile
 260 265 270
 Glu Gly Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln
 275 280 285
 75 Gly Phe Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr
 290 295 300

198/490

Asn Glu Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp
 305 310 315 320
 Ile Thr Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu
 325 330 335
 5 Val Ala Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr
 340 345 350
 Arg Ala Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val
 355 360 365
 10 Gly Glu Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val
 370 375 380
 Arg Arg Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu
 385 390 395 400
 Gln Gly Asn Gly Glu Cys Lys Leu Leu Asn Glu Glu Asn Arg Leu
 405 410 415
 15 Ile Gly Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr
 420 425 430
 Ala Ala Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg
 435 440 445
 20 Ile Ile Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu
 450 455 460
 Ala Gly Gly
 465
 (2) INFORMATION FOR SEQ ID NO:282
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 945 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...945
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282
 Pro Lys Ile Leu Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu
 1 5 10 15
 Leu Val Gly Phe Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro
 20 25 30
 Leu Pro Thr Asp Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu
 35 40 45
 50 Thr Tyr Phe Ile Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe
 50 55 60
 Phe Ile Ala Gln Lys Val Gly Ser Ile Leu Glu Glu Asp Ser Gln Ser
 65 70 75 80
 Gly Leu Ala His Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn
 85 90 95
 55 Phe Pro Gly Lys Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg
 100 105 110
 Phe Gly Gln Asn Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr
 115 120 125
 60 Thr Ile Met Asp Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys
 130 135 140
 Leu Leu Ile Leu His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His
 145 150 155 160
 65 Glu Ile Asp Glu Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg
 165 170 175
 Arg Asp Ala Asn Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met
 180 185 190
 Pro Gly Asn Lys Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val
 195 200 205
 70 Val Leu Asn Phe Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp
 210 215 220
 Tyr Arg Pro Asp Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val
 225 230 235 240
 75 Asp Tyr Val Glu Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala
 245 250 255

Pro Val Asn Pro Ala Glu Arg Ile Tyr Thr Pro Val Glu Asp Asn Asp
260 265 270
Glu Pro Ile Val Ala Ile Ala Thr Asp Ala Glu Ala Thr Thr Thr Gln
275 280 285
5 Leu Ser Ile Ser Phe Lys Ser Asp Pro Thr Pro Gln Glu Val Arg Gly
290 295 300
Ser Ile Phe Gly Leu Val Glu Asp Tyr Met Lys Gln Val Ile Thr Thr
305 310 315 320
10 Ala Val Asn Glu Arg Leu Ser Glu Ile Thr His Lys Pro Asn Ala Pro
325 330 335
Phe Leu Ser Ala Gly Ala Phe Phe Ser Asn Phe Met Tyr Ile Thr Gln
340 345 350
Thr Lys Asp Ala Phe Asn Phe Val Ala Thr Val Arg Glu Gly Glu Ala
355 360 365
15 Glu Lys Ala Met Asn Ala Leu Val Ala Glu Ile Glu Ser Leu Arg Gln
370 375 380
Phe Gly Ile Thr Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu
385 390 395 400
20 Lys Arg Tyr Glu Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn
405 410 415
Ala Tyr Ala Asn Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile
420 425 430
Pro Gly Ile Glu Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln
435 440 445
25 Val Pro Leu Glu Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro
450 455 460
Val Lys Asn Ala Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala
465 470 475 480
30 Lys Ile Pro Ser Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg
485 490 495
Gln Gln Lys Val Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu
500 505 510
Met Glu Lys Ala Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp
515 520 525
35 Gln Lys Phe Gly Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val
530 535 540
Tyr Leu Lys Lys Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala
545 550 555 560
40 Leu Ser Pro Gly Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser
565 570 575
Val Met Asn Ser Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala
580 585 590
Ile Gln Leu Asp Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro
595 600 605
45 Ser Leu Ser Leu Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu
610 615 620
Asp Met Glu Thr Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn
625 630 635 640
50 Arg Lys Asp Pro Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn
645 650 655
Asn Leu Lys Asn Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser
660 665 670
Ile Arg His Thr Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys
675 680 685
55 Ala Ala Asp Val Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr
690 695 700
Asn Glu Arg Phe Ala Asp Ala Gly Asp Phe Met Phe Phe Ile Gly
705 710 715 720
60 Asn Leu Asp Glu Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala
725 730 735
Ser Leu Pro Asn Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val
740 745 750
Pro Ala Ala Arg Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met
755 760 765
65 Asp Thr Pro Ser Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu
770 775 780
Tyr Thr Leu Lys Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met
785 790 795 800
70 Asp Gln Val Tyr Thr Ala Thr Val Arg Glu Lys Glu Gly Gly Ala Tyr
805 810 815
Ser Val Ala Ala Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala
820 825 830
Leu Met Gln Ile Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met
835 840 845
75 Asn Ala Ile Val Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro

200/ 490

850
 Asn Val Glu Tyr Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His
 865
 Lys Glu Ser Leu Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala
 5
 Ser Phe Phe Glu Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu
 900
 Asn Gly Leu Thr Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu
 915
 10 Lys Gln Gln Asn Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala
 930
 Gln
 945
 15 (2) INFORMATION FOR SEQ ID NO:283
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 686 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 20
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 25
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...686
 30
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283
 35 Tyr Thr Met Ser Lys Lys Gly Thr Ile Gly Val Thr Ser Asp Asn Ile
 1 5 10 15
 Phe Pro Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu
 20 25 30
 40 Arg Glu Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr
 35 40 45
 Leu Thr Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val
 50 55 60
 Thr Val Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg
 65 70 75 80
 45 Gly Val Gly Met Thr Glu Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile
 85 90 95
 Ala Phe Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys
 100 105 110
 50 Ala Ala Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met
 115 120 125
 Val Ser Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala
 130 135 140
 Thr Ala Val Lys Trp Ser Cys Asp Gly Ser Pro Glu Tyr Thr Leu Glu
 145 150 155 160
 55 Pro Ala Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp
 165 170 175
 Glu Glu Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu
 180 185 190
 60 Gly Lys Tyr Cys Lys Phe Leu Thr Val Pro Ile Ile Phe Gly Lys Lys
 195 200 205
 Gln Glu Trp Lys Asp Gly Lys Met Gln Asp Thr Asp Glu Asp Asn Gln
 210 215 220
 Ile Asn Asp Thr His Pro Ala Trp Thr Lys Lys Pro Ala Asp Leu Lys
 225 230 235 240
 65 Asp Glu Asp Tyr Lys Glu Phe Tyr Arg Ser Leu Tyr Pro Met Ser Glu
 245 250 255
 Glu Pro Leu Phe Trp Ile His Leu Asn Val Asp Tyr Pro Phe Asn Leu
 260 265 270
 70 Thr Gly Ile Leu Tyr Phe Pro Lys Ile Lys Asn Asn Leu Asp Leu Gln
 275 280 285
 Arg Asn Lys Ile Gln Leu Tyr Cys Asn Gln Val Tyr Val Thr Asp Glu
 290 295 300
 Val Gln Gly Ile Val Pro Asp Phe Leu Thr Leu Leu His Gly Val Ile
 305 310 315 320
 75 Asp Ser Pro Asp Ile Pro Leu Asn Val Ser Arg Ser Tyr Leu Gln Ser

201/ 490

				325						330					335	
	Asp	Ala	Asn	Val	Lys	Lys	Ile	Ser	Ser	His	Ile	Thr	Lys	Lys	Val	Ala
				340					345					350		
5	Asp	Arg	Leu	Glu	Glu	Ile	Phe	Lys	Asn	Asp	Arg	Pro	Thr	Phe	Glu	Glu
			355					360					365			
	Lys	Trp	Asp	Ser	Leu	Lys	Leu	Phe	Val	Glu	Tyr	Gly	Met	Leu	Thr	Asp
		370					375					380				
	Glu	Lys	Phe	Tyr	Glu	Arg	Ala	Ala	Lys	Phe	Phe	Leu	Phe	Thr	Asp	Met
	385					390					395				400	
10	Asp	Gly	His	Lys	Tyr	Thr	Phe	Asp	Glu	Tyr	Arg	Thr	Leu	Val	Glu	Gly
				405						410					415	
	Val	Gln	Thr	Asp	Lys	Asp	Gly	Gln	Val	Val	Tyr	Leu	Tyr	Ala	Thr	Asp
			420						425					430		
	Lys	His	Gly	Gln	Tyr	Ser	His	Val	Lys	Arg	Ala	Ser	Asp	Lys	Gly	Tyr
15			435				440					445				
	Ser	Val	Met	Leu	Leu	Asp	Gly	Gln	Leu	Asp	Pro	His	Ile	Val	Ser	Leu
	450					455					460					
	Leu	Glu	Gln	Lys	Leu	Glu	Lys	Thr	His	Phe	Val	Arg	Val	Asp	Ser	Asp
	465					470					475				480	
20	Thr	Ile	Asn	Asn	Leu	Ile	Arg	Lys	Glu	Glu	Arg	Ala	Glu	Val	Lys	Leu
				485						490					495	
	Ser	Asp	Thr	Glu	Arg	Ala	Thr	Leu	Val	Lys	Leu	Phe	Glu	Ala	Arg	Leu
			500						505					510		
25	Pro	Arg	Asp	Glu	Lys	Lys	His	Phe	Asn	Val	Ala	Phe	Glu	Ser	Leu	Gly
			515					520				525				
	Ala	Glu	Gly	Glu	Ala	Ile	Leu	Ile	Thr	Gln	Ala	Glu	Phe	Met	Arg	Arg
		530				535					540					
	Met	Arg	Asp	Met	Ala	Gln	Leu	Gln	Pro	Gly	Met	Ser	Phe	Tyr	Gly	Glu
	545				550				555						560	
30	Leu	Pro	Asp	Ser	Tyr	Asn	Leu	Val	Leu	Asn	Thr	Asp	His	Pro	Leu	Ile
				565					570					575		
	Asp	Arg	Val	Leu	Ser	Gly	Glu	Lys	Glu	Ser	Val	Glu	Pro	Ser	Leu	Thr
			580						585				590			
35	Glu	Leu	Arg	Ala	Lys	Ile	Ala	Glu	Leu	Lys	Ala	Glu	Glu	Ala	Lys	Leu
			595					600					605			
	Leu	Asp	Glu	Glu	Lys	Gly	Lys	Lys	Pro	Glu	Glu	Ile	Pro	Val	Ala	Thr
		610				615					620					
	Lys	Glu	Ala	Lys	Glu	Asn	Asn	Ala	Val	Glu	Gln	Ala	Lys	Thr	Glu	Gly
	625				630					635					640	
40	Ser	Ile	Asn	Asp	Gln	Leu	Thr	Lys	Tyr	Ala	Gln	Asp	Asn	Glu	Leu	Ile
				645						650					655	
	Gly	Gln	Leu	Ile	Asp	Leu	Ala	Leu	Leu	Gly	Ser	Gly	Leu	Leu	Thr	Gly
			660					665						670		
45	Glu	Ala	Leu	Ala	Glu	Phe	Ile	Arg	Arg	Ser	Gln	Arg	Leu	Leu		
			675					680					685			

(2) INFORMATION FOR SEQ ID NO:284

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 482 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- 60 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...482
- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

	Asp	Ile	Arg	Gln	Lys	Arg	Pro	Cys	Phe	Asn	Ala	Asn	Leu	Tyr	Phe	Tyr
	1				5					10					15	
70	Arg	Ala	Met	Glu	Lys	Leu	Ile	Asp	Ile	Leu	Val	Val	Asp	Asp	Asp	Val
			20					25					30			
	Ala	Val	Cys	Ala	Ala	Leu	Arg	Leu	Val	Leu	Lys	Arg	Ala	Gly	Tyr	Asn
			35					40					45			
	Pro	Val	Ile	Ala	Asn	Ser	Pro	Asp	Glu	Ala	Leu	Ser	Ile	Met	Arg	Asn
		50					55					60				
75	Pro	Asp	Gly	Gly	Cys	Lys	Pro	Ala	Val	Ile	Leu	Met	Asp	Met	Asn	Phe

	65					70				75						80
	Ser	Leu	Ser	Thr	Ser	Gly	Arg	Glu	Gly	Leu	Glu	Leu	Leu	Glu	Lys	Met
					85					90					95	
5	Gln	Ile	Phe	Thr	Ser	Cys	Pro	Val	Ile	Leu	Met	Thr	Ala	Trp	Ala	Ser
				100					105					110		
	Ile	Pro	Leu	Ala	Val	Glu	Gly	Met	Arg	Leu	Gly	Ala	Phe	Asp	Phe	Ile
			115					120					125			
	Gly	Lys	Pro	Trp	Asp	Asn	Asp	Arg	Leu	Leu	Arg	Thr	Ile	Asp	Thr	Ala
		130				135						140				
10	Leu	His	Leu	Ala	Ala	Pro	Ser	Ala	Val	Ala	Asn	Pro	Ser	Glu	Gln	Ser
		145				150					155					160
	Asp	Arg	Asp	Thr	Ala	Arg	Gln	Pro	Lys	Ala	Thr	Val	Gln	Glu	Asn	Asp
				165						170					175	
15	Pro	Cys	Ala	His	Ile	Ile	Gly	Arg	Ser	Asp	Ala	Ile	Cys	Lys	Ile	Lys
				180					185					190		
	Glu	Arg	Ile	Arg	Arg	Ile	Ala	Pro	Thr	His	Ala	Ser	Val	Leu	Ile	Thr
			195					200					205			
	Gly	Glu	Ser	Gly	Thr	Gly	Lys	Glu	Leu	Ile	Ala	Glu	Ala	Leu	His	Arg
		210				215						220				
20	Gly	Ser	Lys	Arg	Ala	Ser	Ala	Pro	Phe	Val	Lys	Val	Asn	Leu	Gly	Gly
		225				230					235				240	
	Ile	Pro	Glu	Ser	Leu	Phe	Glu	Ser	Glu	Leu	Phe	Gly	His	Lys	Lys	Gly
				245					250					255		
25	Ala	Phe	Thr	Asn	Ala	Phe	Ser	Asp	Arg	Lys	Gly	Arg	Phe	Glu	Leu	Ala
			260						265					270		
	Asp	Gly	Gly	Thr	Ile	Phe	Leu	Asp	Glu	Ile	Gly	Glu	Leu	Pro	Val	Gly
			275					280					285			
	Asn	Gln	Val	Lys	Leu	Leu	Arg	Val	Leu	Gln	Glu	Gln	Thr	Phe	Glu	Pro
		290					295					300				
30	Leu	Gly	Glu	Ser	Val	Ser	His	Arg	Val	Asp	Ile	Arg	Val	Val	Ser	Ala
		305				310					315					320
	Thr	Asn	Ala	Ser	Leu	Glu	Arg	Met	Val	Ala	Glu	Gly	Arg	Phe	Arg	Glu
				325						330					335	
35	Asp	Leu	Tyr	Tyr	Arg	Ile	Asn	Leu	Ile	His	Leu	His	Leu	Pro	Pro	Leu
			340						345					350		
	Arg	Glu	Arg	Gln	Glu	Asp	Ile	Gln	Leu	Leu	Val	Glu	Ala	Phe	Ser	Glu
			355					360					365			
	Ala	Phe	Ala	Gln	Ser	Asn	Gly	Leu	Pro	His	Ala	Val	Trp	Ser	Ala	Glu
		370					375					380				
40	Ala	Met	Arg	Arg	Ile	Cys	Ala	Met	Pro	Leu	Pro	Gly	Asn	Val	Arg	Glu
		385				390					395					400
	Leu	Lys	Asn	Val												

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...263
```

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:285

Arg Ser Leu Gln Ser Phe Gln Asn Lys Lys His Ser Ser Met Leu Lys

[illegible]

```

35      (2) INFORMATION FOR SEQ ID NO:286

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 462 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: protein

          (iii) HYPOTHETICAL: YES

45      (vi) ORIGINAL SOURCE:
              (A) ORGANISM: Porphyromonas gingivalis

          (ix) FEATURE:
              (A) NAME/KEY: misc_feature
              (B) LOCATION 1...462

50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

```

55	Ser	Met	Ala	Lys	Glu	Lys	Thr	Ile	Tyr	Val	Cys	Arg	Ser	Cys	Gly	Thr
	1			5						10					15	
	Lys	Tyr	Ala	Lys	Trp	Gln	Gly	Asn	Cys	Asn	Ala	Cys	Gly	Glu	Trp	Asn
				20					25					30		
60	Cys	Ile	Asp	Glu	Glu	Lys	Val	Pro	Ala	Pro	Ala	Ser	Gly	Lys	His	Ala
			35					40					45			
	Ala	Lys	Ser	Phe	Met	Pro	Arg	Glu	Gln	Asp	Asn	Arg	Pro	Arg	Leu	Leu
			50				55					60				
	Gln	Asp	Val	Glu	Ser	Gly	Asp	Glu	Glu	Arg	Ile	Arg	Leu	Gly	Asp	Glu
			65			70				75					80	
65	Glu	Phe	Asp	Arg	Val	Leu	Gly	Gly	Gly	Ile	Val	Lys	Gly	Ala	Phe	Val
					85					90				95		
	Leu	Leu	Gly	Gly	Glu	Pro	Gly	Ile	Gly	Lys	Ser	Thr	Leu	Ile	Leu	Gln
				100					105					110		
70	Thr	Val	Leu	Arg	Leu	Pro	Gln	Leu	Arg	Thr	Leu	Tyr	Val	Ser	Gly	Glu
				115				120					125			
	Glu	Ser	Ala	Arg	Gln	Leu	Lys	Met	Arg	Ala	Glu	Arg	Leu	Gly	Gln	Ala
				130			135						140			
	Met	Asn	Gly	Cys	Tyr	Val	Tyr	Cys	Glu	Thr	Asn	Ile	Glu	Arg	Ile	Leu
						150					155				160	
75	Ser	Arg	Ala	Glu	Glu	Leu	Thr	Pro	Asp	Leu	Leu	Val	Ile	Asp	Ser	Ile

204/ 490

165 170 175
Gln Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly
180 185 190
5 Gln Ile Arg Glu Cys Ala Ala Leu Leu Leu Lys Tyr Cys Lys Thr Thr
195 200 205
Gly Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile
210 215 220
Ala Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe
225 230 235 240
10 Asp Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn
245 250 255
Arg Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp
260 265 270
15 Gly Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn
275 280 285
Arg Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile
290 295 300
Arg Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr
305 310 315 320
20 Ala Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn
325 330 335
Met Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln
340 345 350
25 Lys Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro
355 360 365
Ala Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp
370 375 380
Ile Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser
385 390 395 400
30 Gly Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala
405 410 415
Arg Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg
420 425 430
35 Gln Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys
435 440 445
Val Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu
450 455 460

(2) INFORMATION FOR SEQ ID NO:287

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

60 Gly Ser Cys Gly Ser Ser Pro Ala Ile Gly Arg Ser Gly Cys Ser Arg
1 5 10 15
Cys Asp Arg Arg Ile Gly His Gly Leu Ser Thr Ser Ala Phe Arg Thr
20 25 30
Tyr Ala Gly Leu Val Cys His Ser Arg Leu Arg Asp Gln Ser Ser Cys
35 40 45
65 Arg Val Cys Gly Met Arg Pro Ile Gly Gln Leu Phe Phe Pro Ser Cys
50 55 60
Pro Arg Arg Ser Ala Ser Asp Ala Gly Arg Thr Glu Arg Ile Gln Ser
65 70 75 80
70 Pro Leu Gln Asn Leu Leu Gln Glu Met Gln Phe Ser Pro Thr Asn Arg
85 90 95
Arg Asn Pro Phe Asp Asn Met Asn Ser Arg His Leu Thr Ile Thr Ile
100 105 110
Ile Ala Gly Leu Ser Leu Phe Val Leu Thr Leu Gly Gly Cys Ser Val
115 120 125
75 Ala Gln Gln Asp Thr Gln Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser

205 / 490

130 135 140
 Ala Trp Ile Gln Arg Ser Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala
 145 150 155 160
 Tyr Asn Ile Ala Thr Glu Arg Val Asp Ala Leu Pro Ala Glu Arg Lys
 165 170 175
 Gln Gly Asp Arg Pro Tyr Ala Ile Val Thr Asp Ile Asp Glu Thr Ile
 180 185 190
 Leu Asp Asn Thr Pro Asn Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp
 195 200 205
 10 Tyr Asp Glu Glu Thr Trp Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp
 210 215 220
 Thr Leu Ala Gly Ala Leu Ser Phe Phe Leu His Ala Ala Asn Lys Gly
 225 230 235 240
 Ile Glu Val Phe Tyr Val Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala
 245 250 255
 15 Thr Leu Gln Asn Leu Gln Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu
 260 265 270
 His Leu Leu Thr Thr His Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu
 275 280 285
 20 Lys Ile Gln Glu Gln Tyr Glu Ile Val Leu Leu Ile Gly Asp Asn Leu
 290 295 300
 Gly Asp Phe His His Phe Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys
 305 310 315 320
 Gln Ala Leu Gly Leu Thr Ala Gly Glu Phe Gly Arg His Phe Ile Met
 325 330 335
 25 Leu Pro Asn Pro Asn Tyr Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly
 340 345 350
 Lys Tyr Pro Pro Leu Pro Glu Arg Asp Lys Ala Leu Lys Gln Leu His
 355 360 365
 30 Ser Gln Asn Ser Arg
 370

(2) INFORMATION FOR SEQ ID NO:288

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 426 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) LOCATION 1...426
 50 (xii) SEQUENCE DESCRIPTION: SEQ ID NO:288

Arg Trp Gly Phe Ser Asn Phe Val Ala Met Ser Thr Asn Ile Asp Val
 1 5 10 15
 55 Gln Gln Ile Lys Gln Arg Phe Gly Ile Ile Gly Ser Ser Pro Leu Met
 20 25 30
 Glu His Ala Ile Arg Val Ala Ala Gln Val Ala Pro Thr Asp Met Ser
 35 40 45
 60 Val Leu Val Thr Gly Glu Ser Gly Ser Gly Lys Glu Phe Phe Pro Gln
 50 55 60
 Ile Ile His Tyr Tyr Ser Ala Arg Lys His His Ser Tyr Ile Ala Val
 65 70 75 80
 Asn Cys Gly Ala Ile Pro Glu Gly Thr Ile Asp Ser Glu Leu Phe Gly
 85 90 95
 65 His Arg Lys Gly Ser Phe Thr Gly Ala Val Ser Asp Arg Lys Gly Tyr
 100 105 110
 Phe Glu Glu Ala Ser Gly Gly Thr Ile Phe Leu Asp Glu Val Gly Glu
 115 120 125
 70 Leu Pro Leu Pro Thr Gln Ala Arg Leu Leu Arg Val Leu Glu Thr Gly
 130 135 140
 Glu Phe Ile Pro Val Gly Ala Ser Gln Ser Gln Lys Thr Asp Val Arg
 145 150 155 160
 Ile Val Ala Ala Thr Asn Val Asn Leu Lys Glu Ala Val Ala Asn Gly
 165 170 175
 75 Lys Phe Arg Glu Asp Leu Phe Phe Arg Leu Asn Thr Val Pro Ile Glu

206/ 490

180 185 190
 Val Pro Ala Leu Arg Met Arg Pro Asp Asp Val Pro Leu Leu Phe Arg
 195 200 205
 Arg Phe Ala Ala Asp Ser Ala Glu Lys Tyr Arg Met Pro Pro Leu Arg
 210 215 220
 Leu Ser Asp Glu Ala Arg Thr Ile Leu Met Arg Tyr Arg Trp Pro Gly
 225 230 235 240
 Asn Val Arg Glu Leu Arg Asn Ile Thr Asp Arg Leu Ser Ile Leu Glu
 245 250 255
 10 Glu Glu Arg Thr Val Ser Ala Glu Thr Ile Thr Arg Tyr Leu Asp Ala
 260 265 270
 Glu Gly Met Gln Asp Leu His Pro Val Val Ile Arg Arg Asn Glu Thr
 275 280 285
 15 Thr Glu Ala Asp Lys Gln Ile Pro His Tyr Glu Arg Glu Ile Ile Tyr
 290 295 300
 Gln Val Leu Tyr Asp Met Lys Lys Glu Ile Ala Asp Leu Lys Gly Met
 305 310 315 320
 Met Asn Arg Leu Ala His His Glu Gln Pro Ser Trp Pro Val Gly Ser
 325 330 335
 20 Asp Val Trp Gly Asn Asp Asp Lys Arg Thr Ala Asp Pro Lys Trp Gly
 340 345 350
 Val Ser Thr His Lys Ala Pro Ile Ala Asn Ala Ala Glu Pro Val Glu
 355 360 365
 25 Pro Ile Gln Glu Ala Ser Glu Tyr Thr Glu Asp Pro Val Ser Leu Glu
 370 375 380
 Glu Val Glu Lys Lys Met Ile Ser Leu Ala Leu Glu Arg His Gly Gly
 385 390 395 400
 Arg Arg Lys Gln Thr Ala Glu Glu Leu Lys Ile Ser Glu Arg Thr Leu
 405 410 415
 30 Tyr Arg Lys Ile Lys Glu Tyr Gly Leu Glu
 420 425

(2) INFORMATION FOR SEQ ID NO:289

- 35 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 653 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...653
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

Lys Asn Leu Pro Arg Tyr Ala Pro Ala Phe Gly Arg Asn Arg Lys Arg
 1 5 10 15
 55 Glu Gln Pro Asp Pro Asp Asn Asp Asp Ser Arg Gly Arg Ser His Arg
 20 25 30
 Gln Ser Gly Arg Ala Val Thr Val Val Cys Arg Arg Ile Gln Thr Pro
 35 40 45
 60 Leu Pro His Met Ile Leu Leu Phe Gly Gly Thr Thr Glu Gly Arg Ala
 50 55 60
 Ala Ala Arg Val Leu Asp Glu Ala Gly Ser Pro Phe Phe Tyr Ser Thr
 65 70 75 80
 Lys Gly Asn Leu Gln Glu Ile Gln Ser Ser His Gly His Arg Leu Thr
 85 90 95
 65 Gly Ala Met Thr Val Ala Asp Met Val Ser Phe Cys Arg Lys Glu Glu
 100 105 110
 Ile Arg Leu Ile Val Asp Ala Ala His Pro Phe Ala Glu Glu Leu His
 115 120 125
 70 Ala Ser Val Ala Glu Ala Ser Glu Gln Thr Gly Ile Pro Val Val Arg
 130 135 140
 Tyr Glu Arg Gln Tyr Pro Pro Arg Glu Glu Gly Ile Val Trp Cys Ala
 145 150 155 160
 Asn Tyr Asp Thr Ala Ala Glu Arg Met Leu Gly Asp Gly Val Gln Arg
 165 170 175
 75 Leu Leu Met Leu Thr Gly Val Asn Thr Ile Pro Lys Leu Ala Ala Phe

207/ 490

180 185 190
 Trp Lys Glu Arg Thr Thr Phe Cys Arg Ile Leu Lys Arg Asp Glu Ser
 195 200 205
 5 Val Ala Leu Ala Glu Lys Asn Gly Phe Pro Ala Glu Arg Ile Val Phe
 210 215 220
 Phe Glu Pro His Ala Asp Glu Leu Met Gln Ala Val Arg Pro Asp
 225 230 235 240
 Ala Ile Ile Thr Lys Glu Ser Gly Glu Ser Gly Tyr Phe Arg Glu Lys
 245 250 255
 10 Ile Glu Ala Ala Arg Arg Met Gly Ile Arg Ile Tyr Ala Val Arg
 260 265 270
 Pro Pro Leu Pro Pro Ser Phe Ile Pro Val Gly Gly Pro Val Gly Leu
 275 280 285
 15 Arg Arg Ala Val Glu Arg Leu Val Pro Gly Phe Phe Ser Leu Arg Ser
 290 295 300
 Gly Phe Thr Thr Gly Thr Thr Ala Thr Ala Val Val Ala Ala Met
 305 310 315 320
 Tyr Arg Leu Met Gly Leu Gly Ser Leu Ala Glu Ala Pro Val Glu Leu
 325 330 335
 20 Pro Ser Gly Glu Ile Val Ser Leu Pro Ile Ala Glu Ile Arg Glu Glu
 340 345 350
 Glu Asp Ala Val Val Ser Ala Val Leu Lys Asp Ala Gly Asp Asp Pro
 355 360 365
 25 Asp Val Thr Asn Gly Met Ala Val Cys Ala Thr Ile Arg Leu Asn Pro
 370 375 380
 Glu His Glu Glu Val Arg Phe Leu Gln Gly Glu Gly Val Gly Val Val
 385 390 395 400
 Thr Leu Pro Gly Leu Gly Leu Glu Val Gly Gly Pro Ala Ile Asn Leu
 405 410 415
 30 Val Pro Arg Arg Met Met Thr Ala Glu Val Arg Arg Leu Tyr Ala Gln
 420 425 430
 Gly Gly Val Asp Ile Thr Ile Ser Val Pro Glu Gly Arg Glu Ala Ala
 435 440 445
 35 Thr Gln Thr Phe Asn Pro Arg Leu Gly Ile Arg Asp Gly Ile Ser Ile
 450 455 460
 Ile Gly Thr Ser Gly Val Val Lys Pro Phe Ser Ala Glu Ala Phe Val
 465 470 475 480
 Gly Ala Ile Arg Lys Gln Val Gly Ile Ala Thr Ala Leu Gly Ala Asn
 485 490 495
 40 His Ile Val Leu Asn Ser Gly Ala Lys Ser Glu Arg Tyr Val Lys Gly
 500 505 510
 Ala Tyr Pro Ala Leu Ile Pro Gln Ala Phe Val Gln Tyr Gly Asn Phe
 515 520 525
 45 Val Gly Glu Ser Leu Ser Cys Val Ala Ser Phe Pro Ser Val Arg Ser
 530 535 540
 Val Thr Val Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly
 545 550 555 560
 Tyr Leu Asp Thr His Ser Lys Lys Val Val Met Asn Arg Asp Phe Leu
 565 570 575
 50 His Glu Leu Ala Arg Gln Ala Gly Cys Ser Glu Asp Ile His Ala Ile
 580 585 590
 Ile Asp Ser Leu Asn Leu Ala Arg Glu Leu Trp Thr Met Pro Ser Ala
 595 600 605
 55 Glu Asp Ser Asp Arg Leu Leu Arg Lys Ile Ala Glu Arg Ser Trp Glu
 610 615 620
 Thr Cys Arg Pro Ser Val Pro Ser Ala Glu Leu Glu Leu Leu Ile
 625 630 635 640
 Asp Glu Ser Gly Ala Ile Arg Phe Arg Ile Gly Gly Glu
 645 650

(2) INFORMATION FOR SEQ ID NO:290

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 451 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

208/490

(A) NAME/KEY: misc_feature
(B) LOCATION 1...451

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:290

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Gln Gln Arg Pro His Arg Ile Ile Met Leu Arg Thr Phe Arg Ile Gly
1 5 10 15
Gly Ile His Pro Pro Glu Asn Lys Leu Ser Ala Gly Lys Pro Val Glu
20 25 30
Val Leu Pro Ile Pro Ser Gln Val Val Ile Pro Leu Gly Gln His Ile
35 40 45
Gly Ala Pro Ala Thr Ala Thr Val Lys Lys Gly Asp Glu Val Lys Val
50 55 60
Gly Thr Ile Ile Ala Gln Ala Gly Gly Phe Val Ser Ala Asn Ile His
65 70 75 80
Ser Ser Val Ser Gly Lys Val Leu Lys Ile Asp Asn Val Tyr Asp Ser
85 90 95
Ser Gly Tyr Pro Lys Pro Ala Val Phe Ile Ser Val Glu Gly Asp Glu
100 105 110
Trp Glu Glu Gly Ile Asp Arg Ser Pro Ala Ile Val Lys Glu Cys Asn
115 120 125
Leu Asp Ala Lys Glu Ile Val Ala Lys Ile Ser Ala Ala Gly Ile Val
130 135 140
Gly Leu Gly Gly Ala Thr Phe Pro Thr His Val Lys Leu Ser Pro Pro
145 150 155 160
Pro Gly Asn Lys Ala Glu Ile Leu Ile Ile Asn Ala Val Glu Cys Glu
165 170 175
Pro Tyr Leu Thr Ser Asp His Val Leu Met Leu Glu His Gly Glu Glu
180 185 190
Ile Met Ile Gly Val Ser Ile Leu Met Lys Ala Ile Gln Val Asn Lys
195 200 205
Ala Val Ile Gly Val Glu Asn Asn Lys Lys Asp Ala Ile Ala His Leu
210 215 220
Thr Lys Leu Ala Thr Ala Tyr Pro Gly Ile Glu Val Met Pro Leu Lys
225 230 235 240
Val Gln Tyr Pro Gln Gly Gly Glu Lys Gln Leu Ile Asp Ala Val Ile
245 250 255
Arg Lys Gln Val Lys Ser Gly Ala Leu Pro Ile Ser Thr Gly Ala Val
260 265 270
Val Gln Asn Val Gly Thr Val Phe Ala Val Tyr Glu Ala Val Gln Lys
275 280 285
Asn Lys Pro Leu Val Glu Arg Ile Val Thr Val Thr Gly Lys Lys Leu
290 295 300
Ser Arg Pro Ser Asn Leu Leu Val Arg Ile Gly Thr Pro Ile Ala Ala
305 310 315 320
Leu Ile Glu Ala Ala Gly Gly Leu Pro Glu Asn Thr Gly Lys Ile Ile
325 330 335
Gly Gly Gly Pro Met Met Gly Arg Ala Leu Leu Ser Pro Asp Val Pro
340 345 350
Val Thr Lys Gly Ser Ser Gly Val Leu Ile Leu Asp Arg Glu Glu Ala
355 360 365
Val Arg Lys Pro Met Arg Asp Cys Ile Arg Cys Ala Lys Cys Val Gly
370 375 380
Val Cys Pro Met Gly Leu Asn Pro Ala Phe Leu Met Arg Asp Thr Leu
385 390 395 400
Tyr Lys Ser Trp Glu Thr Ala Glu Lys Gly Asn Val Val Asp Cys Ile
405 410 415
Glu Cys Gly Ser Cys Ser Phe Thr Cys Pro Ala Asn Arg Pro Leu Leu
420 425 430
Asp Tyr Ile Arg Gln Ala Lys Lys Thr Val Met Gly Ile Gln Arg Ala
435 440 445
Arg Lys Gln
450

(2) INFORMATION FOR SEQ ID NO:291

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

WO 99/29870

PCT/AU98/01023

209/490

(vii) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

10 Met Asn Ser Gln Lys Lys Glu Ala Phe Asn Met Lys Arg Ile Gln Leu
1 5 10 15
Thr Leu Ile Ala Leu Phe Ala Ala Val Ala Gly Leu Val Ala Gln Asn
20 25 30
Ala Tyr Glu Gly Val Ile Ser Tyr Lys Ile Ser Leu Asp Lys Thr Gly
15 35 40 45
Asn Lys Val Val Leu Asn Gly Ala Ala Asp Met Ser Asn Leu Lys Leu
50 55 60
Lys Ser Thr Gln Met Ile Ile Val Thr Pro Ile Leu Arg Ser Glu Asp
65 70 75 80
20 Gly Thr Ser Arg Val Glu Phe Pro Ser Val Val Ile Thr Gly Arg Asn
85 90 95
Arg Thr Lys Ala Leu Lys Arg Glu Ile Ala Phe Ser Ser Ala Leu Pro
100 105 110
Gln Ala Lys His Ala Ala Gln Tyr Ile Arg Arg His Asn Gly Lys Ser
115 120 125
25 Glu Gln Phe Ala Phe Thr Gly Glu His Ala Tyr Ala Ser Trp Met Met
130 135 140
Asp Ala Lys Phe Val Val Arg Glu Glu Val Arg Gly Cys Ala Lys Cys
145 150 155 160
30 Pro Val Gly Leu Ser Ser Asn Ile Val Pro Phe Asp Pro Leu Phe Asn
165 170 175
Pro Ala Glu Ala Pro Tyr Leu Leu Ala His Ile Thr Pro Ala Glu Glu
180 185 190
35 Val Glu Lys Gln Arg Glu Ser Ser Phe Asp Ala Tyr Ile Asn Phe Lys
195 200 205
Val Asn Lys Ala Asp Val Leu Pro Glu Tyr Arg Asn Asn Lys Ala Glu
210 215 220
Leu Glu Lys Ile Lys Glu Phe Val Ser Thr Val Lys Ala Asn Pro Asn
225 230 235
40 Tyr Ser Val Asn Lys Met Ile Ile Glu Gly Phe Ala Ser Pro Glu Ala
240 245 250 255
Ser Ile Ala His Asn Lys Ala Leu Ser Glu Arg Arg Ala Lys Arg Leu
260 265 270
45 Ala Glu Glu Leu Val Arg Lys Tyr Gly Lys Thr Leu Pro Asn Ile Thr
275 280 285
Thr Glu Phe Gly Gly Glu Asp Trp Lys Gly Leu Lys Leu Ala Ile Glu
290 295 300
Lys Ser Asp Ile Ala Asp Arg Asp Arg Val Leu Glu Ile Ile Asn Ser
305 310 315 320
50 Asp Lys Tyr Ala Asp Asp Asp Ala Arg Glu Gln Ala Leu Lys Gln Leu
325 330 335
Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile Tyr Pro Asn Leu Arg Arg
340 345 350
55 Asn Thr Ile Thr Met Gly Tyr Ile Val Arg Asp Tyr Thr Leu Glu Glu
355 360 365
Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys Glu Leu Ser Glu Ala Glu
370 375 380
Met Tyr Arg Val Ala Met Ser Tyr Pro Glu Gly His Gln Glu Arg Leu
385 390 395 400
60 Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe Pro Glu Ser Val Thr Gly
405 410 415
Arg Ile Asn Leu Ala Val Ala Ala Phe Asn Gly Gly Asp Val Gln Gln
420 425 430
65 Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr Glu Lys Gly Val Ser Asn
435 440 445
Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly Asp Phe Ala Arg Ala Glu
450 455 460
Thr Phe Phe Arg Lys Ala Val Ala Glu Gly Asp Ala Asn Ala Gln Arg
465 470 475 480
70 Asn Leu Asp Met Leu Leu Gly Lys Lys
485

(2) INFORMATION FOR SEQ ID NO:292

75 (i) SEQUENCE CHARACTERISTICS:

210/ 490

(A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...384

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

Asp Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys
1 5 10 15
20 Asn Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile
20 25 30
Gln Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His
35 40 45
25 Phe Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys
50 55 60
Arg Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala
65 70 75 80
Gly Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser
85 90 95
30 Arg Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Gly Phe Ser
100 105 110
Asp Met Gly Gly Gly Ser Arg Arg Val Arg Arg Gly Ser Asp Leu
115 120 125
35 Arg Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu
130 135 140
Lys Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly
145 150 155 160
Asp Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His
165 170 175
40 Gly Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met
180 185 190
Gln Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile
195 200 205
45 Thr Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu
210 215 220
Glu Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Glu Gly Met Gln
225 230 235 240
Met Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn
245 250 255
50 Gly Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile
260 265 270
Arg Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu
275 280 285
55 Ala Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala
290 295 300
Lys Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu
305 310 315 320
Arg Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln
325 330 335
60 Leu Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp
340 345 350
Glu Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr
355 360 365
65 Asp Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp
370 375 380

(2) INFORMATION FOR SEQ ID NO:293

70 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

75 (ii) MOLECULE TYPE: protein

WO 99/29870

PCT/AU98/01023

211/ 490

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

Arg Phe Asp Ser Thr Thr Asn Val Ser Gln Ile Asn Leu Arg Thr Glu
1 5 10 15
Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met
20 25 30
Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala
35 40 45
Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr
50 55 60
Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Tyr Pro Asp Gln Arg
65 70 75 80
Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln
85 90 95
Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala
100 105 110
Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro
115 120 125
Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala
130 135 140
Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr
145 150 155 160
Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln
165 170 175
Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr
180 185 190
Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys
195 200 205
Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser
210 215 220
Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val
225 230 235 240
Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp
245 250 255
Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala
260 265 270
Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala
275 280 285
Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys
290 295 300
Ala Thr Ser Ala Arg
305

(2) INFORMATION FOR SEQ ID NO:294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

Arg Arg Asp Ala Arg Arg Gln Leu Val Arg Arg Arg Arg Lys Glu Leu
1 5 10 15
Ser Gly Thr Ala Asn Thr Arg Cys Arg Arg Arg Val Phe Pro Glu Arg

WO 99/29870

PCT/AU98/01023

212/ 490

20 25 30
 Arg Ser Ala Ile Arg Trp Cys Phe Pro Arg Leu Arg Asp Gly Leu Gln
 35 40 45
 Pro Ile Arg Phe Gly Ser Leu Leu Ala Asn Pro Gln Gln Leu Ser Arg
 50 55 60
 Gly Val Arg Leu Arg Ser Phe Glu Ser Arg Arg Gln Pro Ile Cys Arg
 65 70 75 80
 Phe Gln Gly Ile Gln Gly Lys Arg Arg Asp Ile Leu Gln Pro Glu Gly
 85 90 95
 10 Asn Ser Leu Leu Arg Thr His Ala His Ala Ser Arg Leu Gly Ala Gly
 100 105 110
 Arg Ser Tyr Arg Tyr Leu Ala Pro Arg Thr Thr Ser Arg Pro Pro Thr
 115 120 125
 15 Ala Phe Leu Leu Phe Ala Pro Met Thr Ser Val Ser His Leu Arg Thr
 130 135 140
 Ile Ser Val Ala Gly Ile Leu Ala Ala Leu Gly Ala Val Leu Ile
 145 150 155 160
 Leu Phe Gly Val Asn Leu Phe Leu Gly Ser Val Ala Ile Pro Met Ser
 165 170 175
 20 Glu Ile Phe Arg His Leu Phe Ser Asp Arg Pro Glu Gly Gly Glu Ala
 180 185 190
 Leu Val His Tyr Asn Ile Leu Trp Lys Ser Arg Leu Pro Glu Ala Leu
 195 200 205
 Thr Ala Ala Phe Ala Gly Ala Gly Leu Ser Val Ser Gly Leu Gln Met
 210 215 220
 25 Gln Thr Val Phe Arg Asn Pro Leu Ala Gly Pro Ser Val Leu Gly Ile
 225 230 235 240
 Ser Ser Gly Ala Ser Leu Gly Val Ala Leu Val Val Leu Leu Ser Gly
 245 250 255
 30 Ser Leu Gly Gly Val Ala Leu Ser Ser Leu Gly Tyr Met Gly Glu Val
 260 265 270
 Ala Met Asn Ile Ala Ala Ala Val Gly Ser Leu Ala Val Met Gly Leu
 275 280 285
 35 Ile Val Phe Val Ser Thr Lys Val Arg Ser His Val Thr Leu Leu Ile
 290 295 300
 Ile Gly Val Met Ile Gly Tyr Val Ala Thr Ala Val Ile Gly Val Phe
 305 310 315 320
 Lys Phe Phe Ser Ile Glu Glu Asp Ile Arg Ala Tyr Val Ile Trp Gly
 325 330 335
 40 Leu Gly Ser Phe Ser Arg Ala Thr Asp Ser Gln Leu Ser Phe Phe Ala
 340 345 350
 Ile Leu Met Leu Ile Phe Ile Pro Ala Gly Met Leu Leu Val Lys Gln
 355 360 365
 45 Leu Asn Leu Leu Leu Gly Glu Ser Tyr Ala Arg Asn Leu Gly Leu
 370 375 380
 Asn Thr Arg Arg Ala Arg Leu Leu Val Ile Ser Ser Ala Gly Leu Leu
 385 390 395 400
 Ile Ala Thr Val Thr Ala Tyr Cys Gly Pro Ile Gly Phe Leu Gly Met
 405 410 415
 50 Ala Val Pro His Leu Ala Arg Val Ile Phe His Thr Ser Asp His Arg
 420 425 430
 Ile Leu Met Pro Ala Thr Cys Leu Ile Gly Ser Ala Leu Ala Leu Phe
 435 440 445
 55 Cys Asn Ile Ile Ala Arg Met Pro Gly Phe Glu Gly Ala Leu Pro Val
 450 455 460
 Asn Ser Val Thr Ala Leu Val Gly Ala Pro Ile Ile Val Thr Val Leu
 465 470 475 480
 Phe Arg Arg Arg Arg Phe Lys Glu Glu Thr Asp
 485 490

(2) INFORMATION FOR SEQ ID NO:295

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 763 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

SUBSTITUTE SHEET (Rule 26) (RO/AU)

214/ 490

Pro Gln Met Ser Asp Tyr Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly
 565 570 575
 Pro Ile Ser Phe Ser Ala Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu
 580 585 590
 5 Ile Ser Phe Met Asp Ile Pro Thr Ser Pro Glu His Glu Ala Gln Gly
 595 600 605
 Ile Lys Lys Thr Lys Gln Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg
 610 615 620
 10 Gly Leu Asp Val Leu Cys Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu
 625 630 635 640
 Gly Ala Gly Tyr Ser Leu Val Glu Ala Lys Asn Leu Gln Thr Asp Glu
 645 650 655
 Trp Leu Glu Gly Ala Ala Arg His Arg Ala Asn Val His Ala Asp Trp
 660 665 670
 15 Val His Tyr Trp Gly Gln Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg
 675 680 685
 Ile Gln Ser Glu Arg Tyr Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr
 690 695 700
 20 Leu Trp Arg Leu Ala Thr Ser His Arg Phe Ala His Phe Arg His Ile
 705 710 715 720
 Ile Leu Asp Gly Thr Leu Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp
 725 730 735
 Asp Arg Pro Met Gly Val Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr
 740 745 750
 25 Phe Phe Ala Gln Ile Ala Ile Arg Phe Asn Asn
 755 760

(2) INFORMATION FOR SEQ ID NO:296

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 40 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...365
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

Cys Cys Ala Arg Leu Arg Asp Thr Ser Pro Arg Lys Lys Ser Phe Arg
 1 5 10 15
 50 Asn Asp Thr Val Phe Pro Tyr Phe Val Ile His Leu Ile Lys His Ile
 20 25 30
 Ile Ile Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe
 35 40 45
 55 Leu Leu Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe
 50 55 60
 Met Leu Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr
 65 70 75 80
 Glu Tyr Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg
 85 90 95
 60 Val Ser Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile
 100 105 110
 Glu Ala Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu
 115 120 125
 Ala Ala Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser
 130 135 140
 65 Glu Gln Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly
 145 150 155 160
 Val Ala Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp
 165 170 175
 70 Gln Gly Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg
 180 185 190
 Asp Ala Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met
 195 200 205
 75 Ala Arg Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu
 210 215 220

216/490

Ile Asn Gln Asn Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr
 290 295 300
 Leu Val Ser Ile Ser Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys
 305 310 315 320

5

(2) INFORMATION FOR SEQ ID NO:298

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:

(A) NAME/KEY: misc feature
 (B) LOCATION 1...502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

25

Ser Lys Ile Val Leu Arg Lys Phe Cys Thr Leu Ala Arg Met Lys Lys
 1 5 10 15
 Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr Gly Ser Phe
 20 25 30
 Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu Thr Glu Glu
 35 40 45
 Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val Leu Ser Asn
 50 55 60
 Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile Ser Ile Lys
 65 70 75 80
 His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly Leu Asp Pro
 85 90 95
 Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu Lys Leu Met
 100 105 110
 Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser Gln Arg Pro
 115 120 125
 Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met Pro Ala Asp
 130 135 140
 Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile Asp Gly Lys
 145 150 155 160
 Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala Leu Lys Gly
 165 170 175
 Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr Gly Glu Thr
 180 185 190
 Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile Met Asn Ser
 195 200 205
 Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr Ile Arg Leu
 210 215 220
 Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr Ala Leu Leu
 225 230 235 240
 Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu Asp Leu Arg
 245 250 255
 Gly Asn Gly Gly Leu Met Gln Ala Ala Ile Glu Ile Val Asn Leu
 260 265 270
 Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly Arg Ile Ala
 275 280 285
 Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile Asp Thr Lys
 290 295 300
 Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser Ser Ser Glu
 305 310 315 320
 Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val Leu Met Gly
 325 330 335
 Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg Gln Leu Pro
 340 345 350
 Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr Ile Pro Ser
 355 360 365
 Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn Arg Thr Gly
 370 375 380
 Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe Tyr Thr Ala
 385 390 395 400

75

WO 99/29870

PCT/AU98/01023

217/490

Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro Asp Ile Glu
405 410 415
Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met Ala Ile Asn
420 425 430
5 Asn Asp Val Phe Asp Phe Val Thr Gly Tyr Val Leu Lys His Lys Thr
435 440 445
Ile Ala Lys Pro Glu Asp Phe Ser Ile Thr Asn Glu Asp Tyr Ala Ala
450 455 460
10 Phe Cys Lys Met Met Glu Glu Lys Lys Phe Asp Tyr Asp Arg Gln Ser
465 470 475 480
Gly Lys Met Leu Asp Lys Leu Glu Glu Leu Ala Lys Ile Glu Gly Tyr
485 490 495
Leu Pro Glu Ala Asn Ser Glu Leu Lys Ala Leu Arg Glu Lys Leu Lys
500 505 510
15 Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu Ile Thr Asn
515 520 525
Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Tyr Glu Arg Gly Ser
530 535 540
20 Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu Ala Ile Lys
545 550 555 560
Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu Ala Ala Pro
565 570 575
Lys Ala Glu Asn Lys Gly
580
25
(2) INFORMATION FOR SEQ ID NO:299
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 985 amino acids
30 (B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
35 (iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
40 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...985
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299
Val Thr Asp Lys Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser
1 5 10 15
Ala Leu Ala Ile Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr
20 25 30
50 Asn Arg Tyr Glu Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met
35 40 45
Ala Tyr Leu Asp Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr
50 55 60
Leu Lys Glu Ala Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys
65 70 75 80
Gly Gly Met Asn Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg
85 90 95
Asn Leu Ser Asn Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu
100 105 110
60 Asn Ala Ala Lys Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val
115 120 125
Lys Glu Tyr Arg Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe
130 135 140
65 Gly Ser Gly Asp Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala
145 150 155 160
Asp Val Val Arg Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala
165 170 175
Ser Phe Asn Val Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala
180 185 190
70 Pro Asn Leu Gln Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu
195 200 205
Pro Gly Val Lys Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser
210 215 220
75 Ala Asn Leu Gln Phe Trp Arg Thr Tyr Lys Phe Glu Glu Val Ser Gly
225 230 235 240

WO 99/29870

PCT/AU98/01023

218/490

	Arg	Leu	Ile	Ala	Ala	Asn	Asp	Arg	Leu	Ser	Glu	Leu	Ala	Met	Asn	Asn
					245					250					255	
	Thr	Asp	Ala	Thr	Pro	Glu	Thr	Glu	Pro	Ala	Thr	Thr	Asp	Ser	Val	Ala
					260				265					270		
5	Ala	Thr	Ala	Asp	Ser	Ala	Ala	Val	Gln	Ala	Val	Ala	Asp	Ser	Ala	Thr
					275				280					285		
	Val	Ala	Gln	Lys	Glu	Ala	Lys	Asp	Ala	Thr	Arg	Lys	Asp	Ala	Leu	Phe
					290				295				300			
10	Ser	Leu	Leu	Thr	Pro	Val	Asn	Arg	Gly	Gly	Ala	Val	Val	Gly	Val	Ala
					305				310						320	
	Arg	Arg	Ala	Asn	Met	Ala	Gln	Ile	Ser	Glu	Met	Leu	Gln	Gln	Ala	His
					325					330					335	
	Asp	Leu	Lys	Val	Thr	Arg	Glu	Asp	Val	Leu	Phe	Leu	Trp	Gly	Ala	Lys
					340				345					350		
15	Ala	Ile	Glu	Asp	Pro	Glu	Thr	Lys	Lys	Glu	Thr	Asp	Leu	Tyr	Glu	Leu
					355				360					365		
	Tyr	Ala	Ile	Arg	Thr	Asn	Arg	Thr	Gly	Asp	Pro	Asp	Leu	Gly	Gly	Asp
					370				375				380			
20	Val	Val	Thr	Ser	Ala	Lys	Ser	Asp	Ile	Gln	Asn	Asp	Phe	Gly	Arg	Ser
					385				390						400	
	Glu	Pro	Ile	Val	Ser	Met	Thr	Met	Asn	Glu	Glu	Gly	Ala	Arg	Lys	Trp
					405					410					415	
	Ala	Arg	Ile	Thr	Lys	Asp	Asn	Val	Gly	Arg	Ala	Ile	Ala	Ile	Val	Leu
					420				425					430		
25	Asp	Gly	Val	Val	Tyr	Ser	Ala	Pro	Asn	Val	Asn	Asp	Glu	Ile	Thr	Gly
					435				440					445		
	Gly	Arg	Ser	Gln	Ile	Ser	Gly	His	Phe	Thr	Val	Glu	Ala	Gly	Asp	
					450				455				460			
30	Leu	Ala	Asn	Val	Leu	Asn	Ser	Gly	Lys	Met	Asp	Ala	Thr	Val	Ser	Ile
					465					470					480	
	Glu	Gln	Glu	Asn	Val	Ile	Gly	Pro	Thr	Leu	Gly	Ala	Glu	Ser	Ile	Lys
					485					490					495	
	Ala	Gly	Phe	Leu	Ser	Phe	Leu	Leu	Ala	Leu	Val	Ile	Leu	Met	Cys	Tyr
					500				505					510		
35	Met	Cys	Leu	Ala	Tyr	Gly	Phe	Leu	Pro	Gly	Leu	Ile	Ala	Asn	Gly	Ala
					515				520					525		
	Leu	Ile	Val	Asn	Ser	Phe	Phe	Thr	Leu	Gly	Val	Leu	Ala	Ser	Phe	His
					530				535					540		
40	Ala	Val	Leu	Thr	Leu	Ser	Gly	Ile	Ala	Gly	Leu	Val	Leu	Thr	Leu	Gly
					545					550				555		
	Met	Ala	Val	Asp	Ala	Asn	Val	Leu	Ile	Phe	Glu	Arg	Ile	Lys	Glu	Glu
					565					570				575		
	Leu	Arg	Ala	Gly	Lys	Thr	Pro	Ile	Arg	Ala	Val	Thr	Asp	Gly	Tyr	Gly
					580				585					590		
45	Asn	Ala	Phe	Ser	Ala	Ile	Phe	Asp	Ser	Asn	Val	Thr	Thr	Ile	Ile	Thr
					595				600					605		
	Gly	Ile	Ile	Leu	Phe	Leu	Tyr	Gly	Thr	Gly	Pro	Ile	Arg	Gly	Phe	Ala
					610				615					620		
50	Thr	Thr	Leu	Ile	Ile	Gly	Leu	Ile	Ala	Ser	Phe	Ile	Thr	Ala	Val	Phe
					625				630					635		
	Leu	Thr	Arg	Ile	Val	Phe	Glu	Lys	Leu	Ala	Lys	Lys	Gly	Arg	Leu	Asp
					645					650				655		
	Lys	Ile	Thr	Phe	Thr	Thr	Ser	Ile	Thr	Arg	Asn	Leu	Leu	Val	Asn	Pro
					660				665					670		
55	Ser	Tyr	Asn	Ile	Leu	Gly	Lys	Arg	Lys	Thr	Gly	Phe	Ile	Ile	Pro	Val
					675				680					685		
	Ile	Ile	Ile	Val	Leu	Gly	Leu	Ile	Ala	Ser	Phe	Thr	Ile	Gly	Leu	Asn
					690				695				700			
60	Arg	Gly	Ile	Glu	Phe	Ser	Gly	Gly	Arg	Asn	Tyr	Val	Val	Lys	Phe	Asp
					705				710					715		
	Gln	Pro	Val	Ser	Ser	Glu	Ala	Val	Arg	Ser	Ala	Leu	Ser	Ser	Pro	Leu
					725					730				735		
	Gln	Glu	Lys	Val	Leu	Val	Thr	Ser	Ile	Gly	Thr	Glu	Gly	Thr	Glu	Val
					740				745					750		
65	Arg	Ile	Ser	Thr	Asn	Tyr	Lys	Ile	Gln	Glu	Glu	Ser	Glu	Glu	Thr	Glu
					755				760					765		
	Ala	Glu	Ile	Thr	Asp	Lys	Leu	Tyr	Gln	Ser	Leu	Lys	Gly	Phe	Tyr	Thr
					770				775					780		
70	Gln	Gln	Pro	Thr	Ala	Asp	Gln	Phe	Leu	Asp	Asn	Ile	Ile	Ser	Ser	Gln
					785				790					795		
	Lys	Val	Ser	Pro	Ser	Met	Ser	Ser	Asp	Ile	Thr	Arg	Gly	Ala	Ile	Trp
					805					810				815		
	Ala	Val	Leu	Leu	Ser	Met	Ile	Phe	Met	Ala	Ile	Tyr	Ile	Leu	Ile	Arg
					820				825					830		
75	Phe	Arg	Asp	Ile	Ser	Phe	Ser	Ala	Gly	Val	Phe	Val	Ser	Val	Ala	Ala

WO 99/29870

PCT/AU98/01023

219/ 490

5 Thr Thr Phe Cys Ile Ile Ala Leu Tyr Ala Leu Leu Trp Lys Ile Leu
850 855 860
Pro Phe Thr Met Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala
865 870 875 880
Ile Ile Gly Tyr Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile
885 890 895
Arg Glu Thr Met Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile
900 905 910
10 Asn Asp Ala Leu Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu
915 920 925
Thr Thr Phe Ile Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr
930 935 940
15 Met Arg Ser Phe Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr
945 950 955 960
Tyr Ser Thr Leu Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys
965 970 975
Arg Lys Leu Asn Lys Ala Ala Lys Lys
980 985
20
(2) INFORMATION FOR SEQ ID NO:300
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1046 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1046
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300
40 Asp Phe Pro Trp Val Arg Val Lys Pro Glu Lys Lys Arg Lys Gln His
1 5 10 15
Asn Ser Asn Asn Phe Lys Phe Asn Ala Lys Glu Lys Ser Met Lys Arg
20 25 30
45 Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met
35 40 45
Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn
50 55 60
Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile
65 70 75 80
50 Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala
85 90 95
Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu
100 105 110
55 Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys
115 120 125
Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu
130 135 140
60 Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala
145 150 155 160
Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala
165 170 175
Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser
180 185 190
65 Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu
195 200 205
Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met
210 215 220
70 Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala
225 230 235 240
Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln
245 250 255
Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala
260 265 270
75 Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met

[illegible]

WO 99/29870

PCT/AU98/01023

222/ 490

	Lys	Thr	Glu	Val	Trp	Ile	Cys	Pro	Leu	Thr	Asn	Pro	Asp	Gly	Ala	Tyr
				260					265					270		
	Arg	Ala	Gly	Asn	His	Thr	Val	Gln	Gly	Ala	Thr	Arg	Tyr	Asn	Ala	Asn
			275					280					285			
5	Asn	Val	Asp	Leu	Asn	Arg	Asn	Phe	Lys	Asp	Asp	Val	Ala	Gly	Asp	His
		290					295					300				
	Pro	Asp	Gly	Lys	Pro	Trp	Gln	Pro	Glu	Ala	Thr	Ala	Phe	Met	Asp	Leu
		305					310				315				320	
10	Glu	Gly	Asn	Thr	Ser	Phe	Val	Leu	Gly	Ala	Asn	Ile	His	Gly	Gly	Thr
				325							330				335	
	Glu	Val	Val	Asn	Tyr	Pro	Trp	Asp	Asn	Lys	Lys	Glu	Arg	His	Ala	Asp
				340				345					350			
	Asp	Glu	Trp	Tyr	Lys	Leu	Ile	Ser	Arg	Asn	Tyr	Ala	Ala	Ala	Cys	Gln
		355					360					365				
15	Ser	Ile	Ser	Ala	Ser	Tyr	Met	Thr	Ser	Glu	Thr	Asn	Ser	Gly	Ile	Ile
		370					375					380				
	Asn	Gly	Ser	Asp	Trp	Tyr	Val	Ile	Arg	Gly	Ser	Arg	Gln	Asp	Asn	Ala
		385					390				395				400	
20	Asn	Tyr	Phe	His	Arg	Leu	Arg	Glu	Ile	Thr	Leu	Glu	Ile	Ser	Asn	Thr
				405						410					415	
	Lys	Leu	Val	Pro	Ala	Ser	Gln	Leu	Pro	Lys	Tyr	Trp	Asn	Leu	Asn	Lys
				420					425					430		
	Glu	Ser	Leu	Leu	Ala	Leu	Ile	Glu	Glu	Ser	Leu	Tyr	Gly	Ile	His	Gly
		435						440					445			
25	Thr	Val	Thr	Ser	Ala	Ala	Asn	Gly	Gln	Pro	Leu	Lys	Cys	Gln	Ile	Leu
		450					455					460				
	Ile	Glu	Asn	His	Asp	Lys	Arg	Asn	Ser	Asp	Val	Tyr	Ser	Asp	Ala	Thr
		465					470				475				480	
30	Thr	Gly	Tyr	Tyr	Val	Arg	Pro	Ile	Lys	Ala	Gly	Thr	Tyr	Thr	Val	Lys
				485						490					495	
	Tyr	Lys	Ala	Glu	Gly	Tyr	Pro	Glu	Ala	Thr	Arg	Thr	Ile	Thr	Ile	Lys
				500					505					510		
	Asp	Lys	Glu	Thr	Val	Ile	Met	Asp	Ile	Ala	Leu	Gly	Asn	Ser	Val	Pro
			515					520					525			
35	Leu	Pro	Val	Pro	Asp	Phe	Thr	Ala	Ser	Pro	Met	Thr	Ile	Ser	Val	Gly
		530					535					540				
	Glu	Ser	Val	Gln	Phe	Gln	Asp	Gln	Thr	Thr	Asn	Asn	Pro	Thr	Asn	Trp
		545					550				555				560	
40	Glu	Trp	Thr	Phe	Glu	Gly	Gly	Gln	Pro	Ala	Met	Ser	Thr	Glu	Gln	Asn
				565						570					575	
	Pro	Leu	Val	Ser	Tyr	Ser	His	Pro	Gly	Gln	Tyr	Asp	Val	Thr	Leu	Lys
				580					585					590		
	Val	Trp	Asn	Ala	Ser	Gly	Ser	Asn	Thr	Ile	Thr	Lys	Glu	Lys	Phe	Ile
		595						600					605			
45	Thr	Val	Asn	Ala	Val	Met	Pro	Val	Ala	Glu	Phe	Val	Gly	Thr	Pro	Thr
		610					615					620				
	Glu	Ile	Glu	Glu	Gly	Gln	Thr	Val	Ser	Phe	Gln	Asn	Gln	Ser	Thr	Asn
		625					630				635				640	
50	Ala	Thr	Asn	Tyr	Val	Trp	Ile	Phe	Asp	Gly	Gly	Thr	Pro	Ala	Thr	Ser
				645						650					655	
	Glu	Asp	Glu	Asn	Pro	Thr	Val	Leu	Tyr	Ser	Lys	Ala	Gly	Gln	Tyr	Asp
				660					665					670		
	Val	Thr	Leu	Lys	Ala	Ile	Ser	Ala	Ser	Gly	Glu	Thr	Val	Lys	Thr	Lys
		675						680					685			
55	Glu	Lys	Tyr	Ile	Thr	Val	Lys	Lys	Ala	Pro	Val	Pro	Ala	Pro	Val	Ala
		690					695					700				
	Asp	Phe	Glu	Gly	Thr	Pro	Arg	Lys	Val	Lys	Lys	Gly	Glu	Thr	Val	Thr
		705					710				715				720	
60	Phe	Lys	Asp	Leu	Ser	Thr	Asn	Asn	Pro	Thr	Ser	Trp	Leu	Trp	Val	Phe
				725						730					735	
	Glu	Gly	Gly	Ser	Pro	Ala	Thr	Ser	Thr	Glu	Gln	Asn	Pro	Val	Val	Thr
				740					745					750		
	Tyr	Asn	Glu	Thr	Gly	Lys	Tyr	Asp	Val	Gln	Leu	Thr	Ala	Thr	Asn	Glu
		755						760					765			
65	Gly	Gly	Ser	Asn	Val	Lys	Lys	Ala	Glu	Asp	Tyr	Ile	Glu	Val	Ile	Leu
		770					775					780				
	Asp	Asp	Ser	Val	Glu	Asp	Ile	Val	Ala	Gln	Thr	Gly	Ile	Val	Ile	Arg
		785					790				795				800	
70	Pro	Gln	Asn	Gly	Thr	Lys	Gln	Ile	Leu	Ile	Glu	Ala	Asn	Ala	Ala	Ile
				805						810					815	
	Lys	Ala	Ile	Val	Leu	Tyr	Asp	Ile	Asn	Gly	Arg	Val	Val	Leu	Lys	Thr
				820					825					830		
	Thr	Pro	Asn	Gln	Leu	Arg	Ser	Thr	Val	Asp	Leu	Ser	Ile	Leu	Pro	Glu
		835					840						845			
75	Gly	Ile	Tyr	Thr	Ile	Asn	Ile	Lys	Thr	Glu	Lys	Ser	Ala	Arg	Thr	Glu

WO 99/29870

PCT/AU98/01023

223/490

850
Lys Ile His Ile Gly
865

855

860

5 (2) INFORMATION FOR SEQ ID NO:302

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

25 Leu Ser Tyr Ser Gly Glu Ser Asp Ala Lys Glu Ser Asp Gln Asn Cys
1 5 10 15
Arg Lys Cys Thr Phe Ile Gly Phe Glu Lys Arg Val Asn Thr Met Arg
20 25 30
30 Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Leu Pro Ile Phe Phe
35 40 45
Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg Phe Thr
50 55 60
Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr Gly Pro
65 70 75 80
35 Gly Lys Gly Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys His Pro
85 90 95
Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro
100 105

40 (2) INFORMATION FOR SEQ ID NO:303

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303

60 Leu Glu Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu
1 5 10 15
Tyr Ser Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln
20 25 30
65 Asp Met Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile
35 40 45
Asp Ile Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu
50 55 60
Ile Glu Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly
65 70 75 80
70 Ser Pro Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr
85 90 95
Asp Ile Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu
100 105 110
75 Leu Leu Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile
115 120 125

WO 99/29870

PCT/AU98/01023

224/ 490

	Phe	Met	Lys	Gln	Gly	Ile	Lys	Tyr	Asp	Thr	Ile	Leu	Ser	Asp	Tyr	Phe
	130						135					140				
	Gly	Gln	Arg	Asn	Pro	Ser	Glu	Gly	Lys	Ser	Pro	Ser	Glu	Met	Glu	Ile
	145					150					155				160	
5	Leu	Asp	Gly	Tyr	Gln	Asp	Asn	Asp	Phe	Asp	Asp	Glu	Glu	Asp	Glu	Ser
					165					170					175	
	Ser	Pro	Pro	Ser	Gly	Asn	Ser	Gly	Thr	Gly	Gly	Gly	Ser	Gly	Asp	Ala
				180					185					190		
10	Pro	Glu	Gln	Asn	Thr	Gly	Gly	Gly	Asp	Thr	Thr	Thr	Thr	Thr	Arg	Ser
				195				200						205		
	Gly	Gly	Asp	Thr	Pro	Ala	Leu	Asp	Thr	Phe	Gly	Thr	Asp	Ile	Thr	Ala
		210				215						220				
	Met	Ala	Ala	Ala	Gly	Lys	Leu	Asp	Pro	Val	Val	Gly	Arg	Glu	Gln	Glu
		225				230						235			240	
15	Ile	Glu	Arg	Val	Ile	Gln	Ile	Leu	Ser	Arg	Arg	Lys	Lys	Asn	Asn	Pro
				245						250					255	
	Val	Leu	Ile	Gly	Glu	Pro	Gly	Val	Gly	Lys	Ser	Ala	Ile	Val	Glu	Gly
				260					265					270		
20	Leu	Ala	Glu	Arg	Ile	Val	Asn	Arg	Lys	Val	Ser	Arg	Ile	Leu	Phe	Asp
			275					280						285		
	Lys	Arg	Ile	Ile	Ser	Leu	Asp	Leu	Ala	Gln	Met	Val	Ala	Gly	Thr	Lys
		290					295					300				
	Tyr	Arg	Gly	Gln	Phe	Glu	Glu	Arg	Leu	Lys	Ala	Val	Leu	Asp	Glu	Leu
		305				310					315				320	
25	Lys	Lys	Asn	Pro	Gln	Ile	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Thr	Ile
				325						330					335	
	Val	Gly	Ala	Gly	Ser	Ala	Ala	Gly	Ser	Met	Asp	Thr	Ala	Asn	Met	Leu
				340					345					350		
30	Lys	Pro	Ala	Leu	Ala	Arg	Gly	Gln	Val	Gln	Cys	Ile	Gly	Ala	Thr	Thr
		355					360						365			
	Leu	Asp	Glu	Tyr	Arg	Lys	Asn	Ile	Glu	Lys	Asp	Gly	Ala	Leu	Glu	Arg
		370					375					380				
	Arg	Phe	Gln	Lys	Val	Pro	Ile	Ala	Pro	Ser	Thr	Ala	Glu	Glu	Thr	Leu
		385				390					395				400	
35	Thr	Ile	Leu	Gln	Asn	Ile	Lys	Glu	Lys	Tyr	Glu	Asp	Tyr	His	Gly	Val
				405						410					415	
	Arg	Tyr	Thr	Asp	Glu	Ala	Ile	Lys	Ala	Ala	Val	Glu	Leu	Thr	Asp	Arg
				420					425					430		
40	Tyr	Val	Ser	Asp	Arg	Phe	Phe	Pro	Asp	Lys	Ala	Ile	Asp	Ala	Met	Asp
			435					440						445		
	Glu	Ala	Gly	Ala	Ser	Val	His	Ile	Thr	Asn	Val	Val	Ala	Pro	Lys	Glu
		450					455					460				
	Ile	Glu	Ile	Leu	Glu	Ala	Glu	Leu	Ala	Ser	Val	Arg	Glu	Asn	Lys	Leu
		465				470					475				480	
45	Ser	Ala	Val	Lys	Ala	Gln	Asn	Tyr	Glu	Leu	Ala	Ala	Ser	Phe	Arg	Asp
				485						490					495	
	Gln	Glu	Arg	Arg	Thr	Gln	Gln	Gln	Ile	Ala	Glu	Glu	Lys	Lys	Lys	Trp
				500					505					510		
50	Glu	Glu	Gln	Met	Ser	Lys	His	Arg	Glu	Thr	Val	Asp	Glu	Asn	Val	Val
			515					520					525			
	Ala	His	Val	Val	Ala	Leu	Met	Thr	Gly	Val	Pro	Ala	Glu	Arg	Leu	Ser
		530					535					540				
	Thr	Gly	Glu	Gly	Glu	Arg	Leu	Arg	Thr	Met	Ala	Asp	Asp	Leu	Lys	Thr
		545				550					555				560	
55	Lys	Val	Val	Gly	Gln	Asp	Thr	Ala	Ile	Glu	Lys	Met	Val	His	Ala	Ile
				565						570					575	
	Gln	Arg	Asn	Arg	Leu	Gly	Leu	Arg	Asn	Glu	Lys	Lys	Pro	Ile	Gly	Ser
				580					585					590		
60	Phe	Leu	Phe	Leu	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr	Tyr	Leu	Ala	Lys
				595				600					605			
	Lys	Leu	Ala	Glu	Tyr	Leu	Phe	Glu	Asp	Glu	Asn	Ala	Met	Ile	Arg	Val
		610					615					620				
	Asp	Met	Ser	Glu	Tyr	Met	Glu	Lys	Phe	Ser	Val	Ser	Arg	Leu	Val	Gly
		625				630					635				640	
65	Ala	Pro	Pro	Gly	Tyr	Val	Gly	Tyr	Glu	Glu	Gly	Gly	Gln	Leu	Thr	Glu
				645						650					655	
	Arg	Val	Arg	Arg	Lys	Pro	Tyr	Ser	Val	Val	Leu	Leu	Asp	Glu	Ile	Glu
				660					665					670		
70	Lys	Ala	His	Ala	Asp	Val	Phe	Asn	Leu	Leu	Leu	Gln	Val	Met	Asp	Glu
			675					680						685		
	Gly	Gln	Leu	Thr	Asp	Ser	Leu	Gly	Arg	Arg	Val	Asn	Phe	Lys	Asn	Thr
			690				695					700				
	Val	Ile	Ile	Ile	Thr	Ser	Asn	Val	Gly	Thr	Arg	Gln	Leu	Lys	Asp	Phe
		705					710				715				720	
75	Gly	Gln	Gly	Ile	Gly	Phe	Arg	Ser	Glu	Lys	Asp	Glu	Glu	Ala	Asn	Lys

WO 99/29870

PCT/AU98/01023

227/ 490

5 260 265 270
 Glu Tyr Met Ala Gln Thr Gly Phe Tyr Ala Val Arg Phe Asp Val Gly
 275 280 285
 Asn Lys His His Val Ser Lys Ile Gln Val Arg
 290 295

(2) INFORMATION FOR SEQ ID NO:306

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

Leu Phe Asn His Lys Lys Ser Trp Tyr Glu Thr Phe Gln Phe Tyr Leu
 1 5 10 15
 Val Val Phe Arg Ser Gly Phe Ile Leu Cys Glu Asn Thr Leu Ala
 20 25 30
 Gln Gln Lys Thr Glu Glu Phe Ala Pro Val Ser Asp Leu Arg Ala Glu
 35 40 45
 Ala Tyr Gly Ser Thr Val Phe Leu His Trp Thr Pro Pro Tyr Asp Asn
 50 55 60
 Pro Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile
 65 70 75 80
 Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu
 85 90 95
 Thr Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr
 100 105 110
 Ile Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro
 115 120 125
 Glu Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val
 130 135 140
 Cys Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser
 145 150 155 160
 Ser Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu
 165 170 175
 Glu Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly
 180 185 190
 Asn Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn
 195 200 205
 Asp Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe
 210 215 220
 Trp Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg
 225 230 235 240
 Arg Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg
 245 250 255
 Asp Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp
 260 265 270
 Thr Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr
 275 280 285
 Leu Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn
 290 295 300
 Ser Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val
 305 310 315 320
 Gly Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr
 325 330 335
 Asp Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr
 340 345 350
 Lys Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr
 355 360 365
 Val Tyr Thr Glu Lys Ile Gln Ile Gln
 370 375

228/ 490

(2) INFORMATION FOR SEQ ID NO:307

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(111) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307

1 Phe Gly Ile Ser Pro Ser Met Lys Lys Ser Phe Leu Leu Ala Ile Val
 5 10 15
 20 Met Leu Phe Gly Ile Ala Met Gln Gly His Ser Ala Pro Val Thr Lys
 25 30 35
 40 Glu Arg Ala Leu Ser Leu Ala Arg Leu Ala Leu Arg Gln Val Ser Leu
 45 50 55
 60 Arg Met Gly Gln Thr Ala Val Ser Asp Lys Ile Ser Ile Asp Tyr Val
 65 70 75
 80 Tyr Arg Gln Gly Asp Ala Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly
 85 90 95
 100 Ser Pro Ala Tyr Phe Tyr Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr
 105 110 115
 120 Ala Leu Val Ala Ala Asp Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser
 125 130 135
 140 Pro Ile Gly Arg Phe Asp Met Asp Ser Met Pro Asp Asn Leu Arg Met
 145 150 155
 160 Trp Leu Gln Ile Tyr Asp Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys
 165 170 175
 180 Ala Gln Leu Asn Glu Glu Ile Leu Arg Thr Glu Gly Val Pro Ala Glu
 185 190 195
 200 Val His Ala Leu Met Asp Asn Gly His Phe Ala Asn Asp Pro Met Arg
 205 210 215
 220 Trp Asn Gln Gly Tyr Pro Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn
 225 230 235
 240 Gly Asn His Ala Tyr Thr Gly Cys Val Ala Thr Ala Ala Ala Gln Ile
 245 250 255
 260 Met Arg Tyr His Ser Trp Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr
 265 270 275
 280 His Ala Gly Ser Leu Val Gly Asn Trp Ser Gly Thr Phe Gly Glu Met
 285 290 295
 300 Tyr Asp Trp Ile Asn Met Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr
 305 310 315
 320 Gln Ser Gln Val Asp Ala Tyr Ala Thr Leu Met Arg Asp Val Ser Ala
 325 330 335
 340 Ser Val Ser Met Ser Phe Tyr Glu Asn Gly Ser Gly Thr Tyr Ser Val
 345 350 355
 360 Tyr Val Val Gly Ala Leu Arg Asn Asn Phe Arg Tyr Lys Arg Ser Leu
 365 370 375
 380 Gln Leu His Val Arg Ala Leu Tyr Thr Ser Gln Glu Trp His Asp Met
 385 390 395
 400 Ile Arg Gly Glu Leu Ala Ser Gly Arg Pro Val Tyr Tyr Ala Gly Asn
 405 410 415
 420 Asn Gln Ser Ile Gly His Ala Phe Val Cys Asp Gly Tyr Ala Ser Asp
 425 430 435
 440 Gly Thr Phe His Phe Asn Trp Gly Trp Gly Gly Val Ser Asn Gly Phe
 445 450 455
 460 Tyr Lys Leu Thr Leu Leu Ser Pro Thr Ser Leu Gly Ile Gly Gly Glu
 465 470 475
 480 Gly Ile Gly Phe Thr Ile Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro
 485 490 495
 500 Ala Lys Thr Pro Ala Glu Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala
 505 510 515
 520 Leu Lys Asp Ile Glu Ala Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val
 525 530 535
 540 Gly Tyr Ser Ile Tyr Asn Thr Gly Glu Glu Gln Ser Asn Leu Asp Leu

WO 99/29870

PCT/AU98/01023

229/ 490

5 Gly Tyr Arg Leu Asn Lys Ala Asp Gly Glu Val Ile Glu Val Lys Thr
435 440 445
450 455 460
Ser Ser Ile Asn Ile Ser Trp Tyr Gly Tyr Gly Glu His Pro Glu Ser
465 470 475 480
Phe Ser Leu Ala Pro Asn Gln Leu Ser Gln Gly Ile Asn Thr Ile Thr
485 490 495
Leu Leu Tyr Arg Arg Thr Gly Thr Glu Gln Trp Glu Pro Val Arg His
500 505 510
10 Ala Gln Gly Gly Tyr Val Asn Ser Ile Lys Val Asn Thr Thr Asp Pro
515 520 525
Asn Asn Val Val Val Thr Val Asp Asn Asn Glu Gly Lys Leu Ser Ile
530 535 540
Val Pro Asn Ser Phe Val Ala Asp Leu Asn Ser Tyr Glu His Ser Thr
545 550 555 560
15 Ile Thr Val Gln Phe Asn Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro
565 570 575
Val Ala Phe Ala Leu Ser Thr Gly Ala Thr Ala Asp Asp Val Ile Ser
580 585 590
20 Leu Gly Trp Val Met Ala Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro
595 600 605
Val Val Trp Ser Lys Asp Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr
610 615 620
25 Leu Tip Tyr Arg Phe Ser Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys
625 630 635 640
Thr Gly Ser Val Ser Val Lys Thr Pro Thr Glu Tyr Thr His Pro Leu
645 650 655
Phe Glu Val Gly His Asn Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala
660 665 670
30 His Asn Arg Val Leu Pro Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro
675 680 685
Phe Asn Gly Glu Leu Val Val Val Phe Arg Gln Thr Gln Ser Ser Ser
690 695 700
35 Gly Ser Leu Trp Ala Ala Gln Glu Thr Val His Ile Lys Gln Gly Glu
705 710 715 720
Thr Phe Val Tyr Lys Pro Val Val Glu Gly Pro Ile Pro Asp Gly Ser
725 730 735
Tyr Arg Ala Thr Leu His Ala Phe Val Asn Gly Gln Gln Gln Leu Tyr
740 745 750
40 Leu Lys Gly Lys Arg Asn Tyr Thr Val Lys Ile Val Asn Gly Thr Ala
755 760 765
Val Glu Ala Ile Glu Ser Ser Glu Glu Ile Arg Val Phe Pro Asn Pro
770 775 780
45 Ala Arg Asp Tyr Val Glu Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr
785 790 795 800
Ser Ile Ile Leu Phe Asp Leu Ser Gly Lys Ile Val Met Lys Asn Ser
805 810 815
Leu Ser Ala Gly His Gly Arg Met Asp Val Ser Arg Leu Pro Asn Gly
820 825 830
50 Ala Tyr Ile Leu Lys Val Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val
835 840 845
His

55 (2) INFORMATION FOR SEQ ID NO:308
(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
60
(11) MOLECULE TYPE: protein
(111) HYPOTHETICAL: YES
65
(111) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(111) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...295
70
(21) SEQUENCE DESCRIPTION: SEQ ID NO:308
75 Thr Lys Lys Thr Leu Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu

WO 99/29870

PCT/AU98/01023

230/ 490

1 Val Met Val Phe Ala Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln
20 25 30
5 Thr Leu Leu Pro Ala Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp
35 40 45
Asn Pro Ser Glu Ile Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val
50 55 60
Leu Ala Glu Glu Phe Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly
65 70 75 80
10 His Arg Lys Leu Ala Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr
85 90 95
Val Val Gly Ile His Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe
100 105 110
15 Arg Thr Glu Ala Gly Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr
115 120 125
Pro Leu Pro Ala Leu Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr
130 135 140
Val Tyr Asp Lys Ser Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln
145 150 155 160
20 Met Glu Gln Lys Ala Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr
165 170 175
Asp Thr Gln Lys Ile Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly
180 185 190
25 Asn Thr Leu Pro Lys Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys
195 200 205
Leu Ile Ala Pro Gln Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu
210 215 220
His Asn His Val Leu Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu
225 230 235 240
30 Phe Val Asn Leu Lys Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu
245 250 255
Ser Gly Met Ser Phe Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val
260 265 270
35 Tyr Asp Val Gln Thr Phe Glu Val Tyr Asp Val Val His Val Lys Ile
275 280 285
Asn Pro Gln Ser Asp Gly Lys
290 295

(2) INFORMATION FOR SEQ ID NO:309

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 amino acids
(E) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...230

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:309

60 Thr Asn Lys Lys Glu Glu Thr Met Lys Lys Ser Ser Val Val Ala Ser
1 5 10 15
Val Leu Ala Val Ala Leu Val Phe Ala Gly Cys Gly Leu Asn Asn Met
20 25 30
Ala Lys Gly Gly Leu Ile Gly Ala Gly Val Gly Gly Ala Ile Gly Ala
35 40 45
65 Gly Val Gly Asn Val Ala Gly Asn Thr Ala Val Gly Ala Ile Val Gly
50 55 60
Thr Ala Val Gly Gly Ala Ala Gly Ala Leu Ile Gly Lys Lys Met Asp
65 70 75 80
Lys Gln Lys Lys Glu Leu Glu Ala Ala Val Pro Asp Ala Thr Ile Gln
85 90 95
70 Thr Val Asn Asp Gly Glu Ala Ile Leu Val Thr Phe Asp Ser Gly Ile
100 105 110
Leu Phe Ala Thr Asn Ser Ser Thr Leu Ser Pro Asn Ser Arg Thr Ala
115 120 125
75 Leu Thr Lys Phe Ala Ala Asn Met Asn Lys Asn Pro Asp Thr Asp Ile

WO 99/29870

PCT/AU98/01023

231/ 490

130 135 140
Arg Ile Val Gly His Thr Asp Asn Thr Gly Ser Asp Lys Ile Asn Asp
145 150 155 160
Pro Leu Ser Glu Arg Arg Ala Ala Ser Val Tyr Ser Phe Leu Asn Ser
5 Gln Gly Val Ser Met Ser Arg Met Ala Ala Glu Gly Arg Gly Ser His
180 185 190
Glu Pro Val Ala Asp Asn Ser Thr Val Ala Gly Arg Ser Ala Asn Arg
195 200 205
10 Arg Val Glu Val Tyr Ile Leu Pro Asn Ala Lys Met Ile Glu Gln Ala
210 215 220
Gln Gln Gly Thr Leu Lys
225 230

15 (2) INFORMATION FOR SEQ ID NO:310

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

25

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

30

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

35 Asn Arg Asn Arg Asn Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys
1 5 10 15
Ser Leu Cys Phe Ile Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn
20 25 30
40 Val Arg Asn Ser Gln Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys
35 40 45
Pro Ser Asp Ser Val Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu
50 55 60
Glu Phe Arg Asn Lys Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu
65 70 75 80
45 Tyr Glu Asn Arg Leu Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp
85 90 95
Leu Tyr Gly Glu Asp Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly
100 105 110
Ala Gly Thr Asp Val Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser
50 115 120 125
Ser Phe Val Met Pro Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly
130 135 140
Tyr Arg Arg Arg Phe Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val
145 150 155 160
55 Asn Arg Gly Asp Thr Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val
165 170 175
Arg Ser Tyr Glu Ala Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His
180 185 190
60 Pro Asn Gly Leu Glu Thr Val Tyr Gly His Met Ser Arg Gln Leu Val
195 200 205
Asp Glu Asn Gln Ile Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly
210 215 220
Ser Thr Gly Arg Ser Thr Gly Pro His Leu His Phe Glu Thr Arg Phe
225 230 235 240
65 Met Gly Ile Pro Ile Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly
245 250 255
Val Pro Leu Arg Asp Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg
260 265 270
70 Tyr Ala Lys Ala Ser Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys
275 280 285
Lys Gly Arg Gln Ala Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly
290 295 300
Asp Thr Leu Glu Thr Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys
305 310 315 320
75 Leu Cys Ala Thr Asn Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly

WO 99/29870

PCT/AU98/01023

233/490

Ser Leu Ser Val Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu
85 90 95
Gln Ile Asn Gly Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu
100 105 110
5 Gln Glu Ile Asn Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe
115 120 125
Asp Val Val Asn Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His
130 135 140
10 Leu Ile Pro Trp Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser
145 150 155 160
Glu Trp Ser Lys Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val
165 170 175
Met Met Ala Phe Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala
180 185 190
15 Gln Ala Ala His Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys
195 200 205
Lys Thr Pro Val Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe
210 215 220
20 Gln Gly Met Ala Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly
225 230 235 240
Phe Asn Ala Ile Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn
245 250 255
Gly Gln Ile Asn Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg
260 265 270
25 Pro Val Ser Cys Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr
275 280 285
Glu Asn Ile Leu Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His
290 295 300
30 Val Val Asp Lys Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe
305 310 315 320
Val Lys Glu Thr Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro
325 330 335
Thr Gly Asn Thr Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys
340 345 350
35 Ala Val Val Asp Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu
355 360 365
Ile Ser Val Glu Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys
370 375 380
40 Ala Trp Asn Arg Val Val Ile Val Arg Ser Lys
385 390 395

(2) INFORMATION FOR SEQ ID NO:313

- (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 387 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 50 (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...387
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

Tyr Lys Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala
1 5 10 15
65 Leu Ala Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr
20 25 30
Thr Gln Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala
35 40 45
Ser Asp His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu
50 55 60
70 Ser Gly Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val
65 70 75 80
Pro Thr Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg
85 90 95
75 Leu Gln Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys
100 105 110

WO 99/29870

PCT/AU98/01023

234/ 490

5 Glu Arg Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe
115 120 125
Asp Leu Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His
130 135 140
15 Ile Ile Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu
145 150 155 160
Asn Ala Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr
165 170 175
10 Val Asn Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp
180 185 190
Phe Asn Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly
195 200 205
Thr Lys Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu
210 215 220
15 Thr Phe Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp
225 230 235 240
Tyr Ala Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly
245 250 255
20 Gln Val Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro
260 265 270
Glu Pro Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val
275 280 285
Tyr Phe Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn
290 295 300
25 Val Tyr Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys
305 310 315 320
Val Val Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met
325 330 335
30 Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys
340 345 350
Tyr Gly Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser
355 360 365
Glu Gln Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr
370 375 380
35 Ala Ala Glu
385

(2) INFORMATION FOR SEQ ID NO:314

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...195
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

60 Val Ile Gly Ile Ile Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val
1 5 10 15
Phe Val Asn Asn Val Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe
20 25 30
Leu Gly Val Ser Lys Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala
35 40 45
65 Val Thr Phe Val Leu Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln
50 55 60
Lys Phe Val Leu Asp Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala
65 70 75 80
Phe Ile Leu Val Ile Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu
85 90 95
70 Lys Lys Val Ser Pro Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro
100 105 110
Leu Ile Thr Thr Asn Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile
115 120 125
75 Gln Lys Asp Tyr Thr Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr
130 135 140

236/ 490

Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg Arg Gly Gly Asp Arg
 370 375 380
 Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala Glu Tyr Leu Gln His
 385 390 395 400
 5 Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln Gly Phe Ser Gly Gly
 405 410 415
 Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln Asp Val Gln Arg Arg
 420 425 430
 10 Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn Leu Leu Asn Gly Ala
 435 440 445
 Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr Asn Asp Ala Phe Thr
 450 455 460
 Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe Asp Leu Gln Gly Gly
 465 470 475 480
 15 Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp Asp Phe Thr Gly Gly
 485 490 495
 Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg Ser Gly Tyr Arg Pro
 500 505 510
 20 Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser Gln Tyr Asp Gln Leu
 515 520 525
 Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile Gly Ala Arg Ile Asp
 530 535 540
 Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr Ile Asp Pro Leu Phe
 545 550 555 560
 25 Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn Pro Asn Lys Asn Leu
 565 570 575
 Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg Ala Pro Gln Tyr Phe
 580 585 590
 30 Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly Thr Pro Ile Ser Arg
 595 600 605
 Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser Arg Ser Ile Ser Ala
 610 615 620
 Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp Gln Phe Asn Ile Met
 625 630 635 640
 35 Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln Phe Lys Pro Ser Asp
 645 650 655
 Lys Val Glu Thr Ser Asp Gly Lys Glu Trp Ile Ile Arg Thr Ile
 660 665 670
 40 Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr Gly Val Asn Leu Glu
 675 680 685
 Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu Gln Leu Gly Gly Thr
 690 695 700
 Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr Ala Val Glu Ala Asp
 705 710 715 720
 45 Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys Asp Tyr Val Arg Thr
 725 730 735
 Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val Arg Pro Thr Glu His
 740 745 750
 50 Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly Lys Met Asp Val Val
 755 760 765
 His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu His Ile Ala Pro Asp
 770 775 780
 Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln Phe Lys Gly Leu Ala
 785 790 795 800
 55 Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala Phe Ala Asp Ile Asp
 805 810 815
 Leu Lys Leu Ser His Asp Phe His Leu Ala Ser Thr Met Thr Leu Glu
 820 825 830
 60 Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser Tyr Gln Lys Asp Thr
 835 840 845
 Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val Tyr Gly Pro Met Gln
 850 855 860
 Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn Phe
 865 870 875

(2) INFORMATION FOR SEQ ID NO:316

(i) SEQUENCE CHARACTERISTICS:

70 (A) LENGTH: 899 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

75 (iii) HYPOTHETICAL: YES

WO 99/29870

PCT/AU98/01023

238/490

515 520 525
Lys Tyr Tyr Gln Gln Tyr Ser Val Thr Phe Met Asp Pro Trp Phe Gly
530 535 540
5 Gly Lys Arg Pro Asp Met Phe Ser Phe Ser Ala Phe Tyr Ser Lys Thr
545 550 555 560
Thr Ala Ile Asp Ser Lys Phe Tyr Asn Ser Asn Ala Gly Asn Tyr Tyr
565 570 575
Asn Ala Tyr Tyr Asn Ser Tyr Tyr Asn Asn Tyr Asn Ser Tyr Tyr Asn
580 585 590
10 Gly Met Ser Asn Tyr Thr Gly Asp Leu Tyr Thr Gln Ala Ser Asp Pro
595 600 605
Asp Arg Ser Leu Gln Met Leu Gly Thr Ser Ile Gly Tyr Gly Lys Arg
610 615 620
15 Leu Thr Trp Pro Asp Asn Trp Phe Gln Ile Tyr Thr Ser Leu Asn Tyr
625 630 635 640
Thr Tyr Tyr Arg Leu Arg Asn Trp Ser Tyr Asn Thr Phe Gln Asn Phe
645 650 655
His His Gly Ser Ala Asn Asp Leu Asn Leu Glu Leu Arg Leu Ser Arg
660 665 670
20 Thr Ser Ile Asp Asn Pro Ile Tyr Thr Arg Ser Gly Ser Arg Phe Met
675 680 685
Val Ser Val Ala Ala Thr Leu Pro Tyr Ser Leu Trp Asp Asn His Asp
690 695 700
25 Tyr Ala Ser Gln Asn Leu Ser Val Ser Asp Arg Tyr Arg Phe Ile Glu
705 710 715 720
Tyr His Lys Trp Lys Phe Arg Gly Arg Val Phe Thr Pro Leu Leu Asn
725 730 735
Pro Ala Thr His Lys Tyr Thr Pro Val Leu Met Ser Arg Val Glu Gly
740 745 750
30 Ala Val Leu Gly Ser Tyr Asn Ser Asn Lys Lys Ser Pro Phe Gly Thr
755 760 765
Phe Tyr Met Gly Gly Asp Gly Met Ser Ser Tyr Tyr Gly Gly Tyr Met
770 775 780
35 Asn Glu Thr Ile Gly Leu Arg Gly Tyr Lys Asn Gly Ser Ile Ala Gly
785 790 795 800
Asn Asn Tyr Asp Tyr Ala Tyr Ala Tyr Met Arg Leu Thr Met Glu Leu
805 810 815
Arg Phe Pro Ile Leu Phe Glu Asn Ser Phe Asn Ala Trp Leu Leu Ala
820 825 830
40 Phe Ala Glu Ala Gly Asn Ala Trp Arg Ser Ile Asp Asn Tyr Asn Pro
835 840 845
Phe Asn Leu Lys Arg Ser Ala Gly Val Gly Leu Arg Val Thr Leu Pro
850 855 860
45 Met Val Gly Met Leu Gly Ile Asp Trp Gly Tyr Gly Phe Asp Arg Pro
865 870 875 880
Asp Asn Ser Leu Gln Arg Gly Gly Ser Asn Val His Phe Val Leu Gly
885 890 895
Gln Glu Phe

50

(2) INFORMATION FOR SEQ ID NO:317

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...177

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317..

75

Gln Ile Asn Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly
1 5 10 15
Phe Ala Leu Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu
20 25 30
Val Asp Met Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met

239/ 490

35 40 45
 Asn Glu Gln Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu
 50 55 60
 5 Ala Leu Glu Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp
 65 70 75 80
 Leu Val Phe Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile
 85 90 95
 Val Lys Lys Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly
 100 105 110
 10 Pro Glu Gly Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile
 115 120 125
 Gln Asp Glu Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn
 130 135 140
 15 Tyr Gln Met Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser
 145 150 155 160
 Pro Ser Ile Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser
 165 170 175
 Lys

20

(2) INFORMATION FOR SEQ ID NO:318

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

35 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...170

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

Arg Ile Asn Lys Gln His Glu Met Lys Lys Phe Phe Leu Met Leu Leu
 1 5 10 15
 Met Ala Leu Pro Leu Ser Leu Leu Ala Gln Lys Val Ala Val Val Asn
 20 25 30
 45 Thr Glu Glu Ile Ile Ser Lys Met Pro Glu Gln Val Ala Ala Thr Lys
 35 40 45
 Gln Leu Asn Glu Leu Ala Glu Lys Tyr Arg Leu Asp Leu Lys Ser Met
 50 55 60
 Asp Asp Glu Phe Ala Lys Lys Thr Glu Glu Phe Val Lys Glu Lys Asp
 65 70 75 80
 Ser Leu Leu Glu Asn Ile Arg Asn Arg Arg Gln Gln Glu Leu Gln Asp
 85 90 95
 Ile Gln Thr Arg Tyr Gln Gln Ser Tyr Gln Thr Met Gln Glu Asp Leu
 100 105 110
 55 Gln Lys Arg Gln Gln Gln Leu Phe Ala Pro Ile Gln Gln Lys Val Ala
 115 120 125
 Asp Ala Ile Lys Lys Val Gly Asp Glu Glu Asn Cys Ala Tyr Ile Met
 130 135 140
 60 Glu Ala Gly Met Met Leu Tyr Thr Gly Ala Thr Ala Ile Asp Leu Thr
 145 150 155 160
 Ala Lys Val Lys Ala Lys Leu Gly Ile Lys
 165 170

65 (2) INFORMATION FOR SEQ ID NO:319

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

70 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75 (vi) ORIGINAL SOURCE:

240/ 490

(A) ORGANISM: Porphyromonas gingivalis

(1X) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...828

5

(21) SEQUENCE DESCRIPTION: SEQ ID NO:319

10 Ile Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn
 1 5 15
 Gly Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser
 20 25 30
 Gln Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp
 35 40 45
 15 Arg Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr
 50 55 60
 Gly Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met
 65 70 75 80
 20 Lys Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr
 85 90 95
 Gln Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu
 100 105 110
 Asn Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val
 115 120 125
 25 Gln Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg
 130 135 140
 Asp Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile
 145 150 155 160
 Ser Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr
 165 170 175
 30 Ser Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly
 180 185 190
 Val Glu Val Tyr Arg Pro Leu Leu Val Arg Ser Ala Gln Gln Glu Gly
 195 200 205
 35 Leu Ser Phe Val Asn Pro Asp Leu Thr Gln Ser Val Gln Phe Ser Ala
 210 215 220
 Gly Gly Phe Thr Ala Asp Tyr Gly Asp Lys Met Ser Ser Val Leu Asp
 225 230 235 240
 40 Ile Arg Tyr Lys Gln Pro Gln Glu Lys Glu Gly Ala Val Leu Leu Gly
 245 250 255
 Met Leu Gln Ser Ser Ala Tyr Tyr Gly Ser Ser Ala Gly Ala Phe Ser
 260 265 270
 Gln Ile Thr Gly Val Arg Tyr Lys Ser Ala Lys Ser Leu Leu Gly Thr
 275 280 285
 45 Thr Asp Thr Lys Ala Glu Tyr Asp Pro Ile Tyr Ala Asp Gly Gln Thr
 290 295 300
 Phe Met Thr Tyr Arg Phe Ser Pro Lys Leu Ser Val Ser Phe Leu Gly
 305 310 315 320
 50 Asn Ile Ser Gln Thr Arg Tyr Lys Phe Val Pro Gln Thr Arg Glu Thr
 325 330 335
 Ser Phe Gly Thr Leu Ser Asp Ala Lys Lys Leu Lys Ile Phe Phe Asp
 340 345 350
 Gly Gln Glu Gln Asp Arg Phe Leu Thr Tyr Phe Gly Ala Phe Ser Met
 355 360 365
 55 Asn Phe Val Pro Asp Asp Lys Gln Arg His Thr Val Thr Leu Ser Ala
 370 375 380
 Phe Asn Ser Asn Glu Arg Glu Thr Tyr Asp Ile Gln Gly Glu Tyr Phe
 385 390 395 400
 60 Leu Asn Asp Val Gln Leu Gly Ala Asp Gly Thr Ala Ser Met Ala Ser
 405 410 415
 Gly Ser Glu Asn Ser Asn Gly Leu Gly Ile Gly Arg Asn His Glu His
 420 425 430
 Ala Arg Asn Arg Leu Ser Tyr Arg Val Leu Asn Met Gly Tyr Arg Gly
 435 440 445
 65 Glu Met Lys Leu Asn Glu Lys His Arg Leu Gln Ala Gly Val Ser Ala
 450 455 460
 Gln Met Glu Lys Ile Ala Asp His Ile Ser Glu Trp Glu Arg Arg Asp
 465 470 475 480
 70 Ser Val Gly Tyr Asn Leu Pro His Ser Glu Thr Val Leu Leu Met Tyr
 485 490 495
 Asn Asn Leu Tyr Ala Asp Thr Gln Met Arg Gly Thr Arg Leu Ser Ala
 500 505 510
 Phe Val Gln Asp Arg Phe Asn Phe Ser Met Gly Gly Gly Thr Phe Ser
 515 520 525
 75 Leu Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu

WO 99/29870

PCT/AU98/01023

241/ 490

530 535 540
 Leu Val Ser Pro Arg Ile Ser Val Gly Tyr Ser Pro Glu Ser Asn Pro
 545 550 555
 Ala Leu Val Leu Arg Ala Ala Ala Gly Leu Tyr Tyr Gln Ala Pro Phe
 565 570 575
 Tyr Lys Glu Leu Arg Gln Thr His Lys Asp Ala Glu Gly Asn Asn Val
 580 585 590
 Val Val Leu Asn Glu Lys Ile Arg Ser Gln Gly Ala Phe His Ile Leu
 595 600 605
 10 Ala Gly Ala Asp Tyr Thr Phe Glu Met Gly Gly Arg Lys Tyr Lys Phe
 610 615 620
 Thr Ala Glu Ala Tyr Tyr Lys Ser Leu Phe Asn Ile Asn Pro Tyr Ile
 625 630 635
 15 Ile Glu Asn Val Lys Ile Arg Tyr Leu Gly Glu Asn Ile Gly Ser Gly
 645 650 655
 Tyr Ala Ala Gly Ile Asp Leu Lys Leu Phe Gly Glu Leu Val Pro Gly
 660 665 670
 Val Asp Ser Trp Leu Thr Ala Ser Ile Ile Lys Ala Arg Gln Lys Leu
 675 680 685
 20 Asp Gly Tyr Gly Ser Leu Pro Leu Met Asn Ala Pro Thr Tyr Asn Phe
 690 695 700
 Ser Phe Phe Leu Gln Glu Tyr Val Pro Gly Asn Lys Arg Ile Thr Ala
 705 710 715 720
 25 Thr Leu Arg Ala Ala Leu Ser Gly Gly Leu Pro Gln Leu Asn Pro Ser
 725 730 735
 Lys Gly Leu Ser Ser Pro Ala Phe Thr Ala Pro Ala Tyr Lys Arg Val
 740 745 750
 Asp Leu Gly Val Met Tyr Lys Trp Leu Asp Pro Asp Asp Ser Phe Ala
 755 760 765
 30 Gly Arg Ser Lys Trp Leu Met Gly Val Lys Gly Ala Tyr Ile Gly Ala
 770 775 780
 Asp Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp
 785 790 795 800
 35 Val Ser Asp Ala Tyr Gln Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr
 805 810 815
 Arg Arg Gln Phe Asn Leu Arg Leu Leu Val Glu Phe
 820 825

40 (2) INFORMATION FOR SEQ ID NO:320
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 679 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 50 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 55 (B) LOCATION 1...679
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

60 Pro Ile Pro Phe Leu Leu Asn Met Tyr Ser Gly His His Lys Ile His
 1 5 10 15
 Tyr Pro Phe Leu Ile Leu Leu Val Cys Leu Ala Phe Ala Ala Cys Lys
 20 25 30
 Ser Val Lys Leu Lys Asp Ala Glu Lys Ala His Asp Arg Gln Glu Tyr
 35 40 45
 65 Thr Lys Ala Ala Asp Met Tyr Asn Thr Leu Tyr Arg Arg Thr Arg Arg
 50 55 60
 Lys Gln Val Glu Met Lys Ala Tyr Thr Ala Phe Arg Ser Gly Glu Asn
 65 70 75 80
 70 Tyr Arg Ala Ala Gly Arg Gln Ala Lys Ala Leu Arg Gly Tyr Leu Asn
 85 90 95
 Ala Arg Arg Tyr Gly Tyr Pro Asp Ser Val Val Leu Leu Arg Leu Ala
 100 105 110
 Gln Thr Tyr Gln Gln Gly Gly Asn Tyr Lys Glu Ala Glu Val Leu Phe
 115 120 125
 75 Arg Gly Tyr Leu Glu Ala Tyr Pro Lys Ser Tyr Phe Ala Ala Ile Gly

242/ 490

130 135 140
 Leu Glu Gly Cys Leu Phe Ala Arg Gln Gln Lys Glu Tyr Pro Thr Arg
 145 150 155 160
 Tyr Arg Ile Arg Arg Ala Ala Glu Trp Asn Ser Ala Arg Gly Asp Phe
 165 170 175
 Gly Pro Ala Tyr Ala Pro Asp Ala Ser Ala Leu Tyr Phe Thr Ser Ser
 180 185 190
 Arg Ser Lys Asp Asp Gly Leu Asp Asn Ser Ser Ile Thr Gly Leu Lys
 195 200 205
 Pro Asn Asp Ile Tyr Ile Ile Lys Arg Asp Ala Gln Gly Arg Trp Gly
 210 215 220
 Arg Pro Asp Ser Val Ser Gly Gly Ile Asn Thr Pro Trp Asp Glu Gly
 225 230 235 240
 Val Pro Thr Ile Thr Pro Asp Gly Ser Thr Ile Tyr Tyr Thr Leu Ala
 245 250 255
 Gln Gln Gly Ala Asp Tyr Asp Arg Thr Val Gln Ile Tyr Ser Ala Ala
 260 265 270
 Arg Ser Gly Glu Gly Gly Trp Ser Asn Gly Ser Leu Val Asp Ile Met
 275 280 285
 Arg Asp Ser Leu Arg Met Ala Ala His Pro Ser Met Ser Ala Ser Gly
 290 295 300
 Asp Tyr Leu Tyr Phe Val Ser Asn Ile Gly Gly Ser Tyr Gly Gly Lys
 305 310 315 320
 Asp Ile Tyr Arg Val Lys Val Ser Asp Arg Ser Tyr Gly Ser Pro Glu
 325 330 335
 Asn Leu Gly Pro Asp Ile Asn Thr Pro Gly Asp Glu Met Phe Pro Phe
 340 345 350
 Ile Asp Gly Asp Ser Thr Leu Phe Phe Ala Ser Asp Gly His Ala Gly
 355 360 365
 Leu Gly Gly Leu Asp Ile Phe Lys Ala Thr Leu Asp Ser Thr Gly Gln
 370 375 380
 Trp His Val Val Asn Met Gly Gln Pro Val Asn Ser Ser Ala Asp Asp
 385 390 395 400
 Phe Gly Leu Ala Val Glu Pro Lys Gly Lys Asn Lys Glu Glu Ala Leu
 405 410 415
 Pro Asp Asn Gly Val Lys Gly Val Phe Cys Ser Asn Arg Gly Asp Ala
 420 425 430
 Arg Gly Trp Pro His Leu Phe His Phe Glu Leu Pro Ala Ile Tyr Thr
 435 440 445
 Glu Ile Gln Gly Tyr Val Met Asp Arg Glu Glu Asn Pro Ile Ala Gly
 450 455 460
 Ala Thr Val Arg Ile Val Gly Glu Arg Gly Pro Val Gly Gln Gly Phe
 465 470 475 480
 Val Thr Thr Arg Asp Asp Gly Ser Tyr Lys Met Ser Val Gln Gly Asp
 485 490 495
 Thr Arg Tyr Val Met Leu Ala Gly Ala Ser Gly Tyr Leu Asn Gln Tyr
 500 505 510
 Val Glu Leu Lys Thr Asp Thr Ala Lys Gln Ser Glu Thr Tyr Tyr Val
 515 520 525
 Asp Phe Phe Leu Ala Ser Arg Glu Lys Ala Glu Gly Leu Gln Asn Ile
 530 535 540
 Phe Tyr Asp Phe Asp Lys Ala Thr Leu Arg Pro Glu Ser Met Lys Ser
 545 550 555 560
 Leu Asp Glu Leu Ile Arg Ile Leu Thr Asp Asn Pro Asp Ile Arg Ile
 565 570 575
 Glu Leu Gly Ser His Ala Asp Arg Lys Gly Pro Asp Ala Tyr Asn Leu
 580 585 590
 Gly Leu Ser Asp Arg Arg Ala Lys Ser Val Val Asp Tyr Leu Thr Ser
 595 600 605
 Arg Gly Ile Ala Ala Asp Arg Leu Thr Trp Lys Gly Tyr Gly Lys Ser
 610 615 620
 Val Pro Lys Thr Val Thr Ala Lys Ile Ala Glu Arg His Asp Phe Leu
 625 630 635 640
 Lys Glu Gly Asp Val Leu Thr Glu Glu Phe Val Ala Pro Leu Thr Glu
 645 650 655
 Glu Gln Gln Ser Val Cys Asp Gln Leu Asn Arg Arg Thr Glu Phe Arg
 660 665 670
 Val Ile Glu Glu Glu Leu Arg
 675

(2) INFORMATION FOR SEQ ID NO:321

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 772 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

15 Pro Ala Gln Pro Lys Thr Tyr Cys Ile Arg Tyr Phe Arg Arg Glu Val
1 5 10 15
Ser Pro Arg Arg Gln Thr Glu Arg Thr Leu Tyr Ala Asp Lys Met Arg
20 20 25 30
Arg His Ile Val Lys Cys Cys Pro Ser Ala Ser Ile Leu Leu Gln Glu
35 40 45
Tyr Ser Thr Thr Glu Leu Phe Ile His His Phe Asn Ile Ser Ile Ile
50 55 60
Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln
25 65 70 75 80
Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His
85 90 95
Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu
100 105 110
30 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys
115 120 125
Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser
130 135 140
35 Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg
145 150 155 160
Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile
165 170 175
Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu
180 185 190
40 Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn
195 200 205
Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys
210 215 220
45 Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala
225 230 235 240
Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp
245 250 255
Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser
260 265 270
50 Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val
275 280 285
Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala
290 295 300
55 Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu
305 310 315 320
Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly
325 330 335
Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser
340 345 350
60 Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln
355 360 365
Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala
370 375 380
65 Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly
385 390 395 400
Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu
405 410 415
Gly Val Asp Ser Arg Asn Met Thr Met Glu Ser Glu Arg Phe Glu Gln
420 425 430
70 Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr Asn Asn
435 440 445
Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp Ala Leu
450 455 460
75 Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Phe Asp Leu Lys
465 470 475 480

WO 99/29870

PCT/AU98/01023

244/ 490

Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val
485 490 495
Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr
500 505 510
5 Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln
515 520 525
Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro
530 535 540
10 Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr
545 550 555 560
Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe
565 570 575
His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn
580 585 590
15 Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile
595 600 605
Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe
610 615 620
20 Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met
625 630 635 640
Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg
645 650 655
Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu
660 665 670
25 Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn
675 680 685
Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu
690 695 700
30 Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro
705 710 715 720
Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr
725 730 735
Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr
740 745 750
35 Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val
755 760 765
Met Val Asn Phe
770

40 (2) INFORMATION FOR SEQ ID NO:322
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 484 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
50
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...484
55
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

60 Gly Arg Ala Ser Ser Pro Tyr Arg Gln Met Asp Gly Ile Leu Asn Asp
1 5 10 15
Glu Tyr Arg Gln Ala Ser Met Asn Arg Phe Ser Asn His Trp Pro Cys
20 25 30
65 Ile Leu Val Gly Phe Val Leu Trp Phe Val Ser Ala Ser Arg Thr Val
35 40 45
Ala Gln Asn Ala Ser Glu Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala
50 55 60
Val Leu Ser Glu Ala Asp Val Leu Arg Ile Ala Leu Ser Glu Asn Ala
65 70 75 80
70 Thr Val Lys Val Ala Asp Met Asp Val Arg Lys Gln Glu Tyr Ala Arg
85 90 95
Arg Ala Ala Arg Ala Asp Leu Phe Pro Lys Val Asp Leu Asn Gly Val
100 105 110
75 Tyr Ser His Thr Leu Lys Lys Gln Val Leu Tyr Ile Asp Met Pro Gly
115 120 125

WO 99/29870

PCT/AU98/01023

246/490

5 Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln
 65 70 75 80
 Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr
 85 90 95
 10 Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro
 100 105 110
 Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu
 115 120 125
 15 Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe
 130 135 140
 20 Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser
 145 150 155 160
 Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro
 165 170 175
 25 Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly
 180 185 190
 Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg
 195 200 205
 30 Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala
 210 215 220
 Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile
 225 230 235 240
 Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg
 245 250 255
 35 Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala
 260 265 270
 Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly
 275 280 285
 40 Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile
 290 295 300
 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile
 305 310 315 320
 Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg
 325 330 335
 45 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser
 340 345 350
 Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr
 355 360 365
 50 Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp
 370 375 380
 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser
 385 390 395 400
 Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg
 405 410 415
 55 Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu
 420 425 430
 Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys
 435 440 445
 60 Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu
 450 455 460
 His Ser Leu Pro Leu Gly Pro Asp Gly Arg Arg Asp Gly Ala Val Tyr
 465 470 475 480
 Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn
 485 490 495
 65 Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr
 500 505 510
 Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile
 515 520 525
 70 Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln
 530 535 540

(2) INFORMATION FOR SEQ ID NO:324

- 65 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

 70 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 75

WO 99/29870

PCT/AU98/01023

247/ 490

(1.) FEATURE:
(A) NAME/KEY: misc_feature
(P) LOCATION: 1...293

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

Lys Ser Pro Ser Asp Ser Ala Leu Pro Ser Val Trp Ser Ala Asn Thr
1 5 10 15
10 Ile Ser Gly Leu Val Gly Gly Lys Arg Ile Thr Leu Leu Ile Leu Tyr
20 25 30
Ser Met Ala Ile Arg Ser Ser Asn Ile Glu Ser Ile Gln Cys Phe Val
35 40 45
Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe
50 55 60
15 Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg
65 70 75 80
Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys
85 90 95
20 Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp
100 105 110
Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
115 120 125
Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
130 135 140
25 Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln
145 150 155 160
Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
165 170 175
30 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
180 185 190
Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
195 200 205
Ala Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
210 215 220
35 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
225 230 235 240
Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
245 250 255
40 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
260 265 270
Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
275 280 285
Ser Phe Ala Leu Lys
290

45 (2) INFORMATION FOR SEQ ID NO:325

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

60 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...280

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

Gly Lys Leu Gln Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu
1 5 10 15
Leu Ala Leu Gly Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala
20 25 30
70 Val Ser Glu Lys Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly
35 40 45
Gln Asp Phe Ala Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro
50 55 60
75 Ile Asp Ser Val Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr
65 70 75 80

248/ 490

Thr Arg Phe Ser Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala
 85 90 95
 Arg Gln Leu Ala His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala
 100 105 110
 5 Met Arg Ala Ala Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro
 115 120 125
 Ala Asp Ala Gln Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg
 130 135 140
 10 Glu Asn Asn Met Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu
 145 150 155 160
 Tyr Ile Asp Thr Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr
 165 170 175
 Gly Leu Ala Tyr Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser
 180 185 190
 15 Leu Ala Asp Thr Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly
 195 200 205
 Lys Glu Phe Asp Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly
 210 215 220
 20 Val Ile Lys Gly Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln
 225 230 235 240
 Lys Val Arg Val Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly
 245 250 255
 Asn Tyr Thr Ile Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu
 260 265 270
 25 Ile Gly Ile Lys Pro Gly Lys Lys
 275 280

(2) INFORMATION FOR SEQ ID NO:326

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 803 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...803
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

Cys Arg Lys Gln Lys Leu Ser Asn Pro Lys Arg Ser Arg Tyr Pro Cys
 1 5 10 15
 50 Arg Arg Ile Ser Phe Arg Gln Ser Asp Lys Asn Pro Met Lys Val Leu
 20 25 30
 Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu Thr Gly Ala Cys
 35 40 45
 55 Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu Tyr Ile Gly Met
 50 55 60
 Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His Ala Gly Gln Gln
 65 70 75 80
 Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr Pro Asn Gly Ala
 85 90 95
 60 Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile Pro Phe Gly Leu
 100 105 110
 Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val Ile Ser Lys Trp
 115 120 125
 65 Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile Ser Gln Val Lys
 130 135 140
 Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu Arg Glu His Gly
 145 150 155 160
 Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr Leu Lys Lys Asp
 165 170 175
 70 Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met Ala Ser Pro Tyr
 180 185 190
 His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr Phe Pro Asp Ser
 195 200 205
 75 Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg Lys Gly Asp Gln
 210 215 220

WO 99/29870

PCT/AU98/01023

250/ 490

(C) INFORMATION FOR SEQ ID NO:327

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 783 amino acids
 (B) TYPE: amino acid
 (E) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

1	Ser	Leu	Ser	Pro	Tyr	Ile	Arg	Phe	Pro	Met	Ser	Ser	His	Ser	Val	Arg
5																
10	Tyr	Leu	Ile	Gly	Ile	Ala	Gly	Cys	Leu	Leu	Met	Leu	Ala	Ser	Ser	
15																
20	Cys	Ser	Val	Thr	Arg	Tyr	Val	Pro	Asp	Gly	Ser	Arg	Leu	Leu	Asp	Arg
25																
30	Val	Thr	Ile	Ala	Ser	Glu	Thr	Gly	Ser	Ile	Ala	Leu	Pro	Glu	Asp	Ile
35																
40	Arg	Asp	Tyr	Thr	Leu	Gln	Gln	Pro	Asn	Tyr	Arg	Leu	Phe	Gly	Met	Thr
45																
50	Arg	Trp	Leu	Leu	Arg	Val	Tyr	Ser	Ser	Ser	Asn	Pro	Asn	Ser	Asn	Ser
55																
60	Trp	Trp	Asn	Arg	Ser	Leu	Arg	Lys	Met	Gly	Glu	Pro	Pro	Val	Leu	Ile
65																
70	Asp	Ser	Val	Leu	Thr	Asp	Arg	Thr	Ala	Asn	Arg	Leu	Ala	Lys	Ala	Met
75																
80	Ala	Gly	Asp	Gly	Phe	Leu	Asp	Ala	Thr	Ala	Arg	Ala	Val	Val	Asp	Thr
85																
90	Gly	Leu	Tyr	Lys	Lys	Ala	Arg	Ile	Thr	Tyr	Leu	Ile	Gln	Pro	Gly	Ser
95																
100	Arg	Tyr	Tyr	Ile	Arg	Asn	Met	Ala	Leu	Asp	Val	Lys	Asn	Pro	Leu	Leu
105																
110	Pro	Pro	Val	Ala	Leu	Gly	Asn	Ser	Leu	Pro	Ser	Ala	Tyr	Lys	Val	Gly
115																
120	Ile	Ser	Glu	Gly	Ser	Pro	Leu	Ser	Pro	Ile	Val	Leu	Asp	Glu	Glu	Arg
125																
130	Lys	Ala	Ile	Ala	Arg	His	Met	Arg	Asn	Asn	Gly	Phe	Trp	Lys	Phe	Ser
135																
140	Ala	Glu	Asp	Val	Tyr	Tyr	Glu	Ala	Asp	Thr	Thr	Val	Ser	Gly	Gly	Ser
145																
150	Gly	Thr	Lys	Ser	Ala	Asp	Leu	Lys	Leu	Val	Val	Asn	Gly	Ile	Gly	Arg
155																
160	Tyr	Pro	Tyr	Arg	Ile	Gly	Arg	Val	Phe	Phe	His	Ala	Asp	Tyr	Asp	Pro
165																
170	Leu	Glu	Ser	Asp	Phe	Arg	Val	Gln	Glu	Leu	Pro	Arg	Ile	Asp	Ser	Ile
175																
180	Ser	Arg	Gly	Asp	Tyr	Thr	Val	Tyr	Tyr	Gly	Ser	Arg	Gly	Arg	Tyr	Ile
185																
190	Arg	Ala	Ser	Ala	Leu	Thr	Arg	Ser	Val	Ser	Val	Thr	Pro	Gly	Ala	Phe
195																
200	Phe	Cys	Glu	Asp	Asp	Val	Glu	Arg	Ser	Tyr	Ile	Lys	Leu	Asn	Ala	Leu
205																
210	Pro	Ile	Val	Arg	Asn	Val	Asn	Ile	Arg	Phe	Val	Glu	His	Asn	Gly	Lys
215																
220	Asp	Glu	Ile	Ala	Leu	Ala	Asp	Ser	Ser	Arg	Leu	Val	Asp	Cys	Tyr	Ile
225																
230	Leu	Thr	Val	Pro	Ala	Lys	Ser	Lys	Ser	Phe	Glu	Ala	Glu	Val	Leu	Gly
235																
240	Thr	Asn	Ser	Ala	Gly	Asp	Phe	Gly	Ala	Ala	Leu	Ser	Leu	Gly	Phe	Thr
245																
250	Asp	Arg	Asn	Leu	Phe	Arg	Gly	Ala	Glu	Met	Phe	Asn	Ile	Lys	Leu	Lys
255																
260	Gly	Ala	Tyr	Glu	Ala	Ile	Arg	Lys	Gly	Ser	His	Ser	Phe	Met	Glu	Tyr
265																
270	Gly	Val	Glu	Ser	Ser	Leu	Arg	Phe	Pro	Arg	Leu	Leu	Phe	Pro	Phe	Ile
275																

WO 99/29870

PCT/AU98/01023

251/ 490

5 Ser Asp 435 Thr Arg Arg Arg 440 Leu Arg Ala Ser Thr 445 Gln Trp Lys Ile
150 455 460
Gly Tyr Asn Tyr Gln Thr Arg Pro Glu Phe Asp Arg Val Ile Leu Ser
465 470 475 480
Ala Gln Leu Asn Tyr Ser Trp Gln Thr Tyr Leu His Asn Arg Leu Arg
485 490 495
His Thr Ile Arg Leu Leu Asp Val Asp Tyr Leu His Leu Pro Tyr Ile
500 505 510
10 Asp Pro Asp Phe Ala Gln Ser Leu Pro Pro Thr Thr Ala Leu Tyr Asn
515 520 525
Tyr Thr Glu Gln Phe Ile Leu Gly Ser Ala Tyr Ile Leu Asn Tyr Thr
530 535 540
15 Thr Ala Ser Ser Met Glu Arg Thr Val Ser Asn Pro Phe Thr Ala Arg
545 550 555 560
Phe Ser Ile Gln Thr Ala Gly Asn Leu Leu Gln Ala Ile Ser Tyr Leu
565 570 575
20 Thr Asp Ser Pro Lys Asp Glu His Gly Leu Tyr Lys Met Phe Gly Leu
580 585 590
His Tyr Ala Gln Phe Val Lys Leu Asp Leu Asp Leu Ala Lys Thr Val
595 600 605
Leu Leu Glu Lys Asp Asn Thr Leu Ala Leu His Leu Gly Phe Gly Leu
610 615 620
25 Ala Phe Pro Tyr Gly Asn Ala Arg His Ile Pro Phe Glu Leu Arg Tyr
625 630 635 640
Phe Ala Gly Gly Ser Asn Ser Val Arg Gly Trp Ser Val Arg Thr Leu
645 650 655
Gly Pro Gly Ser Met Lys Met Thr Pro Asp Lys Thr Phe Phe Asp Gln
660 665 670
30 Met Gly Asp Ile Arg Leu Asp Leu Asn Val Glu Tyr Arg Thr Lys Leu
675 680 685
Phe Trp Lys Phe Arg Ala Ala Phe Val Asp Ala Gly Asn Val Trp
690 695 700
35 Thr Ile Lys Glu Tyr Glu Asn Gln Glu Asp Gly Leu Phe Arg Phe Asp
705 710 715 720
Arg Phe Tyr Lys Glu Ile Ala Leu Ala Tyr Gly Leu Gly Leu Arg Leu
725 730 735
Asp Phe Asp Tyr Phe Leu Val Arg Leu Asp Ala Gly Leu Lys Ala Tyr
740 745 750
40 Asp Pro Gln Gln Thr Gly Arg Tyr Lys Trp Ala Ile Thr Arg Pro Asn
755 760 765
Leu Ser Ser Asn Phe Ala Trp His Ile Ala Val Gly Tyr Pro Phe
770 775 780

45 (2) INFORMATION FOR SEQ ID NO:328

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 875 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES

55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

60 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328

65 Val Glu Ser Lys Leu Leu Cys Leu Met Arg Lys Arg Ile Leu Gln Leu
1 5 10 15
Phe Leu Thr Ala Leu Leu Leu Ala Leu Gly Ser Ser Leu Ala Ile Ala
20 25 30
70 Gln Thr Val Val Thr Gly Lys Val Ile Asp Ser Glu Thr Ser Glu Pro
35 40 45
Leu Ile Gly Val Ser Val Ser Thr Gly Gln Gly Ala Ser Leu Arg Gly
50 55 60
Val Thr Thr Asp Met Asp Gly Gly Phe Arg Phe Glu Val Pro Ala Lys
65 70 75 80
75 Ser Val Leu Thr Phe Arg Cys Val Gly Tyr Ala Thr Val Thr Arg Ser

252 / 490

[illegible]

WO 99/29870

PCT/AU98/01023

253/490

5 His Cys Gly Val Glu Ala Glu Val Ser Tyr Arg Pro Ile Arg Gln Ile
 690 695 700
 Asp Leu Arg Gly Met Phe Ser Leu Gly Asp Trp Thr Trp Gln Asn Asn
 705 710 715 720
 Val Ser Tyr Thr Ser Tyr Asp Glu Ala Gly Asn Glu Thr Gly Gln Asp
 725 730 735
 Ile Thr Tyr Ile Lys Gly Leu His Val Gly Asp Ala Ala Gln Met Thr
 740 745 750
 10 Ala Ala Val Ser Ala Asp Ile Glu Leu Phe Lys Gly Phe His Val Ile
 755 760 765
 Gly Lys Tyr Asn Phe Leu Gly Lys Asn Tyr Ala Gly Phe Asn Pro Ala
 770 775 780
 Thr Arg Asn Ala Gln Gln Tyr Glu Ala Asp Gly Lys Glu Ile Val Glu
 785 790 795 800
 15 Ser Trp Lys Leu Pro Asp Val Gly Leu Phe Asp Leu Ser Ala Ser Tyr
 805 810 815
 Asn Phe Lys Leu Gly Ser Leu Ser Thr Thr Phe Tyr Phe Asn Met Asp
 820 825 830
 20 Asn Val Ala Asp Lys Arg Tyr Val Ser Asp Ala Asp Asp Asn Ile Ile
 835 840 845
 Gly Lys Lys His Asp Glu Ala Ser Ala Leu Val Trp Tyr Gly Phe Gly
 850 855 860
 Arg Thr Trp Ser Thr Gly Ile Arg Val Asn Phe
 865 870 875

(2) INFORMATION FOR SEQ ID NO:329

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 460 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

45 Asn Arg Cys Asn Pro Ser Arg Gln Tyr Phe His Leu Ser Gln Asn Asp
 1 5 10 15
 Val Gly Arg Ser Leu Arg Ala Phe Leu Ile His Leu Ser Met Lys Phe
 20 25 30
 50 Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser Ala Phe Ile
 35 40 45
 Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg Leu Glu Lys
 50 55 60
 55 Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp Arg Glu Leu
 65 70 75 80
 Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His Leu Asn Leu
 85 90 95
 Leu Asn Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln Leu Leu Asp
 100 105 110
 60 Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met Thr Gly Val
 115 120 125
 Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp Glu Tyr Ala
 130 135 140
 65 Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu Asp Arg Ile
 145 150 155 160
 Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met Arg Arg Met
 165 170 175
 Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala Ser Val Arg
 180 185 190
 70 Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala Thr Val Glu
 195 200 205
 Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg Glu Glu Glu
 210 215 220
 75 Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg Gln Val Gln
 225 230 235 240

254/ 490

Ala Leu Gly Ala Lys Gln Lys Asp Leu Glu Ala Gln Leu Arg Lys Gln
 245 250 255
 Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys Gln Ile Ala
 260 265 270
 5 Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu Arg Glu Arg
 275 280 285
 Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro Ala Glu Pro
 290 295 300
 10 Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp Ala Ser Glu
 305 310 315 320
 Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg Leu Pro Gly
 325 330 335
 Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly Val His Gln
 340 345 350
 15 His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly Ile Asp Ile
 355 360 365
 Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp Gly Val Val
 370 375 380
 20 Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val Met Val Arg
 385 390 395 400
 His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys Val Tyr Val
 405 410 415
 Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly Arg Ala Tyr
 420 425 430
 25 Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu Ile Trp Lys
 435 440 445
 Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg
 450 455 460

30 (2) INFORMATION FOR SEQ ID NO:330

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

40 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

45 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

50 Ser Phe Tyr Gln Glu Ile Asp Arg Leu Met Lys Lys Tyr Leu Leu Tyr
 1 5 10 15
 Ala Ser Leu Leu Thr Ser Val Leu Leu Phe Ser Cys Ser Lys Asn Asn
 20 25 30
 55 Pro Asn Glu Pro Val Glu Asp Arg Ser Ile Glu Ile Ser Ile Arg Val
 35 40 45
 Asp Asp Phe Thr Lys Thr Gly Glu Ala Val Arg Tyr Glu Arg Asn Gln
 50 55 60
 Gly Ser Ala Ala Glu Arg Leu Ile Thr Asn Leu Tyr Leu Leu Phe
 65 70 75 80
 60 Asp Gln Ser Gly Ala Asn Pro Ala Lys Tyr Tyr Ile Thr Gly Asn Thr
 85 90 95
 Phe Thr Gly Gly Thr Trp Leu Pro Asp Asp Met Lys Val Lys Leu Asp
 100 105 110
 65 Met Thr Gln Ser Glu Ala Gly Glu Arg Lys Val Tyr Val Val Ala Asn
 115 120 125
 Val Asp Asn Ala Val Lys Thr Ala Leu Asp Ala Val Ala Asn Glu Ser
 130 135 140
 Asp Leu Gln Thr Val Lys Arg Thr Thr Ala Met Pro Trp Ser Thr Asp
 145 150 155 160
 70 Ile Ala Ser Pro Phe Leu Met Ser Gly Asn Lys Thr His Asp Phe Leu
 165 170 175
 Ala Asn Arg Leu Leu Asp Asn Val Pro Leu Val Arg Ala Ile Ala Lys
 180 185 190
 75 Val Glu Leu Asn Ile Ser Leu Ser Glu Lys Phe Gln Ile Val Pro Ile
 195 200 205

WO 99/29870

PCT/AU98/01023

255/490

Ile Val Asn Gly Ser Leu Ser Glu Phe Lys Phe Arg Tyr Val Asn Phe
 210 215 220
 Asp Lys Glu Thr Tyr Val Val Lys Pro Thr Thr Lys Pro Asp Asn Leu
 225 230 235 240
 5 Ile Ser Ser Ala Asn Gly Val Trp Pro Gln Ile Thr Asp Trp Thr Val
 245 250 255
 Trp Gly Ala Ser Leu Asn Thr Ser Pro Ala Pro Asp Ala Gly Thr Gly
 260 265 270
 10 Tyr Thr Leu Asp Ala Asn Gly Lys Val Thr Ala Leu Arg Ile Val Thr
 275 280 285
 Tyr Leu Asn Glu Arg Asp Ser Lys Gly Ala Thr Val Glu Val Ala Leu
 290 295 300
 Pro Arg Val Asp Asp Gly Thr Leu Pro Pro Pro Glu Phe Gly Pro Glu
 305 310 315 320
 15 Leu Tyr Arg Leu Pro Leu Pro Asp Lys Ile Leu Arg Asn His Trp Tyr
 325 330 335
 Lys Tyr Glu Val Glu Ile
 340
 20 (2) INFORMATION FOR SEQ ID NO:331
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...329
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331
 40 Asn Leu Arg Thr Gln Pro Phe Phe Leu Val Asp Leu Gln Ser Met Ile
 1 5 10 15
 Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser Arg Gly
 20 25 30
 45 Ala Thr Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala Ala Thr
 35 40 45
 Ala Leu Pro Ala Cys Gly Gly Thr Ala Ser Gly Ser Asp Arg Thr
 50 55 60
 Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser Ile Ala
 65 70 75 80
 50 Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser Asn Pro
 85 90 95
 Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser Glu Ala
 100 105 110
 55 Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg Asn Leu
 115 120 125
 Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu Met Gly
 130 135 140
 Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser Cys Thr
 145 150 155 160
 60 Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr Trp Ser
 165 170 175
 Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp Ala Leu
 180 185 190
 65 Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly His Asp
 195 200 205
 Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp Thr Met
 210 215 220
 Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His Pro Ser
 225 230 235 240
 70 Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val Ile Glu
 245 250 255
 Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val Ile Asp
 260 265 270
 75 Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro Glu Phe
 275 280 285

258/490

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...206

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

10 Lys Gln Ile Val Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu
1 5 10 15
Thr Leu Ile Gly Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln
20 25 30
Ser Leu Phe Ser Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu
35 40 45
15 Tyr Gly Glu Ser Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu
50 55 60
Ser Ala Phe Pro Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe
65 70 75 80
20 Leu Gly Lys Pro Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp
85 90 95
Cys Ser Gly Tyr Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu
100 105 110
Pro Arg Gly Ala Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg
115 120 125
25 Glu Asp Val Arg Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala
130 135 140
Arg Ser Asn Arg Ile Gly His Val Ala Leu Val Ser Val Asp Glu
145 150 155 160
30 Asp Asp Ile Thr Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile
165 170 175
Glu Lys Leu Asn Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr
180 185 190
Gly Arg Val Pro Gly Ala Lys Arg Val Ile Pro Arg Lys Ser
195 200 205

35

(2) INFORMATION FOR SEQ ID NO:334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

50

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...467

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

55 Lys Gly Thr Trp Asn Arg Lys Asn Arg Arg Glu Glu Met Lys Arg Thr
1 5 10 15
Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu Ser Leu Leu Arg
20 25 30
60 Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met Ser Gly Leu Ser
35 40 45
Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn Leu Asn Leu Arg
50 55 60
Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser Leu Asp Ala Ala
65 70 75 80
Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile Gly His Asn Tyr
85 90 95
Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr Val Asp Arg Ser
100 105 110
70 Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val Glu Val Phe Ser
115 120 125
Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys Tyr Asn Val Glu
130 135 140
Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp Leu Ser Leu Gln
145 150 155 160

75

260/490

Thr Leu Phe Asp Gly Leu Gln Ser Val Tyr Arg Leu Arg Met Ala His
115 120 125
Ala Arg Arg Glu Ala Ser Arg Leu Ser Val Arg Glu Gln Gln Glu Leu
130 135 140
5 Ala Ala Leu Gly Thr Thr Glu Ala Tyr Tyr Asp Leu Val Tyr Ala Arg
145 150 155 160
Gln Met Gln Glu Leu Ala Met Gln Lys Tyr Glu Glu Ser Ser Arg Leu
165 170 175
10 His Arg Gln Thr Ala Arg Met Glu Glu Leu Gly Met Lys Ser Arg Pro
180 185 190
Asp Val Leu Glu Met Gln Ser Arg Met Ala Gly Asp Arg Leu Ala Leu
195 200 205
Thr Gln Ala Asp Asn Gln Cys Ile Ile Ala Leu Ile Arg Leu Lys Glu
210 215 220
15 Lys Met Asn Phe Pro Ile Asp Asp Glu Leu Val Val Asp Asp Met Pro
225 230 235 240
Ala Asp Ser Leu Ser Ala Asp Met Ala Glu Ser Asp Ser Ser Ala Gly
245 250 255
20 Val Phe Ala Arg Ala Ala His His His Pro Val Leu Leu Arg Ala Lys
260 265 270
Leu Asp Glu Gln Ala Ala Thr Asp Arg Leu Arg Ala Ala Arg Gly Ala
275 280 285
Phe Leu Pro Ser Val Ser Val Ser Gly Gly Trp Asn Thr Gly Phe Ser
290 295 300
25 Arg Phe Leu Asn Gly Ser Asp Tyr Thr Pro Phe Ser Glu Gln Phe Arg
305 310 315 320
Asn Arg Arg Gly Glu Tyr Val Ser Leu Asn Leu Ser Ile Pro Ile Phe
325 330 335
30 Ser Gly Phe Ser Leu Val Ser His Leu Arg Gln Ala Arg Ala Glu Arg
340 345 350
Arg Ala Ala Ile Val Arg Arg Gly Glu Ala Glu Arg Arg Leu Tyr Ser
355 360 365
Glu Ile Ala Gln Ala Met Ala Asp Arg Asp Ala Ala Leu Ala Ser Tyr
370 375 380
35 Arg Gln Ala Lys Glu His Thr Asp Ala Met Gln Thr Ala Tyr Glu Ala
385 390 395 400
Val Leu Gln Arg Tyr Glu Glu Gly Leu Asn Thr Ala Ile Asp Leu Thr
405 410 415
40 Thr Gln Ala Asn Arg Leu Leu Asp Ala Arg Val Gln Arg Leu Arg Ala
420 425 430
Ala Met Thr Tyr Arg Leu Lys Cys Lys Leu Ile Ala Tyr Tyr Gly Cys
435 440 445
Leu Ser Asp
450

45 (2) INFORMATION FOR SEQ ID NO:336
(1) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 962 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(11) MOLECULE TYPE: protein
55 (111) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
60 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...962
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:336
65 Ala Ile Phe Val Val Ser Leu Gln Ile Glu Lys Ile Thr Glu Asn Lys
1 5 10 15
Tyr Asn Ser Asp Lys Ser Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln
20 25 30
70 Ser Gly Leu Ala Ala Phe Val Ser Met Ala Thr Ala Leu Thr Ala Ser
35 40 45
Ala Gln Ile Ser Phe Gly Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser
50 55 60
75 Ala Gly Thr His Ser Phe Asp Asp Ala Met Thr Ile Arg Leu Thr Pro
65 70 75 80

WO 99/29870

PCT/AU98/01023

261/ 490

	Asp	Phe	Asn	Pro	Glu	Asp	Leu	Ile	Ala	Gln	Ser	Arg	Trp	Gln	Ser	Gln
					85					90					95	
	Arg	Asp	Gly	Arg	Pro	Val	Arg	Ile	Gly	Gln	Val	Ile	Pro	Val	Asp	Val
					100					105					110	
5	Asp	Phe	Ala	Ser	Lys	Ala	Ser	His	Ile	Ser	Ser	Ile	Gly	Asp	Val	Asp
					115					120					125	
	Val	Tyr	Arg	Leu	Gln	Phe	Lys	Leu	Glu	Gly	Ala	Lys	Ala	Ile	Thr	Leu
					130					135					140	
	Tyr	Tyr	Asp	Ala	Phe	Asn	Ile	Pro	Glu	Gly	Gly	Arg	Leu	Tyr	Ile	Tyr
10					145					150					155	
	Thr	Pro	Asp	His	Glu	Ile	Val	Leu	Gly	Ala	Tyr	Thr	Asn	Ala	Thr	His
					165					170					175	
	Arg	Arg	Asn	Gly	Ala	Phe	Ala	Thr	Glu	Pro	Val	Pro	Gly	Ser	Glu	Leu
					180					185					190	
15	Ile	Met	Asp	Tyr	Glu	Val	Ser	Arg	Gly	Gly	Thr	Leu	Pro	Asp	Ile	Lys
					195					200					205	
	Ile	Ser	Gly	Ala	Gly	Tyr	Ile	Phe	Asp	Lys	Val	Gly	Gly	Arg	Pro	Val
					210					215					220	
20	Thr	Asp	Asn	His	Tyr	Gly	Ile	Gly	Glu	Asp	Asp	Ser	Asp	Ser	Asp	Cys
					225					230					235	
	Glu	Ile	Asn	Ile	Asn	Cys	Pro	Glu	Gly	Ala	Asp	Trp	Gln	Ala	Glu	Lys
					245					250					255	
	Asn	Gly	Val	Val	Gln	Met	Ile	Met	Val	Lys	Gly	Gln	Tyr	Ile	Ser	Met
					260					265					270	
25	Cys	Ser	Gly	Asn	Leu	Leu	Asn	Asn	Thr	Lys	Gly	Asp	Phe	Thr	Pro	Leu
					275					280					285	
	Ile	Ile	Ser	Ala	Gly	His	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val
					290					295					300	
30	Thr	Gln	Ser	Glu	Leu	Asp	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys
					305					310					315	
	Arg	Gly	Cys	Ser	Asn	Gly	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile
					325					330					335	
	Ile	Gly	Ala	Ser	Met	Lys	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp
					340					345					350	
35	Gly	Leu	Leu	Gln	Gln	Leu	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val
					355					360					365	
	Tyr	Tyr	Asn	Gly	Trp	Asp	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala
					370					375					380	
40	Gly	Ile	His	His	Pro	Ala	Gly	Asp	Ala	Met	Lys	Ile	Ser	Ile	Leu	Lys
					385					390					395	
	Lys	Thr	Pro	Ala	Leu	Asn	Thr	Trp	Ile	Ser	Ser	Ser	Gly	Ser	Gly	Gly
					405					410					415	
	Thr	Asp	Asp	His	Phe	Tyr	Phe	Lys	Tyr	Asp	Gln	Gly	Gly	Thr	Glu	Gly
					420					425					430	
45	Gly	Ser	Ser	Gly	Ser	Ser	Leu	Phe	Asn	Gln	Asn	Lys	His	Val	Val	Gly
					435					440					445	
	Thr	Leu	Thr	Gly	Gly	Ala	Gly	Asn	Cys	Gly	Gly	Thr	Glu	Phe	Tyr	Gly
					450					455					460	
50	Arg	Leu	Asn	Ser	His	Trp	Asn	Glu	Tyr	Ala	Ser	Asp	Gly	Asn	Thr	Ser
					465					470					475	
	Arg	Met	Asp	Ile	Tyr	Leu	Asp	Pro	Gln	Asn	Asn	Gly	Gln	Thr	Thr	Ile
					485					490					495	
	Leu	Asn	Gly	Thr	Tyr	Arg	Asp	Gly	Tyr	Lys	Pro	Leu	Pro	Ser	Val	Pro
					500					505					510	
55	Arg	Leu	Leu	Gln	Ser	Thr	Gly	Asp	Gln	Val	Glu	Leu	Asn	Trp	Thr	
					515					520					525	
	Ala	Val	Pro	Ala	Asp	Gln	Tyr	Pro	Ser	Ser	Tyr	Gln	Val	Glu	Tyr	His
					530					535					540	
60	Ile	Phe	Arg	Asn	Gly	Lys	Glu	Ile	Ala	Thr	Thr	Lys	Glu	Leu	Ser	Tyr
					545					550					555	
	Ser	Asp	Ala	Ile	Asp	Glu	Ser	Ile	Ile	Gly	Ser	Gly	Ile	Ile	Arg	Tyr
					565					570					575	
	Glu	Val	Ser	Ala	Arg	Phe	Ile	Tyr	Pro	Ser	Pro	Leu	Asp	Gly	Val	Glu
					580					585					590	
65	Ser	Tyr	Lys	Asp	Thr	Asp	Lys	Thr	Ser	Ala	Asp	Leu	Ala	Ile	Gly	Asp
					595					600					605	
	Ile	Gln	Thr	Lys	Leu	Lys	Pro	Asp	Val	Thr	Pro	Leu	Pro	Gly	Gly	Gly
					610					615					620	
70	Val	Ser	Leu	Ser	Trp	Lys	Val	Pro	Phe	Leu	Ser	Gln	Leu	Val	Ser	Arg
					625					630					635	
	Phe	Gly	Glu	Ser	Pro	Asn	Pro	Val	Phe	Lys	Thr	Phe	Glu	Val	Pro	Tyr
					645					650					655	
	Val	Ser	Ala	Ala	Ala	Ala	Gln	Thr	Pro	Asn	Pro	Pro	Val	Gly	Val	Val
					660					665					670	
75	Ile	Ala	Asp	Lys	Phe	Met	Ala	Gly	Thr	Tyr	Pro	Glu	Lys	Ala	Ala	Ile

262/ 490

675 680 685
 Ala Ala Val Tyr Val Met Pro Ser Ala Pro Asp Ser Thr Phe His Leu
 690 695 700
 5 Phe Leu Lys Ser Asn Thr Asn Arg Arg Leu Gln Lys Val Thr Thr Pro
 705 710 715 720
 Ser Asp Trp Gln Ala Gly Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro
 725 730 735
 Phe Pro Val Asn Asn Asp His Met Leu Phe Ala Gly Ile Arg Met Pro
 740 745 750
 10 Asn Lys Tyr Lys Leu Asn Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp
 755 760 765
 Asn Leu Phe Ser Ile Thr Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val
 770 775 780
 15 Ser Phe Glu Gly Tyr Gly Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile
 785 790 795 800
 Lys Tyr Leu Val Val Asn Thr Asp Ala Pro Lys Ile Asp Met Ser Leu
 805 810 815
 Val Gln Glu Pro Tyr Ala Lys Gly Thr Asn Val Ala Pro Phe Pro Glu
 820 825 830
 20 Leu Val Gly Ile Tyr Val Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln
 835 840 845
 Asp Pro Ser Val Thr Thr Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp
 850 855 860
 25 Glu Tyr Glu Ile Lys Leu Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly
 865 870 875 880
 Val Ala Gln Ile Glu Asn Asn Asn Ala Val Val Ala Tyr Pro Ser Val
 885 890 895
 Val Thr Asp Arg Phe Ser Ile Lys Asn Ala His Met Val His Ala Ala
 900 905 910
 30 Ala Leu Tyr Ser Leu Asp Gly Lys Gln Val Arg Ser Trp Asn Asn Leu
 915 920 925
 Arg Asn Gly Val Thr Phe Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr
 930 935 940
 35 Met Leu Val Met Gln Thr Ala Asn Gly Pro Val Ser Gln Lys Ile Val
 945 950 955 960
 Lys Gln

(2) INFORMATION FOR SEQ ID NO:337

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

60 Trp Lys Lys Ser Asn Pro Gln Tyr Arg Gly Arg Thr Ala Asn Tyr Arg
 1 5 10 15
 Asp His Tyr Asn Thr Glu Ser Tyr Leu Ser Leu Arg Arg Asn Gln Thr
 20 25 30
 Met Lys Tyr Leu Ile Arg Leu Phe Leu Ser Leu Met Leu Leu Ser Leu
 35 40 45
 65 Trp Thr Gly Cys Thr His Glu Glu Leu Ser Ile Cys Asp Gly Glu Asn
 50 55 60
 Thr Leu Val Leu Arg Val Glu Thr Gly Lys Ala Pro Asn Ala Arg Ala
 65 70 75 80
 Thr Glu Pro Gly Gln Gly Ile Tyr Asn Glu Asn Lys Val Gly Ser Ile
 85 90 95
 70 Ser Val Leu Phe Tyr Leu Glu Gly Gln Leu Arg Trp Gln Val Lys Ser
 100 105 110
 Thr Asp Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu
 115 120 125
 75 Gln Met Arg Pro Leu Phe Asn Gly Asn Asn Asn Phe Ser Ile Tyr Val

WO 99/29870

PCT/AU98/01023

263/ 490

	130		135		140
	Val Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser				
	145		150		155
	Gln Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro				
5		165		170	175
	Ala Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala				
	180		185		190
	Thr Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala				
10		195		200	205
	Ala Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu				
	210		215		220
	Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly				
	225		230		235
	Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys				
15		245		250	255
	Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile				
	260		265		270
	His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys				
	275		280		285
20		Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro			
	290		295		300
	Asp Asn Thr Ala Lys Pro Tyr Tyr Arg Val Pro Leu Glu Ser Gln				
	305		310		315
	Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile				
25		325		330	335
	Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly				
	340		345		350
	Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu				
	355		360		365
30		Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn			
	370		375		380
	Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile				
	385		390		395
	Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly				
35		405		410	415
	Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr				
	420		425		430
	Ile Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val				
	435		440		445
40		Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala			
	450		455		460
	Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile				
	465		470		475
	Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu				
45		485		490	495
	Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val				
	500		505		510
	Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr				
	515		520		525
50		Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr			
	530		535		540
	Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr				
	545		550		555
	Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala				
55		565		570	575
	Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu				
	580		585		590
	Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn				
	595		600		605
60		Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys			
	610		615		620
	Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp				
	625		630		635
	Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly				
65		645		650	655
	Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln				
	660		665		670
	Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val				
	675		680		685
70		Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys			
	690		695		700

(2) INFORMATION FOR SEQ ID NO:338

75

(1) SEQUENCE CHARACTERISTICS:

WO 99/29870

PCT/AU98/01023

264/ 490

(A) LENGTH: 1312 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
10 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1312

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

Lys Arg Val Asp Ser Tyr Glu Cys Arg Gln Lys Ala Cys Lys Cys Ala
1 5 10 15
20 Ile Cys Val Ile Gln Lys Phe Thr Asn Val Lys Leu Asn Asp Met Arg
20 25 30
Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly Leu Gln
35 40 45
25 Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu Pro Ser
50 55 60
Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu Val Val
65 70 75 80
Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln Val Phe
85 90 95
30 Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu
100 105 110
Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu Phe Ser
115 120 125
35 Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn
130 135 140
Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu Pro Glu
145 150 155 160
Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr
165 170 175
40 Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser Gln Asp
180 185 190
Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe
195 200 205
45 Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu
210 215 220
Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr
225 230 235 240
Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala
245 250 255
50 Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg Gly Thr
260 265 270
Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln Asn Cys
275 280 285
55 Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln Gln Pro
290 295 300
His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr Asn Gly
305 310 315 320
Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser Phe Pro
325 330 335
60 Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn Phe Ile
340 345 350
Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp Gly Lys
355 360 365
Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr Leu Ala
370 375 380
65 Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn Val Ser
385 390 395 400
Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser Asp Tyr
405 410 415
70 Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu Phe Ile
420 425 430
Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu Ile Glu
435 440 445
75 Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His Lys Asn
450 455 460

265/490

Ile Leu Tyr Ala Glu Gly Lys Gly Cys Asp Ala Pro Ile Leu Arg Leu
 465 470 475 480
 Phe Leu Lys Glu Ile Ala Ser Gly Tyr Thr Val Asn Ser Ile Leu Lys
 485 490 495
 5 Ser Asn Gln Val Ser Ala Ile Asp Ser Ile Phe Asp Cys Leu Asn Asn
 500 505 510
 Gly Ser His His Phe Tyr Phe Asn Thr His Gly Met Pro Thr Val Trp
 515 520 525
 10 Gly Ile Gly Gln Gly Leu Asp Val Asn Thr Leu Thr Ala Arg Leu Asn
 530 535 540
 Asn Thr Ser Ser Gln Gly Leu Cys Thr Ser Leu Ser Cys Ser Ser Ala
 545 550 555 560
 Val Ala Asp Ser Thr Ile Arg Ser Leu Gly Glu Val Leu Thr Thr Tyr
 565 570 575
 15 Ala Pro Asn Lys Gly Phe Ser Ala Phe Leu Gly Gly Ser Arg Ala Thr
 580 585 590
 Gln Tyr Ala Val Tyr Leu Glu Gly Pro Cys Pro Pro Ser Glu Phe Tyr
 595 600 605
 20 Glu Tyr Leu Pro Tyr Ser Leu Tyr His Asn Leu Ser Thr Val Val Gly
 610 615 620
 Glu Met Leu Leu Ser Ser Ile Ile Asn Thr Asn Ser Val Asp Thr Tyr
 625 630 635 640
 Ser Lys Phe Asn Phe Asn Leu Leu Gly Asp Pro Ala Leu Asn Ile Met
 645 650 655
 25 Ala His Gly Met Glu Val Ser Asn Cys Ile Thr Leu Pro Asn Asn Thr
 660 665 670
 Ile Ile Ser Ser Pro Ile Thr Ile Lys Asn Gly Gly Cys Leu Lys Ile
 675 680 685
 30 Pro Glu Lys Gly Val Leu His Phe Thr Asn Asn Gly Ser Ile Gln Val
 690 695 700
 Met Ser Gly Gly Thr Leu Glu Ile Gly Asn Gln Ala Lys Ile Ser Gly
 705 710 715 720
 Glu Thr Gly Ala Asn Pro Thr Phe Ile Thr Val Tyr Gly Asp Gly Leu
 725 730 735
 35 Ala Ile Asn Lys Gln Val Glu Ile Asp Asn Ile Asp Arg Leu Asn Leu
 740 745 750
 Phe Ser Thr His Ser Val Met Pro Lys Phe His Phe Asp Ser Val Lys
 755 760 765
 40 Phe Asn Ser Ala Pro Leu Tyr Thr Thr Asn Cys Ile Val Glu Ile Ser
 770 775 780
 Asn Cys Glu Phe Thr Asn Arg Ser Asp Ile Ile Ser Lys Asn Cys Asp
 785 790 795 800
 Leu Ser Val Glu Asn Ser Met Phe Ser Ser Ser Gly Ile Thr Val Phe
 805 810 815
 45 Lys Pro Met Ala Thr Ser Ser Ile Thr Gly Leu Ser Thr Lys Ala Lys
 820 825 830
 Ile Thr Asp Asn Thr Phe Phe Ala Thr Gly Asn Phe Ala Tyr His Ile
 835 840 845
 50 Thr Asn Thr Pro Gly Leu Thr Ala Thr Ser Asn Ala Ala Ile Lys Leu
 850 855 860
 Asp Asn Ile Pro Glu Tyr Tyr Ile Ser Gly Asn Lys Ile Val Asn Cys
 865 870 875 880
 Asp Glu Ala Leu Val Leu Asn Asn Ser Gly Asn Arg Thr Asn Arg Leu
 885 890 895
 55 His Asn Ile Thr Arg Asn Val Ile Lys Asn Cys Arg Ile Gly Ser Thr
 900 905 910
 Leu Tyr Asn Ser Tyr Gly Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn
 915 920 925
 60 His Ile Gly Val Arg Leu Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn
 930 935 940
 Ala Pro Val Ile Asn Glu Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg
 945 950 955 960
 Thr Trp Gln Leu Tyr Ser Ser Asn Gly Thr Phe Pro Leu Asn Phe His
 965 970 975
 65 Tyr Asn Ser Leu Gln Gly Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp
 980 985 990
 Thr Tyr Thr Asn Arg Tyr Ile Asp Val Ser Asn Asn His Trp Gly Asn
 995 1000 1005
 70 Asn Asp Leu Phe Asp Pro Asn Gln Val Phe Asn Thr Pro Asp Leu Phe
 1010 1015 1020
 Ile Trp Ile Pro Phe Trp Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn
 1025 1030 1035 1040
 Ser Ser Ala Glu Ala Val Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly
 1045 1050 1055
 75 Asn Ser Asp Tyr Leu Ser Ala Lys Val Ala Leu Lys Met Met Val Glu

266/ 490

1060 1065 1070
 Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe
 1075 1080 1085
 Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr
 1090 1095 1100
 Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr
 1105 1110 1115 1120
 Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln
 1125 1130 1135
 10 Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr
 1140 1145 1150
 Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn
 1155 1160 1165
 15 Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu
 1170 1175 1180
 Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val Lys Asn
 1185 1190 1195 1200
 Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro
 1205 1210 1215
 20 Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile
 1220 1225 1230
 Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp
 1235 1240 1245
 25 Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser
 1250 1255 1260
 Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser
 1265 1270 1275 1280
 Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr
 1285 1290 1295
 30 Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:339

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 938 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 45 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...938
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

Ser Glu Asn Tyr Arg Tyr Gly Lys Ile Thr Asn Gln Ile Met Ala Ile
 1 5 10 15
 55 Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
 20 25 30
 Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
 35 40 45
 60 Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
 50 55 60
 Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
 65 70 75 80
 Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
 85 90 95
 65 Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly
 100 105 110
 Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
 115 120 125
 70 Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
 130 135 140
 His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe
 145 150 155 160
 Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val
 165 170 175
 75 Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala

268/ 490

Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu
 785 790 795 800
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr
 805 810 815
 5 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala
 820 825 830
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn
 835 840 845
 10 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys
 850 855 860
 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser
 865 870 875 880
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile
 885 890 895
 15 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg
 900 905 910
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr
 915 920 925
 20 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
 930 935

(2) INFORMATION FOR SEQ ID NO:340

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 606 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...606
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

Ile Ile Phe Cys Thr Ile His His Ser Glu Leu Glu Ile Met Asn Ser
 1 5 10 15
 45 Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val
 20 25 30
 Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro
 35 40 45
 Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu
 50 55 60
 Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro
 65 70 75 80
 Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe
 85 90 95
 55 Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu
 100 105 110
 Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile
 115 120 125
 Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp
 130 135 140
 60 Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys
 145 150 155 160
 Ser Ala Phe Asn Thr Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg
 165 170 175
 65 Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu
 180 185 190
 Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg
 195 200 205
 Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val
 210 215 220
 70 Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly
 225 230 235 240
 Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg
 245 250 255
 75 Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His
 260 265 270

WO 99/29870

PCT/AU98/01023

269/ 490

5 Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile
275 280 285
Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn
290 295 300
Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu
305 310 315 320
Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp
325 330 335
10 Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe
340 345 350
Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu
355 360 365
Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val
370 375 380
15 Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu
385 390 395 400
Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln
405 410 415
20 Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr
420 425 430
Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu
435 440 445
Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu
450 455 460
25 Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu
465 470 475 480
Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly
485 490 495
30 Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu
500 505 510
Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val
515 520 525
Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly
530 535 540
35 Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser
545 550 555 560
Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys
565 570 575
40 Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro
580 585 590
Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe
595 600 605

(2) INFORMATION FOR SEQ ID NO:341

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc feature
60 (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

65 Asn Ser His Ala Thr Val Ser Val Ile Cys Ser Met Met Glu Lys Cys
1 5 10 15
Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met Ile Arg Lys His
20 25 30
Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe Ser Ala Gly Ala
35 40 45
70 Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu Pro Ala Thr Ala
50 55 60
Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile Val Asp Asp Asn
65 70 75 80
75 Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly Tyr Glu Ser Gly
85 90 95

WO 99/29870

PCT/AU98/01023

270/ 490

5 Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser Gly Ser His Met
100 105 110
Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg Gly Met Trp Gly
115 120 125
Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln Gly Tyr Asp Gln
130 135 140
Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp Ile Ala Val Gln
145 150 155 160
10 Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg Gly Gly Val Ser
165 170 175
Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser Ser Phe Gly Leu
180 185 190
Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp Lys Gly Tyr Ser
195 200 205
15 Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu Lys Gly Tyr Asn
210 215 220
Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu Gly Phe Ser Arg
225 230 235 240
20 Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr Leu Phe Asn Leu
245 250 255
Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp Leu Ser Lys Met
260 265 270
Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu Phe Thr Pro Ser
275 280 285
25 Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln Ile Ala Gln Asp
290 295 300
Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu Ser Ala Gly Val
305 310 315 320
30 Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser Ala Ala Thr Tyr
325 330 335
His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly Ile Arg Leu Asp
340 345 350
Asp Lys Ser Ile Phe
355

(2) INFORMATION FOR SEQ ID NO:342

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

55 Pro Gln Pro Val Gly Leu Lys Glu Ile Thr Ile Lys Pro Met Cys Leu
1 5 10 15
Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu Gln Glu Leu
20 25 30
60 Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly Asn Glu Ile
35 40 45
Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys Glu Val Gly
50 55 60
65 Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Gly Thr Gly Lys
65 70 75 80
Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser Tyr Lys Gln
85 90 95
Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly Gly Tyr Arg
100 105 110
70 Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly Lys Pro Leu
115 120 125
Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe Leu His Asp
130 135 140
75 Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val Ser Leu Gln
145 150 155 160

271/ 490

Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val Leu Asp Asn
 165 170 175
 Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro Glu Ala Leu
 180 185 190
 5 Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp Arg Arg Ala
 195 200 205
 Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser Asp Pro Glu
 210 215 220
 10 Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile Ser Ala Glu
 225 230 235 240
 Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn Tyr Lys Thr
 245 250 255
 Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro Pro Leu Val
 260 265 270
 15 Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe Gly Thr Ala
 275 280 285
 Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile Phe Ile Ala
 290 295 300
 20 Val Gly Lys Ile Leu Glu Glu Lys Lys Gln Arg His Ile Glu Ser Phe
 305 310 315 320
 Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser Asn Gly Arg
 325 330 335
 Ser

25

(2) INFORMATION FOR SEQ ID NO:343

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

35

(iii) HYPOTHETICAL: YES

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

40

(ix) FEATURE:

- (A) NAME/KEY: misc feature
 (B) LOCATION 1...566

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343

Tyr Asp Gly Ala Arg Leu Val Tyr Thr Leu Phe Arg Asn Arg Asn Asp
 1 5 10 15
 Ile His Pro Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala
 20 25 30
 50 Leu Phe Phe Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln
 35 40 45
 Met Leu Asn Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro
 50 55 60
 Thr Glu Arg Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg
 65 70 75 80
 55 Gly Ala Asp Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr
 85 90 95
 Val Arg Phe Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro
 100 105 110
 60 Tyr Asn Gly Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg
 115 120 125
 Ile Ser Val Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser
 130 135 140
 65 Arg Gly Met His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu
 145 150 155 160
 Ala Tyr Tyr Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His
 165 170 175
 Phe Glu Asp Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg
 180 185 190
 70 Leu Pro Leu Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg
 195 200 205
 Leu Thr Asp Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser
 210 215 220
 75 Cys Ala Thr Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser
 225 230 235 240

272/490

Ala Ala Tyr Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg
 245 250 255
 Pro Gly Gln Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val
 260 265 270
 5 Asp Val Ser Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr
 275 280 285
 Val Asn Gly Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp
 290 295 300
 10 Ala Ile Gly Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg
 305 310 315 320
 Ser Ser Ile Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr
 325 330 335
 Gly Ser Trp His Leu Ser Asp Phe Asp Phe Ser Phe Ser Ala Asp Tyr
 340 345 350
 15 Ala Leu Arg Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp
 355 360 365
 Asp Asn Tyr His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp
 370 375 380
 20 Tyr Met Leu Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile
 385 390 395 400
 Arg Thr Asp Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe
 405 410 415
 Tyr Gly Tyr Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser
 420 425 430
 25 Gly Met Leu Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser
 435 440 445
 Lys Leu Asp Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu
 450 455 460
 30 Thr His Ser Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr
 465 470 475 480
 Gln Leu Ala Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu
 485 490 495
 Val Arg Ser Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg
 500 505 510
 35 Leu Met Thr Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp
 515 520 525
 Gly Ile Ala Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser
 530 535 540
 40 Asp Pro Gln Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys
 545 550 555 560
 Asn Ile Ser Tyr Leu Phe
 565

(2) INFORMATION FOR SEQ ID NO:344
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...819
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

Arg Thr Asn Val Phe Leu Ser Leu Ser His Lys Ile Gly Arg Arg Gly
 1 5 10 15
 Ala Ser Cys Ser Asn Arg Asn Ala Trp Met Ala Glu Asn Lys Pro Ser
 20 25 30
 Ser Pro Glu Pro Asp Asn Thr Gly Val Gly Asn Ser Pro Ser Asp Tyr
 35 40 45
 70 Leu His Gly Glu Ala Ile Ile Pro Pro Leu Ser Ser Leu Ser Asn Phe
 50 55 60
 Asn Asp Lys Arg Phe Met Lys Lys Leu His Met Ile Ala Ala Leu Ala
 65 70 75 80
 75 Val Leu Pro Phe Cys Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu
 85 90 95

WO 99/29870

PCT/AU98/01023

273/ 490

	Ile	Asp	Ser	Leu	Ser	Asn	Val	Gln	Leu	Gln	Thr	Val	Gln	Val	Val	Ala
				100					105				110			
	Thr	Arg	Ala	Thr	Ala	Lys	Thr	Pro	Val	Ala	Tyr	Thr	Asn	Val	Arg	Lys
				115				120					125			
5	Ala	Glu	Leu	Ser	Lys	Ser	Asn	Tyr	Gly	Arg	Asp	Ile	Pro	Tyr	Leu	Leu
				130				135					140			
	Met	Leu	Thr	Pro	Ser	Val	Val	Ala	Thr	Ser	Asp	Ala	Gly	Thr	Gly	Ile
				145				150				155				160
10	Gly	Tyr	Ser	Gly	Phe	Arg	Val	Arg	Gly	Thr	Asp	Ala	Asn	Arg	Ile	Asn
					165						170				175	
	Ile	Thr	Thr	Asn	Gly	Val	Pro	Leu	Asn	Asp	Ser	Glu	Ser	Gln	Ser	Val
					180					185				190		
	Phe	Trp	Val	Asn	Met	Pro	Asp	Phe	Ala	Ser	Ser	Ile	Glu	Asp	Leu	Gln
				195				200					205			
15	Val	Gln	Arg	Gly	Val	Gly	Thr	Ser	Thr	Asn	Gly	Ala	Gly	Ala	Phe	Gly
				210				215					220			
	Ala	Ser	Val	Asn	Met	Arg	Thr	Asp	Asn	Leu	Gly	Leu	Ala	Pro	Tyr	Gly
				225				230				235				240
20	Arg	Val	Asp	Leu	Ser	Gly	Gly	Ser	Phe	Gly	Thr	Phe	Arg	Arg	Ser	Val
					245					250					255	
	Lys	Leu	Gly	Ser	Gly	Arg	Ile	Gly	Arg	His	Trp	Ala	Val	Asp	Ala	Arg
					260					265					270	
	Leu	Ser	Lys	Ile	Gly	Ser	Asp	Gly	Tyr	Val	Asp	Arg	Gly	Ser	Val	Asp
				275				280					285			
25	Leu	Lys	Ser	Tyr	Phe	Ala	Gln	Val	Gly	Tyr	Phe	Gly	Ser	Asn	Thr	Ala
				290				295				300				
	Leu	Arg	Phe	Ile	Thr	Phe	Gly	Gly	Lys	Glu	Val	Thr	Gly	Ile	Ala	Trp
				305				310				315				320
30	Asn	Gly	Leu	Ser	Lys	Glu	Asp	Glu	Ala	Lys	Tyr	Gly	Arg	Arg	Tyr	Asn
					325					330					335	
	Ser	Ala	Gly	Leu	Met	Tyr	Val	Asp	Ala	Gln	Gly	Val	Pro	His	Tyr	Tyr
				340					345					350		
	His	Asn	Thr	Asp	Asn	Tyr	Glu	Gln	Arg	His	Tyr	His	Ala	Ile	Met	Thr
				355				360					365			
35	His	Ser	Phe	Ser	Pro	Ser	Val	Ile	Leu	Asn	Leu	Thr	Ala	His	Tyr	Thr
				370				375				380				
	Ala	Gly	Tyr	Gly	Tyr	Thr	Asp	Glu	Tyr	Arg	Thr	Gly	Arg	Lys	Leu	Lys
				385				390				395				400
40	Glu	Tyr	Ala	Leu	Gln	Pro	Tyr	Val	Glu	Asn	Ser	Val	Thr	Val	Lys	Lys
					405					410					415	
	Thr	Asp	Leu	Ile	Arg	Gln	Lys	Tyr	Leu	Asp	Asn	Asp	Phe	Gly	Gly	Leu
				420					425					430		
	Ile	Gly	Ser	Leu	Asn	Trp	His	Thr	Gly	Ala	Trp	Asp	Leu	Gln	Phe	Gly
				435				440					445			
45	Ala	Ser	Gly	Asn	Ile	Tyr	Lys	Gly	Asp	His	Phe	Gly	Arg	Ile	Thr	Tyr
				450				455				460				
	Ile	Lys	Lys	Tyr	Asn	Gln	Pro	Leu	Ala	Pro	Asp	Phe	Glu	Tyr	Tyr	Arg
				465				470				475				480
50	Asn	Arg	Ala	Asp	Lys	Arg	Glu	Gly	Ala	Ala	Phe	Ala	Lys	Ala	Asn	Trp
					485					490					495	
	Gln	Ile	Thr	Pro	Glu	Leu	Asn	Met	Tyr	Ala	Asp	Leu	Gln	Tyr	Arg	Thr
				500					505					510		
	Ile	Gly	Tyr	Thr	Ile	Asn	Gly	Ile	Thr	Asp	Glu	Tyr	Asp	Glu	Val	Gln
				515				520					525			
55	Gly	Ser	Met	Gln	His	Ile	Asp	Leu	Asp	Lys	Thr	Phe	Arg	Phe	Leu	Asn
				530				535				540				
	Pro	Lys	Ala	Gly	Leu	Thr	Tyr	Ser	Phe	Asp	Asp	Ala	His	Thr	Ala	Tyr
				545				550				555				560
60	Ala	Ser	Val	Ala	Val	Ala	His	Arg	Glu	Pro	Asn	Arg	Thr	Asn	Tyr	Thr
					565					570					575	
	Glu	Ala	Gly	Ile	Gly	Gln	Tyr	Pro	Thr	Pro	Glu	Arg	Leu	Ile	Asp	Tyr
				580					585					590		
	Glu	Leu	Gly	Tyr	Arg	Tyr	Ala	Ser	Pro	Leu	Leu	Ser	Ala	Gly	Val	Gly
				595				600					605			
65	Leu	Tyr	Tyr	Met	Gln	Tyr	Lys	Asp	Gln	Leu	Val	Leu	Asp	Gly	Arg	Leu
				610				615				620				
	Ser	Asp	Val	Gly	Gln	Met	Leu	Thr	Ser	Asn	Val	Pro	Asp	Ser	Tyr	Arg
				625				630				635				640
70	Met	Gly	Leu	Glu	Leu	Thr	Leu	Gly	Trp	Gln	Ile	Leu	Pro	Arg	Leu	Leu
					645					650					655	
	Arg	Trp	Asp	Ala	Ser	Phe	Thr	Met	Ser	Arg	Asn	Lys	Ile	Asp	Arg	Tyr
				660					665					670		
	Val	Gln	Tyr	Thr	Ser	Val	Tyr	Asp	Ala	Asp	Tyr	Asn	Trp	Leu	Glu	Leu
				675				680					685			
75	Lys	Glu	Glu	Thr	Leu	Glu	Ser	Thr	Asp	Ile	Ala	Tyr	Ser	Pro	Asn	Val

274/ 490

690 695 700
 Ile Ala Gly Ser Met Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala
 705 710 715 720
 Trp Thr Ser Arg Phe Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg
 5 725 730 735
 Ser Asp Arg Met Leu Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly
 740 745 750
 Tyr Val Leu Pro Val His Phe Val Lys Arg Val Ala Leu Gly Val Gln
 755 760 765
 10 Leu Asn Asn Leu Phe Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr
 770 775 780
 Asp Ala Gly Tyr Val Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp
 785 790 795 800
 15 Leu Arg Tyr Tyr Pro Gln Ala Gly Phe Asn Ala Leu Gly Ser Leu Thr
 805 810 815
 Ile Asp Phe

(2) INFORMATION FOR SEQ ID NO:345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc feature
 (B) LOCATION 1...532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

Tyr Arg Arg Ser Gly Arg Val Cys Pro Arg Ile Leu Arg Asn Lys Arg
 1 5 10 15
 Ser Tyr Ala Asp Thr Arg Leu Gln Pro Arg Arg Ala Val Arg Leu Arg
 20 25 30
 Ala Gly Thr Arg Thr Lys Met Lys Arg Arg Phe Leu Ser Leu Leu
 35 40 45
 45 Leu Tyr Ile Leu Ser Ser Ile Ser Leu Ser Ala Gln Arg Phe Pro Met
 50 55 60
 Val Gln Gly Ile Glu Leu Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys
 65 70 75 80
 50 Arg Pro Trp Arg Ala Ile Gly Lys Thr Ile Gly Val Asn Leu Ala Val
 85 90 95
 Trp Gly Phe Asp His Phe Ile Met Asn Glu Asp Phe Ala Asp Ile Ser
 100 105 110
 Trp Gln Thr Ile Lys Ser Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn
 115 120 125
 55 Asp Lys Phe Val Thr Asn Leu Phe Ala His Pro Tyr His Gly Ser Leu
 130 135 140
 Tyr Phe Asn Ala Ala Arg Ser Asn Gly Leu Ser Phe Arg His Ser Ala
 145 150 155 160
 60 Pro Phe Ala Phe Phe Gly Ser Leu Met Trp Glu Leu Leu Met Glu Asn
 165 170 175
 Glu Pro Pro Ser Ile Asn Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile
 180 185 190
 Ala Leu Gly Glu Met Gly His Arg Leu Ser Asp Leu Leu Ile Asp Asn
 195 200 205
 65 Arg Thr Thr Gly Trp Glu Arg Met Gly Arg Glu Val Ala Ile Ala Leu
 210 215 220
 Ile Asn Pro Met Arg Phe Leu Asn Arg Leu Thr Ala Gly Glu Val Thr
 225 230 235 240
 Ser Val Gly Ser Arg Ser Gly Gln Ile Phe Gln Ser Val Pro Ile Asn
 245 250 255
 70 Ile Val Val Asp Ala Gly Phe Arg Phe Leu Ala Asp Lys Arg His Ala
 260 265 270
 Arg Thr Gly Ala Thr Ala Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly
 275 280 285
 75 Asp Pro Phe Arg Ser Glu Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe

WO 99/29870

PCT/AU98/01023

275 / 490

290 295 300
Lys Ala Gly Leu Ser Phe Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile
305 310 315 320
Asn Leu Ile Gly Ile Leu Ser Gly Cys Gln Leu Leu Ala His Glu Arg
5 Thr Val Leu Val Gly Gly Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser
325 330 335
340 345 350
Glu Lys Arg Ile Ser Lys Asn Ser Glu Glu Val Leu Val Thr Pro Tyr
355 360 365
10 Arg Ile Ser Gln Val Ala Ala Leu Gly Gly Gly Leu Ile Phe Gln His
370 375 380
His Gly Lys Phe Arg Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr
385 390 395 400
Leu Asn Val Val Pro Met Gly Ala Ser Leu Ser Asp His Tyr Asn Val
15 Asp Asn Arg Asp Tyr Asn Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr
405 410 415
420 425 430
Leu Gly Ala Thr Tyr Asn Asp Leu Trp Ser Trp Leu Leu Gly Val Glu
435 440 445
20 Ser Tyr Arg Leu Tyr Thr Trp Ile Gly Tyr Glu Glu Pro His Gln Lys
450 455 460
Asn Thr Asp Val Ser Ser Phe Met Val Gln Gly Asp Glu Ser Lys Ala
465 470 475 480
Arg Leu Leu Val Thr Ser Ser Glu Phe Ala Phe His Pro Gly Pro Trp
25 His Val Ala Ile Val Ala Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln
485 490 495
500 505 510
Phe Tyr Pro Asn Val Ser Phe Asp Thr Gly Asp Ile Gln Leu Arg Val
515 520 525
30 Gly Phe His Phe
530

(2) INFORMATION FOR SEQ ID NO:346

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...300
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

Lys Arg Arg Lys Lys Gln Met Lys Arg Leu Ile Val Phe Leu Ala Met
1 5 10 15
55 Gly Gly Leu Leu Phe Thr Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala
20 25 30
Ser Asp Thr Pro Lys Lys Asp Trp Thr Ile Lys Gly Val Thr Gly Leu
35 40 45
60 Asn Ala Ser Gln Thr Ser Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn
50 55 60
Thr Val Ala Gly Asn Leu Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys
65 70 75 80
Asp Lys Trp Ser Trp Asp Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr
85 90 95
65 Tyr Thr Thr Ala Asn Lys Trp Asn Lys Ser Val Asp Lys Ile Glu Leu
100 105 110
Phe Thr Lys Ala Gly Tyr Glu Ile Gly Lys His Trp Tyr Gly Ser Ala
115 120 125
70 Leu Phe Thr Phe Leu Ser Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser
130 135 140
Asp His Leu Thr Gly Val Lys His Ile Ser Asn Phe Phe Ala Pro Ala
145 150 155 160
Tyr Leu Thr Leu Gly Ile Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe
165 170 175
75 Ser Leu Tyr Leu Ser Pro Thr Thr Gly Lys Leu Thr Val Val Ala Asp

276/ 490

180 185 190
Asp Tyr Leu Ser Ser Leu Gly Ala Phe Gly Val Lys Val Gly Glu Lys
195 200 205
Thr Met Phe Glu Leu Gly Ala Leu Val Val Gly Ser Ala Asn Ile Asn
210 215 220
Leu Met Glu Asn Val Asn Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala
225 230 235 240
Tyr Thr His Asp Phe Gly Asn Ile Asp Ile Asn Trp Glu Ala Met Leu
245 250 255
10 Ala Met Lys Ile Asn Lys Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu
260 265 270
Ile Tyr Asp Asp Asp Val Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe
275 280 285
15 Lys Glu Val Val Gly Val Gly Val Ala Tyr Thr Phe
290 295 300

(2) INFORMATION FOR SEQ ID NO:347

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
30 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...221

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

Thr Arg Glu Ser Val Leu His Cys Arg Thr Lys Leu Lys Lys Glu Arg
1 5 10 15
40 Lys Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile
20 25 30
Gly Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn
35 40 45
Phe Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn
50 55 60
45 Asn Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala
65 70 75 80
Leu Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met
85 90 95
Arg Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His
100 105 110
50 Tyr Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp
115 120 125
Asn Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val
130 135 140
55 Ala Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp
145 150 155 160
Ala Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu
165 170 175
60 Ser Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu
180 185 190
His Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu
195 200 205
Arg Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe
210 215 220

65 (2) INFORMATION FOR SEQ ID NO:348

70 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

75 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

WO 99/29870

PCT/AU98/01023

279/ 490

	Ala	Leu	Arg	Gly	Glu	Ile	Phe	Ser	Lys	Gly	Ser	Trp	Gly	Ile	Ser	Ala
	305					310					315					320
	Gln	Ser	Lys	Tyr	Lys	Lys	Arg	Tyr	Lys	Tyr	Asn	Gly	Ser	Phe	Glu	Ala
					325					330						335
5	Asn	Tyr	Leu	Val	Ser	Lys	Ser	Gly	Asp	Lys	Tyr	Val	Pro	Gly	Asp	Tyr
				340						345					350	
	Ser	Lys	Thr	Thr	Ser	Leu	Asn	Ile	Arg	Trp	Thr	His	Ser	Gln	Asp	Pro
				355					360					365		
10	Lys	Ala	Asn	Pro	Leu	Gln	Thr	Leu	Ser	Ala	Asn	Val	Asn	Phe	Ala	Thr
				370				375					380			
	Gly	Ser	Tyr	Phe	Gln	Asn	Ser	Leu	Asn	Thr	Thr	Tyr	Asp	Val	Asn	Ala
						390						395				400
	Arg	Thr	Ala	Thr	Thr	Arg	Ser	Ser	Ala	Val	Ser	Tyr	Ser	Arg	Lys	Phe
					405						410				415	
15	Pro	Gly	Thr	Pro	Phe	Ser	Ile	Thr	Gly	Ser	Met	Asp	Ile	Ser	Gln	Asn
				420					425					430		
	Met	Arg	Asp	Thr	Thr	Val	Ser	Leu	Thr	Leu	Pro	Asn	Leu	Ser	Ile	Asn
				435				440					445			
20	Met	Ser	Thr	Arg	Tyr	Pro	Phe	Lys	Arg	Lys	Thr	Arg	Val	Gly	Pro	Glu
				450				455					460			
	Arg	Trp	Tyr	Glu	Lys	Leu	Ser	Val	Gly	Tyr	Ser	Gly	Gln	Leu	Arg	Asn
						470					475					480
	Ser	Ile	Leu	Thr	Lys	Glu	Lys	Asp	Leu	Leu	Gln	Ser	Asn	Leu	Val	Arg
					485						490				495	
25	Asp	Trp	Lys	Asn	Gly	Met	Arg	His	Ser	Val	Pro	Ile	Ser	Leu	Thr	Val
				500					505					510		
	Pro	Leu	Leu	Asp	Tyr	Ile	Asn	Leu	Thr	Met	Gly	Val	Asn	Tyr	Asn	Glu
				515				520					525			
30	Trp	Trp	Tyr	Thr	Lys	Gly	Ile	Arg	Lys	Ser	Trp	Asn	Glu	Asp	Lys	Lys
				530				535					540			
	Thr	Phe	Leu	Pro	Ser	Asp	Thr	Thr	Tyr	Lys	Phe	Arg	Arg	Leu	Tyr	Asp
						550					555					560
	Tyr	Ser	Leu	Ser	Ala	Gly	Leu	Ser	Thr	Thr	Leu	Tyr	Gly	Met	Phe	Lys
						565					570				575	
35	Pro	Trp	Lys	Pro	Phe	Ser	Phe	Gly	Gly	Asn	Leu	Ile	Met	Ile	Arg	His
				580					585					590		
	Arg	Phe	Thr	Pro	Thr	Val	Ser	Phe	Ser	Tyr	Met	Pro	Asp	Phe	Thr	Lys
				595				600					605			
40	Arg	Arg	Tyr	Gly	Phe	Trp	Glu	Leu	Leu	Glu	His	Thr	Asp	Gln	Asn	Gly
				610				615					620			
	Lys	Leu	His	Thr	Leu	Leu	Tyr	Ser	Pro	Tyr	Phe	Glu	Gln	Ile	Phe	Gly
						630					635					640
	Ala	Pro	Ser	Met	Gly	Asn	Ala	Gly	Ser	Val	Asn	Phe	Ser	Phe	Asp	Asn
					645					650					655	
45	Asn	Leu	Glu	Ala	Lys	Ile	Lys	Ser	Lys	Ser	Asp	Ser	Thr	Gly	Ile	Lys
				660					665					670		
	Lys	Ile	Ser	Leu	Ile	Asp	Gln	Phe	Thr	Trp	Ser	Thr	Ser	Tyr	Asn	Met
				675				680					685			
50	Phe	Ala	Asp	Ser	Ile	Arg	Trp	Ser	Asn	Ile	Ser	Ala	Ser	Leu	Ala	Lcu
				690				695					700			
	Arg	Leu	Ser	Lys	Ser	Phe	Thr	Leu	Arg	Leu	Ser	Gly	Leu	Phe	Asp	Pro
						710					715					720
	Tyr	Leu	Thr	Lys	Tyr	Tyr	Glu	Gly	Glu	Asp	Gly	Lys	Ile	Ile	Pro	Tyr
						725					730				735	
55	Lys	Ser	Asn	Asp	Leu	Arg	Ile	Phe	Asn	Gly	Lys	Gly	Leu	Ala	Arg	Leu
					740				745					750		
	Ile	Ser	Thr	Gly	Thr	Ser	Phe	Ser	Tyr	Thr	Leu	Asn	Lys	Glu	Ser	Leu
				755				760					765			
60	Ser	Gly	Leu	Ile	Ala	Leu	Phe	Ser	Gly	Lys	Lys	Glu	Arg	Arg	Asp	Glu
							775						780			
	Lys	Lys	Asn	Thr	Gly	Ala	Thr	Pro	His	Glu	Gly	Asp	Asp	Ala	Ala	Asp
						790					795					800
	Ile	Leu	Glu	Gly	Gly	Arg	Pro	Gln	Asn	Glu	Ser	Gly	Gly	Ser	Leu	Leu
					805						810				815	
65	Glu	Arg	Asn	Arg	Gln	Gly	Gly	Ala	Val	Asp	Gln	Asp	Gly	Tyr	Phe	Ala
				820					825					830		
	Tyr	Ser	Ile	Pro	Trp	Ser	Leu	Ser	Phe	Asp	Tyr	Ser	Trp	Asn	Ile	Ala
					835			840					845			
70	Thr	Asp	Tyr	Asn	Arg	Tyr	Asn	Val	Asn	Lys	Met	Glu	His	Tyr	Tyr	Arg
						850					855					
	Val	Thr	Gln	Asn	Leu	Ser	Phe	Arg	Gly	Asn	Ile	Gln	Pro	Thr	Pro	Asn
						870					875					880
	Trp	Ser	Phe	Gly	Phe	Asn	Ala	Asn	Tyr	Asn	Phe	Asp	Leu	Lys	Lys	Ile
					885					890					895	
75	Thr	Ser	Leu	Thr	Cys	Asn	Val	Thr	Arg	Asp	Met	His	Cys	Trp	Ala	Ile

WO 99/29870

PCT/AU98/01023

280/ 490

5 Ser Ala Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val
900 905 910
915 920 925
Ile Ser Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser
930 935 940
Asn Arg Pro Ile Thr Asn Thr Trp Tyr
945 950

10 (2) INFORMATION FOR SEQ ID NO:351
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1251 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1251

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

30 Lys Trp Lys Leu Ala Cys Ala Phe Asp Cys Ala Cys Cys Phe Asp Pro
1 5 10 15
Phe Val Val Thr Asn Glu Val Ile Ile Met Met Lys Arg Tyr Thr Ile
20 25 30
Ile Leu Ala Val Phe Leu Leu Phe Cys Thr Val Phe Thr Phe Gln Ile
35 40 45
Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp Val Glu Lys Pro Trp Ile
50 55 60
Gln Lys His Ser Met Asp Ser Lys Leu Val Pro Ala Asn Lys Gly Asn
65 70 75 80
Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser Val Ser Glu His Ser Asp
40 85 90 95
Leu Val Ile Ser Pro Val Asn Glu Ile Arg Pro Ala Asn Arg Phe Pro
100 105 110
Ser His Arg Lys Ser Phe Phe Ala Glu Asn Leu Arg Ala Ser Pro Pro
115 120 125
45 Val Val Pro Val Ala Val Asp Lys Tyr Ala Val Pro Val Ala Asn Pro
130 135 140
Met Asp Pro Glu Asn Pro Asn Ala Trp Asp Val Thr Leu Lys Ile Thr
145 150 155 160
Thr Lys Ala Val Thr Val Pro Val Asp Val Val Met Val Ile Asp Gln
50 165 170 175
Ser Ser Ser Met Gly Gly Gln Asn Ile Ala Arg Leu Lys Ser Ala Ile
180 185 190
Ala Ser Gly Gln Arg Phe Val Lys Lys Met Leu Pro Lys Gly Thr Ala
195 200 205
55 Thr Glu Gly Val Arg Ile Ala Leu Val Ser Tyr Asp His Glu Pro His
210 215 220
Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala Phe Leu Cys Gln Lys Ile
225 230 235 240
Arg Ala Leu Thr Pro Ile Trp Gly Thr His Thr Gln Gly Gly Leu Lys
60 245 250 255
Met Ala Arg Asn Ile Met Ala Thr Ser Thr Ala Val Asp Lys His Ile
260 265 270
Ile Leu Met Ser Asp Gly Leu Ala Thr Glu Gln Tyr Pro Val Lys Asn
275 280 285
65 Val Thr Thr Ala Asp Phe Ile Gly Lys Thr Gly Asn Ala Asn Asp Pro
290 295 300
Ile Asp Leu Val Ile Gln Gly Ala Ile Asn Phe Pro Thr Asn Tyr Val
305 310 315 320
Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro Asn Tyr Pro Thr His Ser
70 325 330 335
Ser Lys Val Gly Arg Arg Asn Leu Pro Glu Ser Lys Phe Asp Tyr Ser
340 345 350
Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly Val Ala Gly Ala Leu Val
355 360 365
75 Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr Tyr Tyr Phe Pro Cys Asn

WO 99/29870

PCT/AU98/01023

282/ 490

Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro Asp Arg Ile Pro Ser Met
 980 985 990
 His Ser Phe Leu Val Lys Met Gln Asn Gly Ala Ser Cys Thr Leu Unk
 995 1000 1005
 5 Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr Thr Val Asn Asn Gly Asn
 1010 1015 1020
 Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn Ser Gly Ser Ala Asn Met
 1025 1030 1035 1040
 10 Pro Ser Leu Val Met Asp Val Leu Gly Asn Glu Ser Ala Asp Arg Leu
 1045 1050 1055
 Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe Gly Phe Asp Asn Gly Trp
 1060 1065 1070
 Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu Ser Gln Leu Tyr, Ala Met
 1075 1080 1085
 15 Ser Asp Ile Gly Asn Asp Lys Phe Gln Val Ala Gly Val Pro Glu Leu
 1090 1095 1100
 Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp Lys Asp Gly Gln Tyr Thr
 1105 1110 1115 1120
 20 Leu Glu Phe Ala Leu Ser Asp His Phe Ala Lys Gly Ala Val Tyr Leu
 1125 1130 1135
 His Asp Leu Gln Ser Gly Ala Lys His Arg Ile Thr Asn Ser Thr Ser
 1140 1145 1150
 Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser Gly Ala Arg Phe Arg Leu
 1155 1160 1165
 25 Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp Ser His Val Val Ser Thr
 1170 1175 1180
 Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln Asp Ala Leu Asp Cys Thr
 1185 1190 1195 1200
 30 Val Thr Leu Phe Thr Ile Glu Gly Lys Leu Leu Arg Arg Leu Lys Val
 1205 1210 1215
 Leu Ala Gly His Arg Glu Val Met Lys Val Gln Thr Gly Gly Ala Tyr
 1220 1225 1230
 Ile Val His Leu Gln Asn Ala Phe Thr Asn Asp Val His Lys Val Leu
 1235 1240 1245
 35 Val Glu Tyr
 1250

(2) INFORMATION FOR SEQ ID NO:352

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 426 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

Thr Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp
 1 5 10 15
 60 Phe Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu
 20 25 30
 Gly Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr
 35 40 45
 65 His Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr
 50 55 60
 Arg Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala
 65 70 75 80
 Val Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly
 85 90 95
 70 Leu Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly
 100 105 110
 Leu Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val
 115 120 125
 75 Arg Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala
 130 135 140

WO 99/29870

PCT/AU98/01023

283/490

5 Gln Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser
145 150 155 160
Val Phe Asn Glu Ser Met Lys Val Glu Val Val Leu Pro Val Phe
165 170 175
10 Glu Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe
180 185 190
Ser Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu
195 200 205
Ala Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg
210 215 220
15 Trp Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His
225 230 235 240
Thr Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr
245 250 255
15 Glu Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly
260 265 270
Asp Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala
275 280 285
20 Phe Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu
290 295 300
Gly Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro
305 310 315 320
Gly Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg
325 330 335
25 Tyr Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu
340 345 350
Asn Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe
355 360 365
30 Thr Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala
370 375 380
Asp Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp
385 390 395 400
Phe Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser
405 410 415
35 Glu Leu Trp Phe Lys Ala Arg Tyr Ser Phe
420 425

(2) INFORMATION FOR SEQ ID NO:353

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...464
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

60 Tyr Gly Lys Arg Arg Lys Leu Gly Thr Ser Val Arg Pro Ser Val Leu
1 5 10 15
Thr Gln Ile Arg Phe Ile Leu Asp Leu His Leu Ile Thr Asp Phe Phe
20 25 30
Glu Gly Leu Arg Val Asn Pro Ile Gly Ala Ala Ala Ile Val Ala Phe
35 40 45
65 Ile Ile Asp Leu Leu Leu Leu Cys Cys Ser Ala Phe Met Ser Ser Cys
50 55 60
Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu Gln Asn Ile Arg
65 70 75 80
Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn Leu Leu Asp Asn
85 90 95
70 Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn Asn Val Ile Asn
100 105 110
Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu Gln Thr Phe Val
115 120 125
75 Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr Ile Leu Leu Thr
130 135 140

284/ 490

Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys Val Tyr Ala Arg
 145 150 155 160
 Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala Met Ser Val
 165 170 175
 5 Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu Val Lys Ser Thr
 180 185 190
 Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Tyr Asp Met Ser Val
 195 200 205
 10 Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr Glu Gly Glu Pro
 210 215 220
 Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe Tyr Asn Lys Thr
 225 230 235 240
 Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val Asp Val Asp Leu
 245 250 255
 15 Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val Ser Ser Gly Tyr
 260 265 270
 Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn Ile Lys Gly Val
 275 280 285
 20 Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys Gly Asp Glu Phe
 290 295 300
 Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val Pro Glu Asn Lys
 305 310 315 320
 Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn Lys Val His Val
 325 330 335
 25 Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly Leu Ile Thr Met
 340 345 350
 Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr Asp Glu Tyr Asp
 355 360 365
 30 Glu Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly Ser Tyr Leu Phe
 370 375 380
 Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr Leu Asp Leu Pro
 385 390 395 400
 Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp Thr Leu Ser Gly
 405 410 415
 35 Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val Gly Asp Thr Ala
 420 425 430
 Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met Asp Lys Arg Arg
 435 440 445
 40 Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr Trp Glu Val Glu
 450 455 460

(2) INFORMATION FOR SEQ ID NO:354

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 55 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...266
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

Ile Ile Tyr Arg Ser Thr Met Lys Leu Leu Leu Tyr Leu Leu Leu Val
 1 5 10 15
 Leu Ser Thr Leu Ser Pro Met Tyr Ser Gln Met Leu Phe Ser Glu Asn
 20 25 30
 65 Leu Thr Met Asn Ile Asp Ser Thr Thr Ile Gln Gly Thr Ile Leu
 35 40 45
 Pro Val Leu Asp Phe Lys Thr Glu Lys Glu Asn Val Phe Thr Phe Lys
 50 55 60
 70 Asn Thr Ala Asn Leu Asn Leu Ile Lys His Gly Gln Val Ile Asn
 65 70 75 80
 Leu Ile Asn Lys Leu Glu Phe Ser Thr Tyr Gly Asn Lys Val Thr Val
 85 90 95
 75 Ser Gly Gly Tyr Val His Thr Glu Tyr Arg Tyr Leu Leu His His Val
 100 105 110

WO 99/29870

PCT/AU98/01023

285/ 490

5 Phe Glu Val Tyr Pro Tyr Val Glu Ser Gln Trp Ala Glu Ser Arg Gly
115 120 125
Met Lys Tyr Lys Val Ser Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val
130 135 140
Asn Ser Asp Asn Cys Leu Met Phe Ala Thr Leu Gly Val Phe Phe Glu
145 150 155 160
Phe Glu Lys Trp Glu Gln Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr
165 170 175
Ala Tyr Ser Arg Ser Ile Lys Ser His Leu Ser Ile Ser Phe Arg His
180 185 190
10 Arg Leu Gly Glu His Trp Glu Phe Thr Thr Thr Ala Ile His Gln Gly
195 200 205
Lys Pro Asp Ser Tyr Phe Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp
210 215 220
15 Leu Lys Tyr His Ile Thr Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg
225 230 235 240
Ile Ile Tyr Asp Thr Ala Pro Ile Val Pro Val Arg Lys Asp Tyr Asn
245 250 255
20 Thr Val Asp Val Gly Ile Asp Ile Ser Phe
260 265

(2) INFORMATION FOR SEQ ID NO:355

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 907 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
35 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...907
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

Thr Ile Cys Val Ala Phe Leu Ser Ala Pro Val Ala Ala Leu Arg Glu
1 5 10 15
45 Ser Pro Pro Met Gly Ala Glu Arg Lys Thr Pro Ser Leu Leu Pro Leu
20 25 30
Leu Phe Glu His Ser Asp Lys Gly Lys Gly Phe Asp Tyr Arg Leu Phe
35 40 45
Thr Ser Asn Lys Leu Lys Val Phe Ala Thr Gly Asn Ser Arg Tyr Ile
50 55 60
His Asn Lys Pro Thr Ile Ile Gln Ala Met Lys Arg Ile Val Leu Ser
65 70 75 80
Ser Phe Leu Phe Val Leu Ser Ile Leu Ser Leu Met Ala Gln Asn Asn
85 90 95
55 Thr Leu Asp Val His Ile Ser Gly Thr Ile Lys Asp Ala Ser Ser Gly
100 105 110
Glu Pro Val Pro Tyr Ala Thr Val Ser Ile Arg Leu Thr Gly Ala Asp
115 120 125
Thr Thr Gln Val Phe Arg Gln Val Thr Asp Gly Asn Gly Tyr Phe Val
130 135 140
60 Ile Gly Leu Pro Ala Ala Pro Ser Tyr His Leu Thr Ala Ser Phe Val
145 150 155 160
Gly Met Lys Thr His Thr Met Gln Ile Ser Arg Gly Asn Gly Gln His
165 170 175
Asp Ile Lys Ser Ile Asp Ile Ser Leu Glu Ser Glu Asp Lys Gln Leu
65 180 185 190
Ser Thr Val Thr Val Ser Ala Ala Arg Pro Leu Val Lys Met Glu Ile
195 200 205
Asp Arg Leu Ser Tyr Asn Met Lys Asp Asp Pro Ala Ala Lys Thr Asn
210 215 220
70 Asn Leu Leu Glu Met Leu Arg Asn Val Pro Leu Val Thr Val Asp Gly
225 230 235 240
Gln Gly Asn Ile Gln Val Lys Gly Ser Ser Asn Phe Lys Ile His Leu
245 250 255
75 Asn Gly Arg Pro Ser Thr Met Val Ser Ser Asn Pro Lys Glu Val Phe
260 265 270

WO 99/29870

PCT/AU98/01023

286/490

	Arg	Ser	Ile	Pro	Ala	His	Thr	Ile	Lys	Arg	Val	Glu	Val	Ile	Thr	Asp
		275					280					285				
	Pro	Gly	Val	Lys	Tyr	Asp	Ala	Glu	Gly	Thr	Ser	Ala	Ile	Leu	Asp	Ile
		290				295					300					
5	Val	Thr	Glu	Glu	Gly	Lys	Lys	Leu	Glu	Gly	Tyr	Ser	Gly	Ser	Ile	Thr
		305				310					315					320
	Ala	Ser	Val	Ser	Asn	Asn	Pro	Thr	Ala	Asn	Gly	Ser	Ile	Phe	Leu	Thr
				325						330					335	
10	Ala	Lys	Ser	Gly	Lys	Val	Gly	Leu	Thr	Thr	Asn	Tyr	Asn	Tyr	Tyr	Gly
			340						345					350		
	Gly	Lys	Asn	Lys	Gly	Ser	Arg	Tyr	Phe	Thr	Glu	Arg	Thr	Thr	Ser	Met
			355					360					365			
	Leu	Gln	Thr	Ile	Glu	Glu	Gly	Lys	Gly	Gln	Glu	Thr	Phe	Gly	Gly	His
		370					375					380				
15	Phe	Gly	Asn	Ala	Leu	Leu	Ser	Phe	Glu	Ile	Asp	Ser	Leu	Asn	Leu	Phe
		385				390					395					400
	Thr	Val	Gly	Gly	Asn	Val	Arg	Leu	Trp	Glu	Met	Thr	Thr	Asp	Arg	Asn
				405						410					415	
20	Ser	Val	Glu	Lys	Ser	Phe	Ala	Gly	Ser	Asn	Leu	Met	Ser	Tyr	Ile	Asp
			420						425					430		
	Arg	Lys	Leu	Lys	Thr	Gln	Met	Asp	Ala	Gly	Ser	Tyr	Glu	Leu	Asn	Ala
			435					440						445		
	Asp	Tyr	Gln	His	Ser	Thr	Arg	Leu	Pro	Gly	Glu	Leu	Leu	Thr	Val	Ser
		450					455					460				
25	Tyr	Arg	Phe	Thr	His	Asn	Pro	Asn	Asn	Ser	Glu	Thr	Phe	Ile	Asp	Gln
		465				470					475					480
	Trp	Lys	Arg	Asp	Pro	Leu	Asn	Thr	Ala	Asn	Thr	Ile	Gln	Tyr	Ala	Gly
				485						490					495	
30	Gln	His	Ser	Lys	Ser	Asp	Ala	Gly	Met	Asp	Glu	His	Thr	Ala	Gln	Val
				500					505					510		
	Asp	Tyr	Thr	Arg	Pro	Leu	Gly	Gln	Ala	His	Ser	Leu	Glu	Ala	Gly	Leu
			515					520						525		
	Lys	Tyr	Ile	Tyr	Arg	His	Ala	Thr	Ser	Asp	Pro	Leu	Tyr	Glu	Ile	Arg
		530					535					540				
35	Pro	Ser	Glu	Asp	Ala	Pro	Trp	Gln	Pro	Gly	Ser	Leu	Tyr	Ala	Gln	Asn
		545				550					555					560
	Pro	Ser	Asn	Gly	Lys	Phe	Arg	His	Asp	Gln	Tyr	Ile	Gly	Ala	Ala	Tyr
				565						570					575	
40	Ala	Gly	Tyr	Asn	Tyr	Arg	Lys	Asp	Gln	Tyr	Ser	Leu	Gln	Thr	Gly	Leu
			580					585						590		
	Arg	Val	Glu	Ser	Ser	Arg	Leu	Lys	Ala	Leu	Phe	Pro	Glu	Asn	Ala	Ala
			595					600						605		
	Ala	Asp	Phe	Ser	His	Asn	Ser	Phe	Asp	Trp	Val	Pro	Gln	Leu	Thr	Leu
		610					615					620				
45	Gly	Tyr	Thr	Pro	Ser	Pro	Met	Lys	Gln	Leu	Lys	Leu	Ala	Tyr	Asn	Phe
		625				630					635					640
	Arg	Ile	Gln	Arg	Pro	Ala	Ile	Gly	Gln	Leu	Asn	Pro	Tyr	Arg	Leu	Gln
				645						650					655	
50	Thr	Asn	Asp	Tyr	Gln	Val	Gln	Tyr	Gly	Asn	Pro	Asp	Leu	Lys	Ser	Glu
			660						665					670		
	Lys	Arg	His	His	Val	Gly	Leu	Ser	Tyr	Asn	Gln	Tyr	Gly	Ala	Lys	Val
			675				680						685			
	Met	Leu	Thr	Ala	Ser	Leu	Asp	Tyr	Asp	Phe	Cys	Asn	Asn	Ala	Ile	Gln
		690					695					700				
55	Asn	Tyr	Thr	Phe	Ser	Asp	Pro	Ala	Asn	Pro	Asn	Leu	Phe	His	Gln	Thr
		705				710					715					720
	Tyr	Gly	Asn	Ile	Gly	Arg	Glu	His	Ser	Phe	Ser	Leu	Asn	Thr	Tyr	Ala
				725						730					735	
60	Met	Tyr	Thr	Pro	Ala	Val	Trp	Val	Arg	Ile	Met	Leu	Asn	Gly	Asn	Ile
			740						745					750		
	Asp	Arg	Thr	Phe	Gln	Lys	Ser	Glu	Ala	Leu	Gly	Ile	Asp	Val	Asn	Ser
			755						760					765		
	Trp	Ser	Gly	Met	Val	Tyr	Ser	Gly	Leu	Met	Phe	Thr	Leu	Pro	Lys	Asp
		770						775						780		
65	Trp	Thr	Val	Asn	Leu	Phe	Gly	Gly	Tyr	Tyr	His	Gly	Gly	Arg	Ser	Tyr
		785				790					795					800
	Gln	Thr	Lys	Tyr	Asp	Gly	Asn	Val	Phe	Asn	Asn	Ile	Gly	Ile	Ala	Lys
				805						810					815	
70	Gln	Leu	Phe	Asp	Lys	Lys	Leu	Arg	Val	Ser	Leu	Ser	Ala	Asn	Asn	Ile
			820					825						830		
	His	Ala	Lys	Tyr	Ser	Thr	Trp	Lys	Ser	Arg	Thr	Ile	Gly	Asn	Gly	Phe
			835					840						845		
	Thr	Ile	Tyr	Ser	Glu	Asn	Ala	Gly	Ile	Gln	Arg	Ser	Val	Ser	Leu	Ser
			850				855					860				
75	Leu	Thr	Tyr	Ser	Phe	Gly	Lys	Met	Asn	Thr	Gln	Val	Arg	Lys	Val	Glu

WO 99/29870

PCT/AU98/01023

287/490

865 Arg Thr Ile Val Asn Asp Asp Leu Lys Gln Thr Ser Ser Gln Gly Gln 880
 885 890 895
 5 Gln Gly Gly Gly Gln Gly Asn Pro Thr Gly Asn 900 905

(2) INFORMATION FOR SEQ ID NO:356

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

Trp Cys Gln Ser Asp Pro Ile Pro His Cys His Ala Val Tyr Arg Asn
 1 5 10 15
 30 Ala Gln Gly His Gln Gln Gly Arg Ser Asp Gln Asp Arg Leu Pro Pro
 20 25 30
 Val Arg Gly Tyr Arg Tyr Ala Arg Cys Leu Gly Arg Tyr Glu Gly Phe
 35 35 40 45
 Gly Glu Arg Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met
 50 55 60
 35 Leu Pro Ala Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu
 65 70 75 80
 Arg Leu Glu Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile
 85 90 95
 40 Arg Ser Ala Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val
 100 105 110
 Lys Gly Tyr Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr
 115 120 125
 Ser Leu Pro Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr
 130 135 140
 45 Leu Asn Tyr Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser
 145 150 155 160
 Asp Leu Pro Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile
 165 170 175
 50 Leu Pro Tyr Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu
 180 185 190
 Met Leu Gly Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro
 195 200 205
 Ile Tyr Asn Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val
 210 215 220
 55 Gln Phe Arg Gly Asp Trp Thr Arg Phe Arg Met Arg Val Trp Val Asn
 225 230 235 240
 Trp Met Ser Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val
 245 250 255
 60 Phe Gly Leu Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp
 260 265 270
 Arg Leu Glu Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu
 275 280 285
 Tyr Asn Trp Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala
 290 295 300
 65 Val Gly Leu Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln
 305 310 315 320
 Ile Trp Gly Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr
 325 330 335
 70 Phe Pro Tyr Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp
 340 345 350
 Leu Glu His Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr
 355 360 365
 Val Ser Pro Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys
 370 375 380
 75 Gln Pro Leu Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp

WO 99/29870

PCT/AU98/01023

288/490

385 390 395 400
Tyr Ser Trp Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg
405 410 415
Val Trp Phe Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu
420 425 430
Leu Thr Met Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Glu
435 440 445
Asn His
450

10

(2) INFORMATION FOR SEQ ID NO:357

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

20

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

25

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...447

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

Pro Phe Ser Pro Pro Trp Val Cys Ala Gly Ala Ala Ser Ser Val Arg
1 5 10 15
Thr Arg Pro Cys Ser Thr Val Ser Ser Thr Ala Ala Ser Ser His Arg
20 25 30
35 Arg Ser Glu His Met Arg Ser Ala Asp Ser Ser Pro Ala Tyr Ser Pro
35 40 45
Ile Gly Ser Leu Ser Ser Ser His Ser Phe Asp Ser Ile Pro Asp Gln
50 55 60
40 Arg Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly
65 70 75 80
Met Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu
85 90 95
Pro Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys
100 105 110
45 Leu Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val
115 120 125
Asp Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met
130 135 140
50 Ser Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln
145 150 155 160
Arg Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser
165 170 175
Asn Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val
180 185 190
55 Ser Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr
195 200 205
Asp Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr
210 215 220
60 Met Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro
225 230 235 240
Glu Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe
245 250 255
Ala Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr
260 265 270
65 Pro Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala
275 280 285
Leu His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg
290 295 300
70 Asn Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg
305 310 315 320
Ile Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp
325 330 335
Lys Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp
340 345 350
75 Val Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp

WO 99/29870

PCT/AU98/01023

290/ 490

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...406

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

10 Ile Phe Ile Asp Pro Asp Lys Asn Thr Lys Gln Asn Glu Arg Asn Met
1 5 10 15
Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile Leu
20 25 30
Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn Val
35 40 45
15 Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg Ala
50 55 60
Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr Ser
65 70 75 80
20 Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala Gly
85 90 95
Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp Ile
100 105 110
Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu Asn
115 120 125
25 Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu Glu
130 135 140
Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn Glu
145 150 155 160
Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe Ser
165 170 175
30 Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His Asn
180 185 190
Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala Gly
195 200 205
35 Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp Ser
210 215 220
Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp Gly
225 230 235 240
40 Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr Gly
245 250 255
Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu Glu
260 265 270
Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn Asp
275 280 285
45 Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser Ser
290 295 300
Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu Lys
305 310 315 320
50 Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser Tyr
325 330 335
Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro Thr
340 345 350
Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met Asn
355 360 365
55 Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser Asn
370 375 380
Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp Gly
385 390 395 400
60 Leu Arg Asn Leu Phe His
405

(2) INFORMATION FOR SEQ ID NO:360

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

65

(ii) MOLECULE TYPE: protein

70

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

75

WO 99/29870

PCT/AU98/01023

292/ 490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

10 Gly Leu Tyr Gly Met Ser Val Val Pro Ile Ile Ile Tyr Leu Cys Gly
1 5 10 15
Ile Ser Asn Tyr Ala Arg Leu Met Ile Ile Arg Cys Leu Ile Arg Arg
20 25 30
15 Pro Arg Thr Val Leu Phe Gly Leu Ile Phe Val Val Gly Leu Phe Ser
35 40 45
Ala Met Ala Gln Glu Lys Lys Asp Ser Leu Ser Thr Val Gln Pro Val
50 55 60
20 Pro Asn Ser Ser Met Val Glu Gln Thr Pro Leu Leu Ser Ile Asp His
65 70 75 80
Pro Val Leu Pro Ala Ser Phe Gln Asn Thr Arg Thr Leu Lys Arg Phe
85 90 95
Arg Asp Lys His Leu Ser Asp Ala Leu Leu Asn Gly Leu Lys Pro His
100 105 110
25 Arg Ser Ser Leu Gln Leu Asn Glu Glu Leu Asn Phe Ala Ala Glu Arg
115 120 125
Arg Asp Phe Val Ser Pro Leu Leu Gln Thr Arg His Ala Ala Gly Val
130 135 140
30 Leu Ser Trp Arg Pro Thr Asp Arg Met His Phe Tyr Thr Ser Gly Asn
145 150 155 160
Ile Gly Leu Gly His Asp Leu Leu Thr Gly Val Arg Lys Asp Phe Gly
165 170 175
Trp Asn Ala Gly Ala Asp Phe Leu Leu Ser Gln Asn Leu Thr Ala His
180 185 190
35 Val Gln Gly Gly Trp Gln Gln Asn Phe Gly Phe Ile Pro Met Thr Ala
195 200 205
Val Asn Gly Gln Leu Arg Trp Gln Ala Thr Glu Arg Leu Ser Phe Thr
210 215 220
Thr Gly Ile Asp Tyr Arg Gln Val Gln Trp Asn Ala Phe Asp Asn Arg
225 230 235 240
40 Thr Phe Ser Leu Lys Gly Ser Ala Arg Tyr Glu Val Met Asp Asn Val
245 250 255
Phe Val Asn Gly Phe Gly Ser Tyr Pro Leu Tyr Ser Ser Thr Arg Ser
260 265 270
45 Gly Leu Asn Met Ala Val Pro Met His Gly Phe Gly Pro Gln Tyr Gly
275 280 285
Gly Ser Leu Glu Leu Lys Val Ser Glu Arg Phe Gly Phe Ala Val Gly
290 295 300
50 Met Glu Arg Glu Tyr Asn Ile Trp Thr Arg Arg Trp Glu Thr His Tyr
305 310 315 320
Phe Ala Tyr Pro Val Phe Tyr Gly Asp Lys Lys
325 330

(2) INFORMATION FOR SEQ ID NO:362

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

65 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
70 (B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

75 Glu Thr Asn Ser Trp Val Ser Ser Asp Cys Asn Ser Thr Thr Met Lys
1 5 10 15

294/ 490

Ala Ser Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly
 115 120 125
 Ile His Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg
 130 135 140
 5 Ser Ala Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile
 145 150 155 160
 Arg Ser Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys
 165 170 175
 10 Ser Ser Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys
 180 185 190
 Val Phe Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly
 195 200 205
 Leu Arg Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp
 210 215 220
 15 Ala Ile Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr
 225 230 235 240
 Arg Thr Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln
 245 250 255
 20 Ile Gly Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala
 260 265 270
 Asn Val Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr
 275 280 285
 Asp Leu Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala
 290 295 300
 25 Val Gly Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly
 305 310 315

(2) INFORMATION FOR SEQ ID NO:364

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 614 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...614
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

Pro Tyr Asn Val Gln Ser Ile Ser Asn Lys Thr Ile Lys Lys Gln Met
 1 5 10 15
 50 Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Arg Phe Asn Trp Glu Glu
 20 25 30
 Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln Glu
 35 40 45
 55 Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val Val
 50 55 60
 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val
 65 70 75 80
 Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn
 85 90 95
 60 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln
 100 105 110
 Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala
 115 120 125
 65 Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile
 130 135 140
 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Met Ile Val Asp
 145 150 155 160
 Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg
 165 170 175
 70 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys
 180 185 190
 Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys
 195 200 205
 75 Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly
 210 215 220

WO 99/29870

PCT/AU98/01023

296/ 490

His Ser Ile Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr
35 40 45
Val Glu Asn Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile
50 55 60
5 Asp Met Asp Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile
65 70 75 80
Ser Arg Glu Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu
85 90 95
Tyr Asn Gly Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu
100 105 110
10 Ile Gly Ala Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe
115 120 125
Thr Ile Thr Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr
130 135 140
15 Tyr Gln Ile Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu
145 150 155 160
Thr Phe Asn Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro
165 170 175
20 Ile Gly Gly Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser
180 185 190
Glu Pro Gln Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys
195 200 205
Asp Phe Asn Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe
210 215 220
25 Ala Arg Met Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp
225 230 235 240
Thr Phe Asn

- 30 (2) INFORMATION FOR SEQ ID NO:366
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 amino acids
(B) TYPE: amino acid
35 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 40 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- 45 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...235
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

50 Met Lys Thr Ile Ser Lys Asn His Ala Ala Arg Ile Cys Ala Ala Ile
1 5 10 15
Ala Leu Phe Ala Val Cys Asn Gly Arg Ile Ala Ala Gln Asp Phe Leu
20 25 30
55 Tyr Glu Ile Gly Gly Phe Gly Ala Ala Gln Tyr Phe Gly Asp Ala
35 40 45
Asn Arg Gly Leu Phe Gly Ser Ser Gly Val Gly Leu Glu Leu Val Gly
50 55 60
Arg Tyr Asn Tyr Asn Phe Arg Trp Ala Phe Ser Thr Met Leu Asp Trp
65 70 75 80
60 Arg Thr Leu Arg Gly Asp Thr Asp Lys Ser Gly Asn Val Phe Pro Asp
85 90 95
Phe Ala Gln Ala Asp Phe Lys Val Gly Leu Thr Gln Leu His Val Arg
100 105 110
65 Ser Glu Phe Asn Phe Leu Pro Tyr Ser Asp Gly Tyr Lys Tyr Leu Gly
115 120 125
Thr Ala Arg Leu Ser Pro Tyr Val Ala Ala Gly Leu Ser Leu Gly Phe
130 135 140
Ala Ser Gly Ala Lys Gly Ser Ala Phe Ala Pro Gly Ile Thr Ala Gly
145 150 155 160
70 Met Gly Val Lys Tyr Lys Leu Lys Pro Arg Ile Asn Val Gly Ile Glu
165 170 175
Tyr Ser Phe Thr Gly Leu Leu Thr Asp Ala Leu Asp Ala Leu Thr Asp
180 185 190
75 Lys Ser Val Trp Leu Glu Asp Pro Tyr Lys Ile Asn Asp Ser Trp Val
195 200 205

297/490

Lys Asn Lys Asp Ala Thr Gly Ala Leu Val Leu Arg Ile Thr Tyr Asp
 210 215 220
 Phe Gly Leu Arg Lys Thr Phe Cys Asn Lys Gln
 225 230 235

5 (2) INFORMATION FOR SEQ ID NO:367
 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 15 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 20 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...436
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367
 Asn Ile Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp
 1 5 10 15
 Tyr Ala Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala
 20 25 30
 30 Gln Asn Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly
 35 40 45
 Arg Leu Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu
 50 55 60
 35 Gly Val Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala
 65 70 75 80
 Ser Tyr Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala
 85 90 95
 Ser Thr Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg
 100 105 110
 40 Lys Met Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys
 115 120 125
 Ser Ile Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr
 130 135 140
 45 Gln Phe Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr
 145 150 155 160
 Arg Lys Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile
 165 170 175
 Gly Ala Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser
 180 185 190
 50 Leu Phe Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu
 195 200 205
 Ala Pro Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala
 210 215 220
 55 Lys Phe Asp Phe Gly Met Gln Tyr His Leu Leu Lys Ser Asp Arg
 225 230 235 240
 Ser Leu Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser
 245 250 255
 Glu Leu Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu
 260 265 270
 60 Ser Glu Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro
 275 280 285
 His Thr Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu
 290 295 300
 65 Leu Gly Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr
 305 310 315 320
 Lys Ser Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly
 325 330 335
 Glu Ile Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg
 340 345 350
 70 Tyr Arg Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr
 355 360 365
 Lys Gly Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly
 370 375 380
 75 Ile Gly Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu
 385 390 395 400

WO 99/29870

PCT/AU98/01023

298/490

Glu Tyr Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala
 405 410 415
 Leu Lys Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys
 420 425 430
 5 Leu Lys Leu Asn
 435

(2) INFORMATION FOR SEQ ID NO:368

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 945 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...945
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

Asn Thr Ile Ser Glu Asn Gly Asn Asp Ser Thr Tyr Phe Ser Phe Gln
 1 5 10 15
 30 Thr Phe Leu Met Arg Ser Ile Tyr Gln Leu Leu Ser Ile Leu Leu
 20 25 30
 Ala Ser Leu Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala
 35 40 45
 Gly Arg Val Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val
 50 55 60
 Gln Leu Val Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr
 65 70 75 80
 Asn Glu Lys Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr
 85 90 95
 40 Ile Leu Arg Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile
 100 105 110
 Ser Leu Arg Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn
 115 120 125
 Glu Asp Ala Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala
 45 130 135 140
 Glu Val Val Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr
 145 150 155 160
 Thr Val Ala Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro
 165 170 175
 50 Gly Ala Glu Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp
 180 185 190
 Ile Ser Lys Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro
 195 200 205
 Gln Val Ala Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln
 55 210 215 220
 Val Leu Asn Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp
 225 230 235 240
 Gly Glu Glu Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys
 245 250 255
 60 Lys Gly Leu Phe Gly Thr Leu Gln Ala Gly Tyr Gly Thr Asp Gln Arg
 260 265 270
 Tyr Met Ala Gly Gly Asn Val Asn Arg Phe Asp Gly Asn Lys Gln Trp
 275 280 285
 Thr Leu Ile Gly Ser Ala Asn Asn Thr Asn Asn Met Gly Phe Ser Glu
 65 290 295 300
 Met Asp Ser Glu Met Gly Ser Met Thr Phe Phe Ser Pro Gln Gly Gly
 305 310 315 320
 Gly Arg Arg Gly Phe Gly Asn Ser Gly Gly Val Thr Ser Ser Ser Met
 325 330 335
 70 Leu Gly Gly Asn Phe Ser Val Glu Phe Ser Ser Ala Leu Asn Thr Gly
 340 345 350
 Gly Asp Ala Arg Tyr Gly Tyr Asn Asp Lys Ala Ile Glu Thr Thr Lys
 355 360 365
 75 Arg Val Glu Asn Ile Leu Ala Glu Gly Asn Thr Tyr Met Asp Glu Asn
 370 375 380

299/ 490

Ile Leu Glu Arg Ser Phe Ser His Asn Gly Gln Ala Arg Phe Arg Met
 385 390 395 400
 Gln Trp Lys Pro Ser Glu Arg Thr Glu Val Val Phe Glu Pro Asp Leu
 405 410 415
 5 Ser Ile Ser Lys Ile Asp Gly Phe Phe Asn Asp Thr Tyr Glu Thr Lys
 420 425 430
 Asp Ala Thr Gly Ile Ser Ile Asn Lys Gly Ser Ile His Gln Thr Thr
 435 440 445
 10 Gln Gly Asn Asn Phe Arg Leu Asn Gly Glu Leu Asp Ile Ser His Lys
 450 455 460
 Leu Asn Asp Glu Gly Arg Thr Ile Ser Ala Ser Val Ser Gly Gly Leu
 465 470 475 480
 Thr Asp Glu Asp Gly Asp Gly Ile Tyr Gln Ala Val Leu Gln Ser Val
 485 490 495
 15 Glu Thr Asn Gln Lys Gln Phe Asn Asp Asn Ser Asn Leu Gln Tyr Arg
 500 505 510
 Leu Arg Leu Ser Tyr Val Glu Pro Leu Gly Lys Asn Tyr Phe Ala Gln
 515 520 525
 20 Ala Ile Leu Asn Arg Arg Phe Ser Arg Arg Asn Ser Asp Arg Glu Val
 530 535 540
 Tyr Arg Leu Gly Asp Asp Gly Gln Tyr Ser Ile Leu Asp Ser Gln Tyr
 545 550 555 560
 Gly Leu Ser Tyr Ser Asn Glu Phe Thr Gln Tyr Arg Ile Gly Leu Asn
 565 570 575
 25 Leu Lys Lys Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val
 580 585 590
 Asp Pro Asn Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln
 595 600 605
 30 Asp Lys Leu Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile
 610 615 620
 Asn Tyr Lys Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly
 625 630 635 640
 Arg Thr Thr Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile
 645 650 655
 35 Thr Asn Pro Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser
 660 665 670
 Tyr Ser Asn Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser
 675 680 685
 40 Gln Arg Ala Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp
 690 695 700
 Ile Val Pro Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr
 705 710 715 720
 Arg Tyr Glu Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr
 725 730 735
 45 Leu Ser Leu Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu
 740 745 750
 Phe Asn Arg Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn
 755 760 765
 50 Lys Ala Leu Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg
 770 775 780
 Asn Asn Trp Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met
 785 790 795 800
 Ala Asn Asn Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe
 805 810 815
 55 Gly Gly Asn Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile
 820 825 830
 Asp Ser Asp Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe
 835 840 845
 60 Ser Leu Asp Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu
 850 855 860
 Arg Asp Lys Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly
 865 870 875 880
 Gln Arg Ser Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu
 885 890 895
 65 Ser Met Ser Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr
 900 905 910
 Arg Phe Asn Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg
 915 920 925
 70 Gly Asn Met Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro
 930 935 940
 Ser
 945

(2) INFORMATION FOR SEQ ID NO:369

75

SUBSTITUTE SHEET (Rule 26) (RO/AU)

301/490

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

Ser Asn Ser Ser Ser His Lys Trp Leu Ile Tyr Tyr His Ile Glu Lys
1 5 10 15
Thr Lys Ser Ile Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met
20 25 30
Pro Val Ala Ser Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser
35 40 45
Lys Asp Asn Arg Ile Leu Thr Ser Met Gln Ser Ser Leu Asn Arg
50 55 60
Asp Asp Ala Pro Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile
65 70 75 80
Gln Ser Asp Met Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp
85 90 95
Phe Gly Asn Ser Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu
100 105 110
Phe Gly Ala Arg Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu
115 120 125
Pro Glu Met Gly Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr
130 135 140
His Trp Ala Glu Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser
145 150 155 160
Gly Met Val Phe Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn
165 170 175
Ala Val Arg Gly Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg
180 185 190
Val Lys Gly Ile Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly
195 200 205
Lys Val Phe Asn Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu
210 215 220
Leu Asn Val Glu Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His
225 230 235 240
Leu Ala Ile Gly Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp
245 250 255
Ile Phe Val Gly Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu
260 265 270
Asn Val Pro Ile Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu
275 280 285
Ala Leu Tyr Ala Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp
290 295 300
Asn Asp Tyr Ile Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser
305 310 315 320
Tyr Ser Lys Lys Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu
325 330 335
Asn Phe Ala Phe Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met
340 345 350
Ile Asn Tyr Met Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala
355 360 365
Ala Ile Tyr Pro Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln
370 375 380
Gly Glu Leu Arg Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg
385 390 395 400
Tyr Gly Thr Gly Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp
405 410 415
Lys Lys Met Leu Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly
420 425 430
Tyr Thr Val Ser Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile
435 440 445
Asp Val Glu Ile Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu
450 455 460
Thr Tyr Leu Asn Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala

303/ 490

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

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Leu Leu Phe Ser Ser Pro Leu Pro Arg Met Asp Arg Pro Lys Pro Ser
1      5      10      15
Tyr Ile Val Arg Ile Ala Ala Ile Leu Cys Leu Phe Val Gly Arg Pro
20     20     25     30
Leu Phe Ala Gln Ser Tyr Val Asp Tyr Val Asp Pro Leu Ile Gly Thr
35     40     45
Leu Ser Ser Phe Glu Leu Ser Ala Gly Asn Thr Tyr Pro Val Ile Gly
50     55     60
Leu Pro Trp Gly Met Asn Ser Trp Thr Pro Met Thr Gly Val Pro Gly
25     65     70     75     80
Asp Gly Trp Gln Tyr Thr Tyr Ser Ala His Lys Ile Arg Gly Phe Lys
85     90     95
Gln Thr His Gln Pro Ser Pro Trp Ile Asn Asp Tyr Gly Gln Phe Ser
30     100    105    110
Leu Leu Pro Leu Thr Ala Pro Gln Lys Pro Ser Ser Asn Asp Ser Ile
115    120    125
Ala Leu Thr Lys Trp Cys Lys Gln Leu Phe Ser Asp Glu Gln Thr Ser
130    135    140
Trp Phe Ser His Lys Ala Glu Thr Ala Thr Pro Tyr Tyr Tyr Ser Val
35     145    150    155    160
Tyr Leu Ala Asp Tyr Asp Thr Arg Val Glu Met Ala Pro Thr Glu Arg
165    170    175
Ala Ala Ile Phe Arg Ile Arg Tyr Ser Gly Asn Thr Glu Ser Gly Ser
40     180    185    190
Gly Arg Trp Leu Arg Leu Asp Ala Phe Thr Gly Gly Ser Glu Ile Ser
195    200    205
Ile Val Asp Pro His Thr Val Val Gly Ile Ser Arg Lys Asn Ser Gly
210    215    220
Gly Val Pro Ala Asn Phe Ala Cys Tyr Phe Ile Leu Gln Ser Asp Thr
45     225    230    235    240
Pro Met Ala Asp Val Leu Leu Glu Thr Asp Thr Gly Lys Ser Asp Glu
245    250    255
Gly Thr Arg Ala Trp Ala Ala Cys Arg Phe Asp Ser Gln Glu Val Thr
50     260    265    270
Val Arg Val Ala Ser Ser Phe Ile Ser Val Glu Gln Ala Glu Arg Asn
275    280    285
Leu Ala Glu Val Lys Gly Gln Ser Phe Asp Arg Ile Arg Leu Ala Gly
290    295    300
Arg Glu Ala Trp Asn Lys Val Leu Gly Arg Ile His Val Glu Gly Gly
55     305    310    315    320
Thr Lys Asp Glu Arg Thr Thr Phe Tyr Ser Ala Leu Tyr Arg Cys Leu
325    330    335
Leu Phe Pro Arg Arg Phe Tyr Glu Glu Asp Ala Ser Gly Asn Phe Val
60     340    345    350
His Tyr Ser Pro Tyr Asn Gly Glu Val Leu Pro Gly Tyr Leu Tyr Thr
355    360    365
Asp Thr Gly Phe Trp Asp Thr Phe Arg Ala Leu Phe Pro Leu Leu Asn
370    375    380
Leu Leu Tyr Pro Asp Glu Asn Ile Lys Ile Gln Glu Gly Leu Leu Asn
65     385    390    395    400
Val Tyr Arg Glu Ser Gly Phe Phe Pro Glu Trp Ala Ser Pro Gly His
405    410    415
Arg Asp Cys Met Ile Gly Asn Asn Ser Ala Ser Val Leu Ala Asp Ala
70     420    425    430
Tyr Leu Lys Gly Val Arg Val Glu Asp Thr Arg Thr Leu Met Asn Gly
435    440    445
Leu Leu His Ala Thr Lys Ala Val His Pro Lys Ile Ser Ser Thr Gly
450    455    460
Arg Lys Gly Trp Glu Trp Tyr Asn Ser Leu Gly Tyr Val Pro Ala Asp
75

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WO 99/29870

PCT/AU98/01023

304/ 490

465 470 475 480
Ala Gly Ile Asp Glu Ser Ala Ala Arg Thr Leu Glu Tyr Ala Tyr Asn
485 490 495
5 Asp Trp Cys Ile Leu Arg Leu Gly Arg Thr Leu Gly Trp Asp Arg Ala
500 505 510
Ala Leu Asp Thr Leu Ala His Arg Ser Met Asn Tyr Arg His Leu Phe
515 520 525
10 Asp Pro Glu Thr Lys Leu Met Arg Gly Arg Asn Gln Asp Gly Ser Phe
530 535 540
Arg Thr Pro Phe Ser Pro Phe Lys Trp Gly Asp Val Phe Thr Glu Gly
545 550 555 560
Asn Ala Trp His Tyr Thr Trp Ser Val Phe His Asp Val Gln Gly Leu
565 570 575
15 Ile Asp Leu Met Gly Gly Asp Arg Pro Phe Val Ser Met Leu Asp Ser
580 585 590
Val Phe Asn Thr Pro Pro Met Phe Asp Glu Ser Tyr Tyr Gly Phe Val
595 600 605
Ile His Glu Ile Arg Glu Met Gln Ile Ala Asp Met Gly Asn Tyr Ala
610 615 620
20 His Gly Asn Gln Pro Ile Gln His Met Ile Tyr Leu Tyr Asn His Ala
625 630 635 640
Gly His Pro Trp Lys Ala Gln Glu Arg Leu Arg Glu Val Met Gly Arg
645 650 655
25 Leu Tyr Arg Pro Thr Pro Asp Gly Tyr Cys Gly Asp Glu Asp Asn Gly
660 665 670
Gln Thr Ser Ala Trp Tyr Val Phe Ser Ala Leu Gly Phe Tyr Pro Val
675 680 685
Thr Pro Ala Thr Asp Gln Tyr Val Leu Gly Ser Pro Ile Phe Ser Lys
690 695 700
30 Val Ile Leu Ser Phe Pro Asp Gly His Lys Thr Val Leu His Ala Pro
705 710 715 720
Ala Asn Ser Ala Asp Thr Pro Tyr Ile Arg Ser Ile Ser Val Glu Gly
725 730 735
35 Lys Glu Trp Ser Cys Asn Tyr Leu Thr His Glu Gln Leu Arg Ser Ser
740 745 750
Ala Ser Ile Gln Trp Met Met Asp Thr Lys Pro Asn Tyr Asn Arg Gly
755 760 765
Met Lys Glu Ser Asp Arg Pro Tyr Ser Phe Ser Thr Glu Gln Gln Arg
770 775 780
40 Arg Ala Asn His Ser Asn
785 790

(2) INFORMATION FOR SEQ ID NO:373

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
50 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
60 (B) LOCATION: 1...286
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

Ile Cys Gly Ser Lys Met Asn Leu Ser Gly Leu Gln Ser Phe Thr Met
1 5 10 15
65 Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
20 25 30
Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
35 40 45
70 Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
50 55 60
Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
65 70 75 80
Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
85 90 95
75 Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr

WO 99/29870

PCT/AU98/01023

305/ 490

100 105 110
 Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
 115 120 125
 5 Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
 130 135 140
 Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
 145 150 155 160
 Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
 165 170 175
 10 Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
 180 185 190
 Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
 195 200 205
 15 Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
 210 215 220
 Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
 225 230 235 240
 Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
 245 250 255
 20 Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala
 260 265 270
 Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
 275 280 285
 25 (2) INFORMATION FOR SEQ ID NO:374
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...378
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374
 45 Gly Ile Ile Ser Val Leu Ser His Val Val Asp Arg Pro Gln Trp Gly
 1 5 10 15
 Ala Ser Pro Glu Ala Ala Gly Thr His Ser Val Tyr Ser Ile Leu His
 20 25 30
 50 Pro Ser Ala Gly Ile Ile Arg Ile Arg Ser Met Gly Ile Ile Ser Ala
 35 40 45
 Cys Arg Ile Ala Ile Leu Ala Gly Lys His Pro Arg Ser Gly Leu Ser
 50 55 60
 Arg Ala Asn Val Gly Ile Leu Ser Tyr Asn Pro Glu Asn Thr Pro Glu
 65 70 75 80
 55 Lys Lys Arg Lys Leu Gln Glu Lys Asn Val Phe Leu Gln Ile Arg Leu
 85 90 95
 Arg Gln Ser Phe Asn Asn Leu Ile Pro Ser Leu Pro Phe Arg Ile Asp
 100 105 110
 60 Asn Thr Lys Lys Ile Thr Glu Met Lys Lys Thr Thr Leu Thr Gly Ser
 115 120 125
 Ile Cys Ala Leu Leu Leu Phe Leu Gly Leu Ser Ala Asn Ala Gln Ser
 130 135 140
 Lys Leu Lys Ile Lys Ser Ile Glu Ala Ala Thr Thr Phe Ser Ser Ala
 145 150 155 160
 65 Thr Ala Gly Asn Gly Phe Gly Gly Asn Ile Phe Gly Met Asp Met Ser
 165 170 175
 Ile Arg Met Arg Val His His Ser Ile Leu Pro Glu Gly Leu Asp Phe
 180 185 190
 70 Ser Val Gly Ile His Glu Arg Arg Ala His Trp Glu Glu Ala Gly Ser
 195 200 205
 Pro Lys Leu Met Tyr Thr Asn Val Pro Ser Ile Ile Gly Ile Val Glu
 210 215 220
 Lys Val Ile Val Phe Glu Asp Ala Glu Asp Phe Phe Asp Lys Lys Ala
 225 230 235 240
 75 Leu Gly Arg Phe Leu Ile Ser Leu Gly Ile Ser Tyr Thr Lys His Leu

WO 99/29870

PCT/AU98/01023

306/490

5 Gly Ala Tyr Trp 245 Gly Trp Thr Asn Asp Ala His Ile Leu Phe Ser Pro
 Ile Pro Lys Ser Lys Val His Tyr Asp Thr Tyr Thr Arg Ala Gly Ser
 Asp Leu Val Leu Gln Ser Glu Asp Val Ala Thr Val Ser Asn Gly Phe
 Ser Pro Gly Ile Gly Leu Lys Ser Ser Ile Trp Trp Lys Met Pro Ile
 10 Lys Ser Lys Tyr Asp Phe Arg Leu Gly Phe Ser Leu Gly Tyr Glu Tyr
 Leu Asn Leu Leu Tyr Pro Tyr Arg Asn Phe Lys Leu Asp Gly Asn Lys
 Pro Leu Ser Ala Leu Ser Pro Arg Met Asn His Ile Gly His Val Gly
 15 Phe Asn Phe Thr Val Gly Leu Trp Thr Asn
 20 (2) INFORMATION FOR SEQ ID NO:375
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1269 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1269
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375
 40 Val Lys Cys Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu
 Phe Pro Phe Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu
 Cys Ala Ser Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp
 45 Leu Glu Lys Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu
 Gly Ile Ser Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly
 Ala Val Val Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr
 50 Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn
 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys
 55 Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser
 Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys
 60 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu
 Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu
 Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu
 65 Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile
 Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg
 70 Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr
 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu
 Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn
 75 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys

WO 99/29870

PCT/AU98/01023

307/ 490

	290		295		300
	Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg				
	305		310		315
5	Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys				
		325		330	335
	Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu				
		340		345	350
	Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu				
		355		360	365
10	Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu				
		370		375	380
	Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile				
		385		390	395
15	Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr				
		405		410	415
	Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala				
		420		425	430
	Ser Leu Thr Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys Leu Glu				
		435		440	445
20	Gly Leu Asp Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser Gly Asn				
		450		455	460
	Asp Ile Gln Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile Leu Glu				
		465		470	475
25	Gln Thr Leu Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val Ala Ser				
		485		490	495
	Ser Gly Leu Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu Ile Lys				
		500		505	510
	Ala Leu Leu Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser Val Glu				
		515		520	525
30	Tyr His Pro Phe Cys Lys Val Met Leu Leu Gly Asn His Ser Ser Gly				
		530		535	540
	Lys Thr Thr Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr Gln Lys				
		545		550	555
35	Asn Thr His Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn Ala Ile				
		565		570	575
	Phe Tyr Asp Phe Gly Gln Asp Tyr Tyr His Gly Ile Tyr Gln Ala				
		580		585	590
	Phe Phe Thr Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala Lys Lys				
		595		600	605
40	Asp Arg Asn Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr Leu Asn				
		610		615	620
	Phe Asn Arg Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys Asn Arg				
		625		630	635
45	Cys Met Ser Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro Gln Thr				
		645		650	655
	Thr Asp Asp Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr Gly Ala				
		660		665	670
	Lys Gln Gln Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu Glu Glu				
		675		680	685
50	Ile Tyr Val Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His Ala Leu				
		690		695	700
	Asn Tyr Leu Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg Ser Lys				
		705		710	715
55	Ser Ile Gln Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala Leu Pro				
		725		730	735
	Thr Ile Ala Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu Ala Leu				
		740		745	750
	Ala Ala Gln Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr Thr Ile				
		755		760	765
60	Glu Tyr Leu Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly Glu Val				
		770		775	780
	Leu Tyr Tyr Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp Leu Asp				
		785		790	795
65	Pro Ala Ala Phe Val Gln Met Ile His Gly Glu Ile Leu Gln Lys Asp				
		805		810	815
	Asn Ile Asn Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys Lys Leu				
		820		825	830
	His Asn Leu Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln Asn Gly				
		835		840	845
70	Asn Met Ile Leu Gln Leu Leu Leu Glu Glu Leu Ile Val Tyr Glu Asp				
		850		855	860
	Lys Asp Cys Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser Asp Asp				
		865		870	875
75	Glu Ala Tyr Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn Phe Val				
		885		890	895

WO 99/29870

PCT/AU98/01023

308/ 490

Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile
 900 905 910
 Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp
 915 920 925
 5 Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu
 930 935 940
 Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr
 945 950 955 960
 10 Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe
 965 970 975
 Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu
 980 985 990
 Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro
 995 1000 1005
 15 Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr
 1010 1015 1020
 Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu
 1025 1030 1035 1040
 20 Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His
 1045 1050 1055
 Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala
 1060 1065 1070
 Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val
 1075 1080 1085
 25 Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr
 1090 1095 1100
 Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu
 1105 1110 1115 1120
 30 Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile
 1125 1130 1135
 Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro
 1140 1145 1150
 Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile
 1155 1160 1165
 35 Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro
 1170 1175 1180
 Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro
 1185 1190 1195 1200
 40 Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln
 1205 1210 1215
 Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala
 1220 1225 1230
 Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala
 1235 1240 1245
 45 Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu
 1250 1255 1260
 Val Asn Thr Asp Glu
 1265

50 (2) INFORMATION FOR SEQ ID NO:376

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

70 Lys Phe Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu
 1 5 10 15
 Phe Ser Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg
 20 25 30
 75 Ser Tyr Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val
 35 40 45

WO 99/29870

PCT/AU98/01023

309/ 490

Pro Pro Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly
50 55 60
Leu Pro Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly
65 70 75 80
5 Asp Ile Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn
85 90 95
Glu Trp Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly
100 105 110
10 Arg Phe Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys
115 120 125
Thr Arg Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu
130 135 140
Ile Pro Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro
145 150 155 160
15 Cys Ile Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp
165 170 175
Asp Thr Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys
180 185 190
20 Pro Phe Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln
195 200 205
Lys Tyr Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala
210 215 220
Gln Thr Val Ser Gln Gln Lys
225 230
25 (2) INFORMATION FOR SEQ ID NO:377

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 563 amino acids
30 (B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
35 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
40 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377
45
Ser Leu Ile Asn Asn Ser Arg Asp Trp Arg Ala Pro Val Arg Leu Ser
1 5 10 15
Leu Lys Lys Lys Thr Lys Thr Met Lys Thr Lys Val Leu Arg Lys Phe
20 25 30
50 Val Val Ala Ala Phe Ala Val Ala Thr Leu Cys Pro Leu Ala Gln Ala
35 40 45
Gln Thr Met Gly Gly Asp Asp Val Lys Val Val Gln Tyr Asn Gln Glu
50 55 60
Lys Leu Val Gln Thr Arg Met Ser Val Ala Asp Asn Gly Trp Ile Tyr
65 70 75 80
55 Val Met Thr His Ser Gly Tyr Asp Thr Gly Asn Ser Asn Val Lys Ile
85 90 95
Phe Arg Ser Lys Asp Gln Gly Ala Thr Tyr Gln Lys Leu Arg Asp Trp
100 105 110
60 Asp Pro Ser Asp Asp Tyr Gln Phe Gln Asp Phe Asp Ile Val Val Thr
115 120 125
Gly Lys Asn Glu Ser Asp Ile Lys Ile Trp Ser Val Glu Leu Met Asn
130 135 140
Lys Pro Gly Gly Tyr Lys Ser Arg Val Ala Val Phe Ser Arg Asp Ala
145 150 155 160
65 Asn Ala Gln Asn Ala Lys Leu Val Tyr Lys Glu Asp Phe Ser Asn Val
165 170 175
Gln Leu Tyr Asp Val Asp Ile Ala Ser Asn Tyr Arg Ser Pro Ser Ser
180 185 190
70 Leu Asn Asn Gly Gly Asn Pro Phe Ala Leu Ala Phe Ala Tyr Thr Gly
195 200 205
Phe Asn Asn Thr His Lys Ile Ser Phe Val Asp Tyr Val Phe Ser Leu
210 215 220
Asn Gly Gly Gln Asn Phe Asn Lys Asn Leu Leu Phe Ser Gln Asp Gly
75 225 230 235 240

WO 99/29870

PCT/AU98/01023

310/ 490

5 Glu Lys Lys Ile Asp Lys Val Asp Leu Ser Leu Gly Ser Thr Ser Glu
245 250 255
Ser Met Gly His Asn Ala Trp Pro Leu Met Gly Val Val Phe Glu Met
260 265 270
10 Asn Lys Gln Gly Gly Lys Ser Asp Ile Gly Phe Leu Ser Asn Phe Val
275 280 285
Asp Asn Asp Pro Glu Phe Gln Trp Ser Gly Pro Ile Lys Val Ser Glu
290 295 300
Ser Asp Met Ser Phe Ser Pro Lys Ile Gln Met Leu Leu Asp Glu Asp
305 310 315 320
15 Asn Asn Thr Ile Asn Gly Glu Ser Cys His Asn Phe Met Ile Thr Tyr
325 330 335
Ser Asp Tyr Asp Ser Glu Tyr Ser Asp Trp Asp Ile Arg Tyr Val Tyr
340 345 350
Pro Lys Lys Ser Phe Lys Tyr Glu Lys Gly Lys Thr Pro Thr Met Asp
355 360 365
20 Asp Leu Val Glu Ala Phe Leu Thr Ala Ser Tyr Gln Ser Glu Thr Asn
370 375 380
Ser Gly Leu Gly Tyr Asp Lys Asn Ala Asn His Tyr Leu Ile Thr Tyr
385 390 395 400
Ala Lys Lys Glu Glu Asn Gly Thr Asn Thr Leu Lys Tyr Arg Trp Ala
405 410 415
25 Asn Tyr Asp Lys Ile His Asn Lys Asp Leu Trp Ser Asp Thr Phe Thr
420 425 430
Tyr Thr Ser Ala Asn Ala Leu Tyr Thr Pro Gln Val Asp Ile Asn
435 440 445
Pro Thr Lys Gly Leu Val Cys Trp Ser Trp Val Glu Tyr Leu Pro Gly
450 455 460
30 Lys Arg Ile Val Trp Ser Asp Thr Gln Trp Thr His Ala Asn Gly Val
465 470 475 480
Glu Asp Ile Val Met Gln Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro
485 490 495
Ala Gln Glu Tyr Ala Val Ile Ser Leu Pro Thr Ala Ala Asn Cys Lys
500 505 510
35 Ala Val Val Tyr Asp Met Gln Gly Arg Val Val Ala Glu Ala Ser Phe
515 520 525
Ser Gly Asn Glu Tyr Arg Leu Asn Val Gln His Leu Ala Lys Gly Thr
530 535 540
40 Tyr Ile Leu Lys Val Val Ser Asp Thr Glu Arg Phe Val Glu Lys Leu
545 550 555 560
Ile Val Glu

(2) INFORMATION FOR SEQ ID NO:378

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

55

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

60

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

65 Ile Val Tyr Leu Cys His Cys Met Asn His Arg Arg Ser Lys Thr Met
1 5 10 15
Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile Ala
20 25 30
Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu Thr
35 40 45
70 Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr Asn
50 55 60
Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe Asn
65 70 75 80
75 Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp Trp
85 90 95

WO 99/29870

PCT/AU98/01023

311/490

Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser His
 100 105 110
 Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu Leu
 115 120 125
 5 Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Tyr Gly Ser
 130 135 140
 Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val Leu
 145 150 155 160
 10 Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr Ala
 165 170 175
 Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu Asn
 180 185 190
 Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe Leu
 195 200 205
 15 Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys Tyr
 210 215 220
 Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser Arg
 225 230 235 240
 20 Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr Val
 245 250 255
 Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp Gly
 260 265 270
 Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser Phe
 275 280 285
 25 Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser Phe
 290 295 300
 Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu Glu
 305 310 315 320
 30 Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala Ile
 325 330 335
 Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val Glu
 340 345 350
 Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala Leu
 355 360 365
 35 Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly Glu
 370 375 380
 Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp Arg
 385 390 395 400
 40 Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro Leu
 405 410 415
 Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr Leu
 420 425 430
 Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu Tyr
 435 440 445
 45 Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val Ile
 450 455 460
 Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr Ala
 465 470 475 480
 50 Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His Pro
 485 490 495
 Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro Leu
 500 505 510
 Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr Leu
 515 520 525
 55 Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys Glu
 530 535 540
 Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr Tyr
 545 550 555 560
 60 Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser Phe
 565 570 575
 Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn Pro
 580 585 590
 Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro His
 595 600 605
 65 Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe Ser
 610 615 620
 Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr Asn
 625 630 635 640
 70 Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys Glu
 645 650 655
 Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His Phe
 660 665 670
 Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr Met
 675 680 685
 75 Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys Pro

WO 99/29870

PCT/AU98/01023

313/490

325 330 335
 Ala Tyr Ile Ala Leu Gly Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala
 340 345 350
 5 Glu Gly Ser Thr Ala Glu Ala Met Pro Val Ala Phe Asp Gly Pro Gly
 355 360 365
 Asp Asn Asp Phe Tyr Glu Met Arg Phe Ser His Gly Arg Leu Tyr Ala
 370 375 380
 Ala Ser Gly Leu Trp Gly Thr Asn Leu Met Gly His Ala Gly Met Val
 385 390 395 400
 10 Lys Leu Tyr Asp Gly Asn Arg Trp Thr Asn Phe Asp Lys Lys Thr Val
 405 410 415
 Gln Glu Gln Leu Gly Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile
 420 425 430
 15 Ala Val Ser Asn Gly Asp Pro Asp His Phe Phe Val Gly Thr Trp Gly
 435 440 445
 Asn Gly Leu Phe Glu Phe Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser
 450 455 460
 Gly Asn Glu Thr Ala Ile Ala Glu Cys Asn Pro Gly Asp Ala Arg Val
 465 470 475 480
 20 Lys Ala Ile Ala Phe Asp Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly
 485 490 495
 Ala Val Gly Lys Asn Ile Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp
 500 505 510
 25 His Ser Phe Ser Tyr Pro Asp Val Ala Asn Leu Ala Ser Phe Gly Asn
 515 520 525
 Met Ile Ile Leu Pro Asn Gly Asp Lys Trp Val Asn Ile Leu His Arg
 530 535 540
 Ser Gly Gly Ser Thr Arg Lys Gly Val Leu Ile Phe Asn Asp Arg Gly
 545 550 555 560
 30 Thr Pro Glu Thr Thr Ser Asp Asp Ser His Leu Tyr Val Glu Gln Phe
 565 570 575
 Val Asn Arg Leu Gly Ala Ala Ile Gly His Lys Thr Ile Tyr Ala Met
 580 585 590
 35 Ala Val Asp His Asn Gly Ser Val Trp Met Gly Ser Asp Ile Gly Ile
 595 600 605
 Phe Gly Val Tyr Asn Ala Ala Gly Val Leu Ser Ser Thr Ser Thr Pro
 610 615 620
 Ile Ala Val Arg Pro Val Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val
 625 630 635 640
 40 Leu Asp Lys Val Thr Val Thr Asp Ile Val Val Asp Lys Leu Asn His
 645 650 655
 Lys Trp Val Ala Thr Gln Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp
 660 665 670
 45 Cys Ser Lys Ile Leu Ala Gln Phe Thr Val Glu Asn Ser Pro Leu Leu
 675 680 685
 Ser Asn Asn Ile Leu Ser Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu
 690 695 700
 Tyr Ile Gly Thr Ala Asp Gly Leu Met Thr Phe Gln Thr Gly Thr Gly
 705 710 715 720
 50 Ser Gly Ser Ala Ser Glu Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro
 725 730 735
 Leu Arg Pro Glu Tyr Pro Asp Gly Val Thr Ile Ala Gly Leu Gln Ala
 740 745 750
 55 Gly Cys Ser Val Lys Ile Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln
 755 760 765
 Thr Glu Ser Val Thr Thr Glu Val Lys Trp Asn Ala Arg Gly Ala Asp
 770 775 780
 Gly Asn Arg Val Ala Ser Gly Val Tyr Ala Val Ala Val Tyr Asp Pro
 785 790 795 800
 60 Val Ser Lys Lys Ser Lys Leu Ile Arg Phe Ala Val Ile Arg
 805 810

(2) INFORMATION FOR SEQ ID NO:380

- 65 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1162 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 70 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 75 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION 1...1162

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

	Ala	Ile	Ser	Gln	Met	Lys	Arg	Ile	Leu	Pro	Ile	Val	Ala	Phe	Leu	Ser
	1				5					10					15	
10	Leu	Phe	Leu	Ala	Leu	Ala	Leu	Pro	Ala	Lys	Ala	Gln	Arg	Ala	Met	Gly
			20						25					30		
	Lys	Thr	Ala	Asp	Arg	Ser	Leu	Met	Ala	Ser	Gly	His	Trp	Val	Lys	Ile
			35					40					45			
15	Arg	Val	Asp	Ala	Ser	Gly	Val	Tyr	Arg	Leu	Thr	Asp	Glu	Gln	Leu	Arg
		50				55						60				
	Ala	Asn	Gly	Phe	Ser	Asp	Pro	Ser	Lys	Val	Gly	Val	Phe	Gly	Tyr	Gly
	65					70				75					80	
	Gly	Gly	Val	Leu	Pro	Glu	Asp	Leu	Ser	Arg	Ile	Thr	Thr	Asp	Asp	Leu
					85					90					95	
20	Pro	Pro	Val	Pro	Val	Leu	Arg	Gln	Gly	Asn	Ala	Leu	Tyr	Phe	Tyr	Ala
				100					105					110		
	Val	Gly	Pro	Val	Thr	Trp	Phe	Tyr	Asn	Pro	Ala	Lys	Thr	Thr	Met	Glu
		115					120						125			
25	His	Thr	Val	Asn	Thr	Tyr	Ser	Thr	His	Gly	Tyr	Tyr	Phe	Leu	Ser	Asp
		130					135					140				
	Ala	Ala	Gly	Ala	Pro	Leu	Gln	Met	Ser	Gln	Tyr	Thr	Gly	Gly	Gly	Ala
	145					150				155					160	
	Ser	Ala	Glu	Ala	Leu	Ile	Asp	Tyr	Tyr	Asp	Glu	Leu	Met	Leu	His	Glu
				165					170					175		
30	Gln	Glu	Leu	Tyr	Ser	Pro	Lys	Glu	Ser	Gly	Arg	Asp	Leu	Tyr	Gly	Glu
				180					185					190		
	Ser	Phe	Ser	Ala	Val	Asn	Thr	Arg	Thr	Val	Lys	Phe	Pro	Leu	Arg	Gly
		195						200					205			
35	Asn	Thr	Arg	Ser	Ser	Gly	Glu	Leu	Gly	Thr	Val	Phe	Ser	Tyr	Ile	Ala
		210				215						220				
	Lys	Ala	Arg	Ser	Ala	Gly	Gly	Gly	Arg	Glu	Met	Ser	Leu	Ser	Ala	Asn
					230					235					240	
	Gly	Ile	Leu	Ile	Phe	Ser	Asp	Pro	Phe	Ser	Met	Thr	Ser	Asn	Glu	Val
					245					250					255	
40	Ser	Asn	Ser	Tyr	Leu	Ala	Gly	Lys	Lys	Arg	Arg	Leu	Tyr	His	Ser	Thr
				260					265					270		
	Pro	Met	Asn	Ser	Leu	Val	Asn	Glu	Leu	Arg	Leu	Asp	Ala	Asn	Tyr	Ser
			275				280						285			
45	Met	Thr	Gly	Asp	Ala	Val	Asn	Leu	Asp	Phe	Ile	Glu	Val	Ala	Thr	Gln
		290					295					300				
	Asn	Asp	Leu	Arg	Tyr	Asp	Gly	Ala	Pro	Met	His	Ile	Arg	Arg	Phe	Ser
		305				310				315					320	
	Asn	Leu	Pro	Val	Leu	Gly	Gly	Glu	Ser	Cys	Arg	Phe	Val	Ile	Ser	Glu
				325					330					335		
50	Val	Pro	Glu	Ser	Leu	Val	Val	Leu	Gln	Ala	Asn	Ser	Ser	Leu	Thr	Ala
				340					345					350		
	Ser	Leu	Val	Pro	Val	Lys	Thr	Val	Gly	Asp	Lys	Thr	Ile	Glu	Phe	Val
				355				360					365			
55	Ala	Pro	Pro	Lys	Gly	Gln	Asp	Arg	Arg	Thr	Ile	Asn	Thr	Phe	Tyr	Ala
		370				375						380				
	Val	Asp	Leu	Ser	Gln	Ala	Ser	Ala	Pro	Glu	Ile	Leu	Gly	Ala	Val	Pro
					390					395					400	
	Asn	Gln	Asn	Leu	His	Gly	Glu	Glu	Ile	Pro	Asp	Leu	Ile	Ile	Val	Ser
				405					410					415		
60	Thr	Gln	Ala	Leu	Leu	Glu	Ala	Asp	Arg	Leu	Ala	Thr	Tyr	Arg	Arg	
				420				425					430			
	Glu	Lys	Asn	Gly	Leu	Lys	Val	Leu	Val	Val	Leu	Gln	Glu	Gln	Val	Phe
			435					440					445			
65	Asn	Glu	Phe	Ser	Gly	Gly	Thr	Pro	Asp	Ala	Thr	Ala	Tyr	Arg	Leu	Phe
		450				455						460				
	Ala	Lys	Met	Phe	Tyr	Asp	Arg	Trp	Lys	Ala	Asn	Ala	Pro	Val	Gly	Glu
		465				470				475					480	
	Thr	Phe	Pro	Met	Gln	Met	Leu	Leu	Phe	Gly	Asp	Gly	Ala	His	Asp	Asn
				485						490				495		
70	Arg	Lys	Val	Ser	Val	Ala	Trp	Gln	Lys	Pro	Tyr	Leu	Gln	Gln	Thr	Glu
				500					505					510		
	Phe	Leu	Leu	Thr	Phe	Gln	Ala	Val	Asn	Ser	Thr	Asn	Val	Asn	Ser	Tyr
				515			520						525			
75	Val	Thr	Asp	Asp	Tyr	Phe	Gly	Leu	Leu	Asp	Asp	Gln	Pro	Ala	Ser	Val
		530					535					540				

WO 99/29870

PCT/AU98/01023

315/ 490

	Asn	Ile	Gly	Trp	Arg	Asn	Tyr	Asn	Met	Ala	Val	Gly	Arg	Phe	Pro	Val
	545					550					555					560
	Arg	Thr	Pro	Ala	Glu	Ala	Arg	Ile	Ala	Val	Asp	Lys	Thr	Ile	Arg	Tyr
					565					570					575	
5	Glu	Glu	Asp	Arg	Glu	Ser	Gly	Ala	Trp	Arg	Ile	Arg	Ala	Cys	Phe	Ala
				580					585					590		
	Ala	Asp	Asn	Gly	Asp	Lys	His	Ala	Thr	Glu	Thr	Ser	Arg	Leu	Ile	Asp
		595						600					605			
10	Thr	Val	Lys	Arg	Tyr	Ala	Pro	Ala	Ile	Met	Pro	Val	Arg	Ala	Phe	Gln
		610					615					620				
	Asp	Val	Tyr	Pro	His	Val	Ile	Glu	Asn	Gly	Leu	His	Ser	Ile	Pro	Gly
		625				630					635					640
	Ala	Lys	Lys	Lys	Met	Leu	Glu	Thr	Leu	Gln	Ser	Gly	Ile	Ile	Leu	Leu
					645					650					655	
15	Asn	Tyr	Ala	Gly	His	Gly	Gly	Pro	Ala	Gly	Trp	Ser	Asp	Glu	His	Leu
				660					665					670		
	Leu	Thr	Leu	Asn	Asp	Ile	His	Lys	Phe	Asn	Tyr	Lys	His	Met	Pro	Ile
		675						680					685			
20	Trp	Ile	Thr	Ala	Thr	Cys	Asp	Phe	Ala	Asn	Tyr	Asp	Ser	Gln	Thr	Thr
		690					695					700				
	Ser	Ala	Gly	Glu	Glu	Val	Phe	Leu	His	Glu	Lys	Ser	Gly	Thr	Pro	Ile
		705				710					715					720
	Met	Phe	Ser	Thr	Thr	Arg	Val	Val	Tyr	Asn	Thr	Gln	Asn	Glu	Lys	Ile
					725					730					735	
25	Asn	Gly	Phe	Met	Leu	Arg	Arg	Met	Phe	Glu	Lys	Ala	Lys	Asp	Gly	Arg
				740					745					750		
	Tyr	Arg	Thr	Met	Gly	Glu	Ile	Ile	Arg	Ser	Ala	Lys	Gln	Gly	Met	Leu
		755						760					765			
30	Ser	Thr	Val	Phe	Pro	Asp	Ser	Ile	Asn	Gln	Leu	Ser	Phe	Phe	Leu	Met
		770					775					780				
	Gly	Asp	Pro	Ser	Val	Arg	Met	Asn	Leu	Pro	Thr	His	Lys	Val	Gln	Leu
		785					790					795				800
	Thr	Ala	Ile	Asn	Gly	Gln	Asp	Pro	Glu	Gly	Gln	Tyr	Gly	Thr	Ile	Met
					805					810					815	
35	Leu	Lys	Ser	Leu	Glu	Arg	Val	Ala	Leu	Lys	Gly	Lys	Val	Thr	Asp	Glu
				820					825					830		
	Lys	Gly	Thr	Phe	Asp	Glu	Thr	Phe	Ser	Gly	Lys	Val	Phe	Leu	Thr	Val
		835						840					845			
40	Phe	Asp	Gly	Arg	Lys	Lys	Met	Thr	Ala	Leu	Glu	Glu	Gly	Asn	Asp	
		850					855					860				
	Leu	Ser	Leu	Val	Tyr	Thr	Asp	Tyr	Pro	Asn	Val	Met	Tyr	Ala	Gly	Ile
		865				870					875					880
	Ala	Glu	Val	Lys	Asp	Gly	Leu	Phe	Glu	Thr	Ser	Phe	Ile	Val	Pro	Lys
				885					890					895		
45	Asp	Val	Asn	Tyr	Ser	Glu	His	Glu	Gly	Arg	Ile	Asn	Leu	Tyr	Ala	Tyr
				900					905					910		
	Asn	Glu	Ser	Thr	Lys	Ala	Glu	Ala	Met	Gly	Val	Asp	Phe	Ser	Ile	Arg
			915					920					925			
50	Val	Gln	Pro	Gly	Ile	Pro	Asp	Glu	Val	Thr	Glu	Asp	Asn	Thr	Pro	Pro
			930				935					940				
	Glu	Ile	Ile	Ser	Cys	Phe	Leu	Asn	Asp	Ser	Thr	Phe	Arg	Ser	Gly	Asp
			945			950					955					960
	Glu	Val	Asn	Pro	Thr	Pro	Leu	Phe	Met	Ala	Glu	Val	Phe	Asp	Leu	Asn
					965					970					975	
55	Gly	Ile	Asn	Ile	Thr	Gly	Ser	Gly	Val	Gly	His	Asp	Ile	Thr	Leu	Cys
				980					985					990		
	Ile	Asp	Gly	Arg	Ala	Asp	Leu	Thr	Tyr	Asn	Leu	Asn	Ala	Tyr	Phe	Thr
			995						1000					1005		
60	Ser	Ser	Ala	Thr	Asp	Ala	Gly	Val	Gly	Thr	Ile	Leu	Phe	Met	Ile	Pro
			1010					1015					1020			
	Ala	Leu	Ala	Glu	Gly	Asp	His	Thr	Ala	Arg	Leu	Thr	Val	Trp	Asp	Ile
			1025				1030					1035				1040
	Phe	Asn	Asn	Ala	Val	His	His	Asp	Phe	Ser	Phe	Arg	Val	Val	Asp	Gly
					1045					1050					1055	
65	Ile	Ala	Pro	Asp	Val	Ala	Asp	Val	Ile	Leu	Phe	Pro	Asn	Pro	Val	Arg
				1060					1065					1070		
	Glu	Ser	Ala	Thr	Phe	Arg	Ile	Phe	His	Asn	Arg	Pro	Gly	Ser	Asp	Leu
			1075					1080					1085			
70	Asn	Val	Ala	Val	Glu	Ile	Tyr	Asp	Phe	Thr	Gly	Arg	Leu	Val	Asn	Ser
				1090				1095					1100			
	Leu	Pro	Val	Lys	Thr	Tyr	Ser	Ser	Ser	Tyr	Gly	Glu	Pro	Ile	Glu	Ile
				1105				1110				1115				1120
	Lys	Trp	Asp	Leu	Thr	Ser	Lys	Tyr	Gly	Val	Lys	Ile	Gly	Asn	Gly	Phe
					1125					1130					1135	
75	Tyr	Leu	Tyr	Arg	Cys	Val	Val	Asn	Ser	Pro	Gly	Gly	Gln	Thr	Ala	Ser

316/ 490

1140 1145 1150
Met Ala Lys Lys Met Ile Val Val Gly Gln
1155 1160

5 (2) INFORMATION FOR SEQ ID NO:381

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 973 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

20 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...973

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:381

25 Phe Tyr Thr Gly Ile Asp Leu His Ile Glu Ser Gln Met Lys Lys Leu
1 5 10 15
Phe Pro Leu Leu Leu Ile Leu Ser Ile Leu Val Gly Cys Gly Lys
20 25 30
30 Lys Glu Lys His Ser Val Thr Glu Ile Ala Arg Glu Lys Lys Arg Ile
35 40 45
Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp Ser Val Lys Gln
50 55 60
Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val Gly Gln Met Leu
65 70 75 80
35 Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met Ser Gln Tyr Thr
85 90 95
Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala Ala Leu Asn Leu
100 105 110
40 Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His Leu Gly Thr Asp
115 120 125
Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp Tyr His Tyr Lys
130 135 140
45 Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln Asn Arg Pro Ala
145 150 155 160
Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly Asn Ile Asn Leu
165 170 175
Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe Leu Lys Ala Leu
180 185 190
50 Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln Ala Ile Asn Tyr
195 200 205
Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu Tyr Asp Lys Ala
210 215 220
Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Met Ala Glu Asn
225 230 235 240
55 Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly Glu Val Asp Glu
245 250 255
Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr Ala Thr Ala Tyr
260 265 270
60 Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp Leu Asn Ser Cys
275 280 285
Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn Glu Arg Leu Tyr
290 295 300
Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys Glu Ile Asn Ser
305 310 315 320
65 Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr Glu Asn Leu Glu
325 330 335
Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe Cys Leu Ser Lys
340 345 350
70 Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val Ser Ser Ile Gln
355 360 365
Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln Lys Glu Leu Glu
370 375 380
Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys Ser Lys Phe Ile
385 390 395 400
75 Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile Leu Leu Ile Ser

WO 99/29870

PCT/AU98/01023

318/490

(A) LENGTH: 563 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
10 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...563

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

20 His His Lys Thr Tyr Gln Thr Met Lys Lys Leu Leu Gln Ala Lys Ala
1 5 10 15
Leu Ile Leu Ala Leu Gly Leu Phe Gln Leu Pro Ala Ile Ala Gln Thr
20 25 30
Gln Met Gln Ala Asp Arg Thr Asn Gly Gln Phe Ala Thr Glu Glu Met
35 40 45
25 Gln Arg Ala Phe Gln Glu Thr Asn Pro Pro Ala Gly Pro Val Arg Ala
50 55 60
Ile Ala Glu Tyr Glu Arg Ser Ala Ala Val Leu Val Arg Tyr Pro Phe
65 70 75 80
Gly Ile Pro Met Glu Leu Ile Lys Glu Leu Ala Lys Asn Asp Lys Val
85 90 95
30 Ile Thr Ile Val Ala Ser Glu Ser Gln Lys Asn Thr Val Ile Thr Gln
100 105 110
Tyr Thr Gln Ser Gly Val Asn Leu Ser Asn Cys Asp Phe Ile Ile Ala
115 120 125
35 Lys Thr Asp Ser Tyr Trp Thr Arg Asp Tyr Thr Gly Trp Phe Ala Met
130 135 140
Tyr Asp Thr Asn Lys Val Gly Leu Val Asp Phe Ile Tyr Asn Arg Pro
145 150 155 160
Arg Pro Asn Asp Asp Glu Phe Pro Lys Tyr Glu Ala Gln Tyr Leu Gly
165 170 175
40 Ile Glu Met Phe Gly Met Lys Leu Lys Gln Thr Gly Gly Asn Tyr Met
180 185 190
Thr Asp Gly Tyr Gly Ser Ala Val Gln Ser His Ile Ala Tyr Thr Glu
195 200 205
45 Asn Ser Ser Leu Ser Gln Ala Gln Val Asn Gln Lys Met Lys Asp Tyr
210 215 220
Leu Gly Ile Thr His His Asp Val Val Gln Asp Pro Asn Gly Glu Tyr
225 230 235 240
Ile Asn His Val Asp Cys Trp Gly Lys Tyr Leu Ala Pro Asn Lys Ile
245 250 255
50 Leu Ile Arg Lys Val Pro Asp Asn His Pro Gln His Gln Ala Leu Glu
260 265 270
Asp Met Ala Ala Tyr Phe Ala Ala Gln Thr Cys Ala Trp Gly Thr Lys
275 280 285
55 Tyr Glu Val Tyr Arg Ala Leu Ala Thr Asn Glu Gln Pro Tyr Thr Asn
290 295 300
Ser Leu Ile Leu Asn Asn Arg Val Phe Val Pro Val Asn Gly Pro Ala
305 310 315 320
Ser Val Asp Asn Asp Ala Leu Asn Val Tyr Lys Thr Ala Met Pro Gly
325 330 335
60 Tyr Glu Ile Ile Gly Val Lys Gly Ala Ser Gly Thr Pro Trp Leu Gly
340 345 350
Thr Asp Ala Leu His Cys Arg Thr His Glu Val Ala Asp Lys Gly Tyr
355 360 365
65 Leu Tyr Ile Lys His Tyr Pro Ile Leu Gly Glu Gln Ala Gly Pro Asp
370 375 380
Tyr Lys Ile Glu Ala Asp Val Val Ser Cys Ala Asn Ala Thr Ile Ser
385 390 395 400
Pro Val Gln Cys Tyr Tyr Arg Ile Asn Gly Ser Gly Ser Phe Lys Ala
405 410 415
70 Ala Asp Met Thr Met Glu Ser Thr Gly His Tyr Thr Tyr Ser Phe Thr
420 425 430
Gly Leu Asn Lys Asn Asp Lys Val Glu Tyr Tyr Ile Ser Ala Ala Asp
435 440 445
75 Asn Ser Gly Arg Lys Glu Thr Tyr Pro Phe Ile Gly Glu Pro Asp Pro
450 455 460

WO 99/29870

PCT/AU98/01023

321/ 490

Gln Asn Ser Ile Ile Asn Lys Lys Leu Asn Val Thr Gln Leu
305 310 315

(2) INFORMATION FOR SEQ ID NO:385

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

Arg Arg Ala Val Lys Ile Arg Ser Pro Pro His Ile His Ser Leu Phe
1 5 10 15
Val Arg Lys Cys Leu Phe Ser Asp Phe Lys Tyr Leu Tyr Leu Ser Arg
20 25 30
Lys Ile Thr Gln Glu Arg Leu Gly Arg Leu Ser Ile Arg Leu Lys Ser
35 40 45
Tyr Asn Pro Ile Ile Ile Ile Glu Met Lys Lys Thr Thr Ile Ile Ser
50 55 60
Leu Ile Val Phe Gly Ala Phe Phe Ala Val Gly Gln Thr Lys Asp
65 70 75 80
Asn Ser Ser Tyr Lys Pro Phe Ser Lys Glu Asp Ile Ala Gly Gly Val
85 90 95
Tyr Ser Leu Pro Thr Gln Asn Arg Ala Gln Lys Asp Asn Ala Glu Trp
100 105 110
Leu Leu Thr Ala Thr Val Ser Thr Asn Gln Ser Ala Asp Thr His Phe
115 120 125
Ile Phe Asp Glu Asn Asn Arg Tyr Ile Ala Arg Asp Ile Lys Ala Asn
130 135 140
Gly Val Arg Lys Ser Thr Asp Ser Ile Tyr Tyr Asp Ala Asn Gly Arg
145 150 155 160
Ile Ser His Val Asp Leu Tyr Ile Ser Phe Ser Gly Gly Glu Pro Ala
165 170 175
Leu Asp Thr Arg Phe Lys Tyr Thr Tyr Asp Asp Glu Gly Lys Met Thr
180 185 190
Val Arg Glu Val Phe Met Leu Val Met Asp Pro Asn Thr Pro Ile Ser
195 200 205
Arg Leu Glu Tyr His Tyr Asp Ala Gln Gly Arg Leu Thr His Trp Ile
210 215 220
Ser Phe Ala Phe Gly Ala Glu Ser Gln Lys Asn Thr Tyr His Tyr Asn
225 230 235 240
Glu Lys Gly Leu Leu Val Ser Glu Val Leu Ser Asn Ala Met Gly Thr
245 250 255
Thr Tyr Ser Asp Thr Gly Lys Thr Glu Tyr Ser Tyr Asp Asp Ala Asp
260 265 270
Asn Met Val Lys Ala Glu Tyr Phe Val Val Gln Gln Gly Lys Ala Trp
275 280 285
Gln Val Leu Lys Arg Glu Glu Tyr Thr Tyr Glu Asp Asn Ile Cys Ile
290 295 300
Gln Tyr Leu Ala Ile Asn Gly Thr Asp Thr Lys Val Tyr Lys Arg Asp
305 310 315 320
Ile Glu Ser Asp Lys Ser Ile Ser Ala Asn Val Ile Asp Ile Pro Ser
325 330 335
Met Pro Glu Gln Thr Trp Pro Asn Met Tyr Gly Phe Asn Ala Lys Arg
340 345 350
Leu Lys Glu Thr Tyr Ser Ser Tyr Glu Gly Asp Val Ala Thr Pro Ile
355 360 365
Phe Asp Tyr Ile Tyr Thr Tyr Lys Ala Leu Thr Ser Met Ala Thr Pro
370 375 380
Ser Thr Glu Ala Gln Val Ala Val Tyr Leu Asn Pro Ser Thr Asp Arg
385 390 395 400
Leu Val Ile Leu Ala Asn Gly Ile Thr His Leu Ser Met Tyr Asp Leu
405 410 415

WO 99/29870

PCT/AU98/01023

322/490

Gln Gly Lys Leu Ile Arg Asp Cys Ala Leu Ser Gly Asp Lys Val Glu
420 425 430
Met Gly Val Gly Ser Leu Thr Lys Gly Thr Tyr Leu Leu Lys Val Asn
435 440 445
5 Thr Asp Gln Gly Ala Phe Val Arg Lys Val Val Ile Arg
450 455 460

(2) INFORMATION FOR SEQ ID NO:386

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
- 20 (iv) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...451
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu Asn Leu Lys
1 5 10 15
30 Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln Ser Pro Thr
20 25 30
Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro Lys Val Thr
35 40 45
Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu Met His His
50 55 60
Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser Gly Glu Val
65 70 75 80
Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser Ile Glu Val
85 90 95
40 Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val Gly Asp Pro
100 105 110
Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Ser Ser Gly
115 120 125
45 Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val Ala Thr Pro
130 135 140
Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe Thr Ala Pro
145 150 155 160
Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu Arg Ala Leu
165 170 175
50 Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly Lys Val Tyr
180 185 190
Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn Ala Glu Ile
195 200 205
55 Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly Val Leu Ile
210 215 220
Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp Thr Leu Lys
225 230 235 240
Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr Gly Lys Ala
245 250 255
60 Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala Ala Ala His
260 265 270
Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala Ser Phe Pro
275 280 285
Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile Asp Gly Asn
290 295 300
65 Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe Leu Ser Ala
305 310 315 320
Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp Val Asp Glu
325 330 335
70 Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser Met Ser Arg
340 345 350
Ala Tyr Phe Ser Trp Leu Gln Gly Lys Asn Lys Glu Tyr Val Leu Asp
355 360 365
75 Ala Arg Ile Lys Gly Gly Glu Arg Ala Met Ile Met Ser Asn Glu Tyr
370 375 380

WO 99/29870

PCT/AU98/01023

324/ 490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:388

5 Met Lys Lys Ala Leu Leu Ile Gly Ala Ala Leu Leu Gly Ala Val Ser
1 5 10 15
Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile Lys Val Gln Asn Asn Ser
20 25 30
Val Gln Gln Pro Arg Glu Glu Ala Thr Ile Gln Val Cys Gly Glu Leu
35 40 45
10 Ala Glu Gln Val Asp Cys Ile Gly Thr Gly Asn Ser Ala Ile Ile Ala
50 55 60
Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu Glu Ser Tyr Val Gly Trp
65 70 75 80
Glu Ile Met Ser Val Asp Phe Phe Pro Gly Tyr Lys Ala Cys Lys Tyr
85 90 95
15 Thr Ser Ala Val Trp Ala Asp Asp Met Thr Ile Leu Gly Gln Ser Glu
100 105 110
Asp Ser Asp Pro Glu Met Gln Thr Ile Asn Asn Leu Ala Leu Lys Thr
115 120 125
20 Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr Ile Val Gly Tyr Ile Ala
130 135 140
Asn Thr Ala Gly Gly His Pro Ile Gly Cys Asp Gln Gly Pro Ala Val
145 150 155 160
Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser Glu Asp Gly Gly Ala Thr
165 170 175
25 Phe Pro Pro Phe Glu Ser Leu His Gln Ala Val Pro Thr Leu Asn Tyr
180 185 190
Asn Ile Tyr Val Val Val His Leu Lys Lys Gly Glu Gly Val Glu Ala
195 200 205
30 Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr Val Gln Asn Gly Val Ile
210 215 220
Tyr Val Ala Gly Ala Asn Gly Arg Gln Val Ser Leu Phe Asp Met Asn
225 230 235 240
35 Gly Lys Val Val Tyr Thr Gly Val Ser Glu Thr Ile Ala Ala Pro Gln
245 250 255
Lys Gly Met Tyr Ile Leu Arg Val Gly Ala Lys Ser Ile Lys Leu Ala
260 265 270
Ile

(2) INFORMATION FOR SEQ ID NO:389

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION 1...554

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:389

60 Met Pro Arg Ile Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala
1 5 10 15
Thr Phe Ala Ile Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp
20 25 30
65 Ile Gly Gly Asp Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly
35 40 45
Tyr Ser Glu Asp Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp
50 55 60
70 Ile Tyr Val Met Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg
65 70 75 80
Leu Tyr Arg Ser Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser
85 90 95
Leu Gly Ser Leu Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe
100 105 110
75 Ile Val Thr Gly Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met

WO 99/29870

PCT/AU98/01023

326/ 490

Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile
1 5 10 15
5 Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp
20 25 30
Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp
35 40 45
Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met
50 55 60
10 Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser
65 70 75 80
Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser Leu Gly Ser Leu
85 90 95
15 Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe Ile Val Thr Gly
100 105 110
Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met Thr Ala Phe Glu
115 120 125
Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu Met His Arg His
130 135 140
20 Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys Lys Asp Phe Pro
145 150 155 160
Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro
165 170 175
25 Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val
180 185 190
Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu
195 200 205
Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln
210 215 220
30 Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro
225 230 235 240
Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met
245 250 255
35 Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val
260 265 270
Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile Ile Ile Glu Glu
275 280 285
Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu
290 295 300
40 Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr Val Gly Gly Glu
305 310 315 320
Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro
325 330 335
45 Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp
340 345 350
Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys
355 360 365
Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg
370 375 380
50 Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser
385 390 395 400
Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg
405 410 415
55 Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp
420 425 430
His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro
435 440 445
Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala
450 455 460
60 Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr
465 470 475 480
Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly
485 490 495
65 Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys
500 505 510
Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser
515 520 525
Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val
530 535 540
70 Glu Lys Ile Ile Val Glu
545 550

(2) INFORMATION FOR SEQ ID NO:391

75

WO 99/29870

PCT/AU98/01023

327/490

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391
- Met Lys Arg Leu Leu Pro Phe Leu Leu Leu Ala Gly Leu Val Ala Val
 1 5 10 15
 Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val His
 20 25 30
 Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser Val
 35 40 45
 Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr Ile
 50 55 60
 Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile Asp
 65 70 75 80
 Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe Asp
 85 90 95
 Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly Ser
 100 105 110
 Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr Pro
 115 120 125
 Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro Phe
 130 135 140
 Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr Leu
 145 150 155 160
 Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln Gln
 165 170 175
 Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu Phe
 180 185 190
 Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu Pro
 195 200 205
 Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr Asp
 210 215 220
 Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr Leu
 225 230 235 240
 Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser Ser
 245 250 255
 Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro Asn
 260 265 270
 Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser Gly
 275 280 285
 Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp Met
 290 295 300
 Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys Ile
 305 310 315 320
 Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln Leu
 325 330 335
 Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala Thr
 340 345 350
 Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro Arg
 355 360 365
 Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile Arg
 370 375 380
 Ala Lys Val Ser Leu Arg
 385 390
- (2) INFORMATION FOR SEQ ID NO:392
- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

328/ 490

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
(A) NAME/KLY: misc_feature
(B) LOCATION 1...411
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392
- Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu Leu
1 5 10 15
Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys Gln
20 25 30
Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro Asp
35 40 45
Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln Glu
50 55 60
Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe Pro
65 70 75
Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly Ile
80 85 90
Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile Ser
100 105 110
Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro Val
115 120 125
Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe Trp
130 135 140
Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp Lys
145 150 155
Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val Ile
160 165 170
Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met Trp
180 185 190
Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu Ser
195 200 205
Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly Tyr
210 215 220
Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp Phe
225 230 235
Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys Cys
240 245 250
Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met Ala
255 260 265
Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu Arg
270 275 280
Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg Lys
285 290 295
Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu Gly
300 305 310
Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala Ile
315 320 325
Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln Ala
330 335 340
Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg Pro
345 350 355
Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu Ile
360 365 370
Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu Thr
375 380 385
Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro
390 395 400
405 410
- (2) INFORMATION FOR SEQ ID NO:393
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

WO 99/29870

PCT/AU98/01023

329/ 490

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

Met	Lys	Val	Gly	Leu	Phe	Ile	Pro	Cys	Tyr	Val	Asn	Ala	Val	Tyr	Pro
1				5					10					15	
Glu	Val	Gly	Ile	Ala	Thr	Tyr	Lys	Leu	Lys	Ser	Leu	Asp	Ile	Asp	
			20					25				30			
Val	Asp	Tyr	Pro	Met	Asp	Gln	Thr	Cys	Cys	Gly	Gln	Pro	Met	Ala	Asn
			35				40					45			
Ala	Gly	Phe	Glu	Gln	Lys	Ala	Gln	Lys	Leu	Ala	Leu	Arg	Phe	Glu	Glu
			50				55					60			
Leu	Phe	Glu	Ser	Tyr	Asp	Val	Val	Val	Gly	Pro	Ser	Ala	Ser	Cys	Val
			65				70					75			80
Ala	Phe	Val	Lys	Glu	Asn	Tyr	Asp	His	Ile	Leu	Arg	Pro	Thr	Gly	His
			85					90						95	
Val	Cys	Lys	Ser	Ala	Ala	Lys	Val	Arg	Asp	Ile	Cys	Glu	Phe	Leu	His
			100					105				110			
Asp	Asp	Leu	Lys	Ile	Thr	Ser	Leu	Pro	Ser	Arg	Phe	Ala	His	Lys	Val
			115				120					125			
Ser	Leu	His	Asn	Ser	Cys	His	Gly	Val	Arg	Glu	Leu	His	Leu	Ser	Thr
			130				135					140			
Pro	Ser	Glu	Val	His	Arg	Pro	Tyr	His	Asn	Lys	Val	Arg	Arg	Leu	Leu
			145				150					155			160
Glu	Met	Val	Gln	Gly	Ile	Glu	Val	Phe	Glu	Pro	Lys	Arg	Ile	Asp	Glu
			165					170						175	
Cys	Cys	Gly	Phe	Gly	Gly	Met	Tyr	Ser	Val	Glu	Glu	Pro	Glu	Val	Ser
			180					185					190		
Thr	Cys	Met	Gly	His	Asp	Lys	Val	Leu	Asp	His	Ile	Ser	Thr	Gly	Ala
			195				200					205			
Glu	Tyr	Ile	Thr	Gly	Pro	Asp	Ser	Ser	Cys	Leu	Met	His	Met	Gln	Gly
			210				215					220			
Val	Ile	Asp	Arg	Glu	Lys	Leu	Pro	Ile	Lys	Thr	Ile	His	Ala	Val	Glu
			225				230				235				240
Ile	Leu	Ala	Ala	Asn	Leu										
				245											

(2) INFORMATION FOR SEQ ID NO:394

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ji) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

Met	Asp	Ile	Val	Ser	Met	Ala	Asp	Lys	Ala	Leu	Val	Val	Glu	Met	Arg
1				5					10					15	
Asp	Val	Thr	Leu	Cys	Gln	Glu	Glu	Asn	Val	Ile	Phe	Gln	Asn	Leu	Asn
			20					25					30		
Leu	Thr	Leu	Ser	Ala	Gly	Asp	Phe	Val	Tyr	Leu	Ile	Gly	Ser	Val	Gly
			35				40					45			
Ser	Gly	Lys	Ser	Thr	Leu	Leu	Lys	Ala	Leu	Tyr	Ala	Glu	Val	Pro	Ile
			50				55					60			
Ser	Ala	Gly	Tyr	Ala	Arg	Val	Ile	Asp	Tyr	Asp	Leu	Ala	Lys	Leu	Lys
			65				70				75			80	

WO 99/29870

PCT/AU98/01023

330/490

Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln
85 90 95
Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe
100 105 110
5 Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg
115 120 125
Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys
130 135 140
Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala
145 150 155 160
10 Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr
165 170 175
Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr
180 185 190
15 Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His Asn Ser
195 200 205
Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn
210 215 220
20 Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg
225 230 235 240
Lys Asn Thr Glu Ile Asp

(2) INFORMATION FOR SEQ ID NO:395

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

Met Ala Asp Lys Ala Leu Val Val Glu Met Arg Asp Val Thr Leu Cys
1 5 10 15
Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala
20 25 30
Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly Ser Gly Lys Ser Thr
35 40 45
50 Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala
50 55 60
Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro
65 70 75 80
55 Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln Asp Phe Gln Leu Leu
85 90 95
Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe Val Leu Arg Ala Thr
100 105 110
Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg Ile Glu Glu Val Leu
115 120 125
60 Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys Arg Pro His Glu Leu
130 135 140
Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala Arg Ala Leu Leu Ala
145 150 155 160
Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser
165 170 175
65 Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln
180 185 190
Gly Thr Ala Val Leu Met Ser Thr His Asn Ser Ser Leu Leu Ser His
195 200 205
70 Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn Gly Asp Ala Ser Ser
210 215 220
Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg Lys Asn Thr Glu Ile
225 230 235
75 Asp

331/ 490

(2) INFORMATION FOR SEQ ID NO:396

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

15 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...232

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile Phe Gln Asn
 1 5 10 15
 Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu Ile Gly Ser
 20 25 30
 Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr Ala Glu Val
 35 40 45
 Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp Leu Ala Lys
 50 55 60
 Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val
 65 70 75 80
 Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu
 85 90 95
 Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu
 100 105 110
 Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala
 115 120 125
 Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly
 130 135 140
 Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu
 145 150 155 160
 Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu
 165 170 175
 Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His
 180 185 190
 Asn Ser Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg
 195 200 205
 Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val
 210 215 220
 Ser Arg Lys Asn Thr Glu Ile Asp
 225 230

(2) INFORMATION FOR SEQ ID NO:397

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...219

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr Glu Glu Ile
 1 5 10 15
 Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp Lys Gly Glu

332/ 490

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      20      25      30
Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu
  35      40      45
5  Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile Tyr Lys Leu
   50      55      60
   Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg Thr Ala Val
   65      70      75      80
   Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn Leu Ile Glu
      85      90      95
10  Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val Tyr Leu Gly
    100      105      110
    Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala Leu Arg Lys
    115      120      125
15  Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln Leu Ser Gly
    130      135      140
    Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val Ala Asn Pro
    145      150      155      160
    Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Lys Asn
    165      170      175
20  Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg Glu Gly Ala
    180      185      190
    Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg Ser Ala Gly
    195      200      205
25  Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg
    210      215

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(2) INFORMATION FOR SEQ ID NO:398

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 595 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...595
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

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Met Lys Glu Phe Phe Lys Met Phe Phe Ala Ser Ile Leu Gly Val Ile
  1      5      10      15
10  Thr Ala Gly Ile Ile Leu Phe Cys Ile Phe Leu Phe Ile Phe Gly
    20      25      30
15  Ile Val Ala Gly Ile Ala Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys
    35      40      45
20  Ile Glu Ala Asn Ser Ile Leu His Ile Unk Asn Ser Ser Phe Pro Glu
    50      55      60
25  Ile Val Ser Ala Asn Pro Trp Ser Met Leu Thr Gly Lys Asp Glu Ser
    65      70      75      80
    Val Ser Leu Ser Gln Ala Val Glu Ala Ile Gly Gln Ala Lys Asn Asn
    85      90      95
30  Pro Asn Ile Thr Gly Ile Phe Leu Asp Leu Asp Asn Leu Ser Val Gly
    100      105      110
35  Met Ala Ser Ala Glu Glu Leu Arg Arg Ala Leu Gln Asp Phe Lys Met
    115      120      125
40  Ser Gly Lys Phe Val Val Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly
    130      135      140
45  Tyr Tyr Leu Ser Ser Ile Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly
    145      150      155      160
50  Met Leu Gly Leu Ile Gly Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp
    165      170      175
55  Ala Leu Asp Lys Phe Gly Val Lys Met Glu Ile Phe Lys Val Gly Thr
    180      185      190
60  Tyr Lys Ala Ala Val Glu Pro Phe Met Leu Asn Arg Met Ser Asp Ala
    195      200      205
65  Asn Arg Glu Gln Ile Thr Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile
    210      215      220
70  Thr Ser Asp Ile Ala Glu Ser Arg Lys Thr Ala Met Asp Ser Val Lys
    225
75

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WO 99/29870

PCT/AU98/01023

333/490

225 230 235 240
Met Phe Ala Asp Lys Gly Glu Met Phe Gly Leu Ala Glu Lys Ala Val
245 250 255
5 Glu Met Lys Leu Val Asp Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys
260 265 270
Glu Leu Lys Lys Met Ser Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe
275 280 285
Val Ser Leu Ser Gln Val Leu Ala Asn Gly Pro Met Asn Lys Thr Lys
290 295 300
10 Gly Ser Arg Ile Ala Val Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu
305 310 315 320
Ile Ile Lys Lys Pro Phe Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu
325 330 335
15 Leu Ala Lys Glu Ile Lys Ala Ala Ala Asp Asp Asp Ile Lys Ala
340 345 350
Val Val Leu Arg Val Asn Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu
355 360 365
Gln Ile Trp Lys Gln Val Ala Asp Leu Lys Ala Lys Lys Pro Ile Val
370 375 380
20 Val Ser Met Gly Asp Val Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys
385 390 395 400
Ala Ala Asn Ser Ile Val Ala Glu His Thr Thr Leu Thr Gly Ser Ile
405 410 415
25 Gly Ile Phe Gly Met Phe Pro Asn Phe Ala Gly Val Ala Lys Lys Ile
420 425 430
Gly Val Asn Met Asp Val Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly
435 440 445
Asn Thr Phe Ala Pro Met Thr Val Glu Asp Arg Ala Leu Ile Gln Arg
450 455 460
30 Tyr Ile Glu Gln Gly Tyr Asp Leu Phe Leu Thr Arg Val Ser Glu Gly
465 470 475 480
Arg Asn Arg Thr Lys Ala Gln Ile Asp Ser Ile Ala Gln Gly Arg Val
485 490 495
35 Trp Leu Gly Asp Lys Ala Leu Ala Leu Gly Leu Val Asp Glu Leu Gly
500 505 510
Gly Leu Asp Thr Ala Ile Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly
515 520 525
Gly Asn Tyr Ser Ile Glu Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu
530 535 540
40 Glu Leu Leu Ser Ser Ser Ala Ala Asp Met Lys Ser Ala Ile Leu Ser
545 550 555 560
Thr Ile Leu Ser Asp Pro Glu Ile Glu Val Leu Arg Glu Leu Arg Ser
565 570 575
45 Met Pro Pro Arg Pro Ser Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe
580 585 590
Met Pro Tyr
595

(2) INFORMATION FOR SEQ ID NO:399

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 589 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

60

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...589

65

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:399

70 Met Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu
1 5 10 15
Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala
20 25 30
Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile
35 40 45
75 Leu His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro

WO 99/29870

PCT/AU98/01023

334/ 490

	50		55		60											
	Trp	Ser	Met	Leu	Thr	Gly	Lys	Asp	Glu	Ser	Val	Ser	Leu	Ser	Gln	Ala
	65					70					75					80
5	Val	Glu	Ala	Ile	Gly	Gln	Ala	Lys	Asn	Asn	Pro	Asn	Ile	Thr	Gly	Ile
					85						90				95	
	Phe	Leu	Asp	Leu	Asp	Asn	Leu	Ser	Val	Gly	Met	Ala	Ser	Ala	Glu	Glu
					100					105				110		
	Leu	Arg	Arg	Ala	Leu	Gln	Asp	Phe	Lys	Met	Ser	Gly	Lys	Phe	Val	Val
					115				120					125		
10	Ser	Tyr	Ala	Asp	Arg	Tyr	Thr	Gln	Lys	Gly	Tyr	Tyr	Leu	Ser	Ser	Ile
					130				135					140		
	Ala	Asp	Lys	Leu	Tyr	Leu	Asn	Pro	Lys	Gly	Met	Leu	Gly	Leu	Ile	Gly
					145						155					160
15	Ile	Ala	Thr	Gln	Thr	Met	Phe	Tyr	Lys	Asp	Ala	Leu	Asp	Lys	Phe	Gly
					165					170					175	
	Val	Lys	Met	Glu	Ile	Phe	Lys	Val	Gly	Thr	Tyr	Lys	Ala	Ala	Val	Glu
					180					185					190	
	Pro	Phe	Met	Leu	Asn	Arg	Met	Ser	Asp	Ala	Asn	Arg	Glu	Gln	Ile	Thr
					195				200					205		
20	Thr	Tyr	Ile	Asn	Gly	Leu	Trp	Asp	Lys	Ile	Thr	Ser	Asp	Ile	Ala	Glu
					210				215					220		
	Ser	Arg	Lys	Thr	Ala	Met	Asp	Ser	Val	Lys	Met	Phe	Ala	Asp	Lys	Gly
					225						235					240
	Glu	Met	Phe	Gly	Leu	Ala	Glu	Lys	Ala	Val	Glu	Met	Lys	Leu	Val	Asp
25					245					250					255	
	Glu	Leu	Ala	Tyr	Arg	Thr	Asp	Val	Glu	Lys	Glu	Leu	Lys	Lys	Met	Ser
					260				265						270	
	Gln	Arg	Gly	Glu	Lys	Asp	Glu	Leu	Arg	Phe	Val	Ser	Leu	Ser	Gln	Val
					275				280					285		
30	Leu	Ala	Asn	Gly	Pro	Met	Asn	Lys	Thr	Lys	Gly	Ser	Arg	Ile	Ala	Val
					290				295					300		
	Leu	Phe	Ala	Glu	Gly	Glu	Ile	Thr	Glu	Glu	Ile	Ile	Lys	Lys	Pro	Phe
					305					310					315	
35	Asp	Thr	Asp	Gly	Ser	Ser	Ile	Thr	Gln	Glu	Leu	Ala	Lys	Glu	Ile	Lys
					325					330					335	
	Ala	Ala	Ala	Asp	Asp	Asp	Asp	Ile	Lys	Ala	Val	Val	Leu	Arg	Val	Asn
					340					345					350	
	Ser	Pro	Gly	Gly	Ser	Ala	Phe	Thr	Ser	Glu	Gln	Ile	Trp	Lys	Gln	Val
					355					360				365		
40	Ala	Asp	Leu	Lys	Ala	Lys	Lys	Pro	Ile	Val	Val	Ser	Met	Gly	Asp	Val
					370					375				380		
	Ala	Ala	Ser	Gly	Gly	Tyr	Tyr	Ile	Ala	Cys	Ala	Ala	Asn	Ser	Ile	Val
					385					390					400	
45	Ala	Glu	His	Thr	Thr	Leu	Thr	Gly	Ser	Ile	Gly	Ile	Phe	Gly	Met	Phe
					405					410					415	
	Pro	Asn	Phe	Ala	Gly	Val	Ala	Lys	Lys	Ile	Gly	Val	Asn	Met	Asp	Val
					420					425					430	
	Val	Gln	Thr	Ser	Lys	Tyr	Ala	Asp	Leu	Gly	Asn	Thr	Phe	Ala	Pro	Met
					435					440					445	
50	Thr	Val	Glu	Asp	Arg	Ala	Leu	Ile	Gln	Arg	Tyr	Ile	Glu	Gln	Gly	Tyr
					450					455					460	
	Asp	Leu	Phe	Leu	Thr	Arg	Val	Ser	Glu	Gly	Arg	Asn	Arg	Thr	Lys	Ala
					465					470					475	
	Gln	Ile	Asp	Ser	Ile	Ala	Gln	Gly	Arg	Val	Trp	Leu	Gly	Asp	Lys	Ala
55					485					490					495	
	Leu	Ala	Leu	Gly	Leu	Val	Asp	Glu	Leu	Gly	Gly	Leu	Asp	Thr	Ala	Ile
					500					505					510	
	Lys	Arg	Ala	Ala	Lys	Leu	Ala	Gln	Leu	Gly	Gly	Asn	Tyr	Ser	Ile	Glu
					515					520					525	
60	Tyr	Gly	Lys	Thr	Lys	Arg	Asn	Phe	Phe	Glu	Glu	Leu	Leu	Ser	Ser	Ser
					530					535					540	
	Ala	Ala	Asp	Met	Lys	Ser	Ala	Ile	Leu	Ser	Thr	Ile	Leu	Ser	Asp	Pro
					545						555				560	
65	Glu	Ile	Glu	Val	Leu	Arg	Glu	Leu	Arg	Ser	Met	Pro	Pro	Arg	Pro	Ser
					565					570					575	
	Gly	Ile	Gln	Ala	Arg	Leu	Pro	Tyr	Tyr	Phe	Met	Pro	Tyr			
					580					585						

(2) INFORMATION FOR SEQ ID NO:400

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

WO 99/29870

PCT/AU98/01023

335 / 490

(ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 10 (B) LOCATION: 1...313
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400
 15 Met Arg Ala Asn Ile Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe
 1 5 10 15
 Phe Gly Thr Ala Ile Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu
 20 20 25 30
 Ala Tyr Val Lys Gln Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg
 35 40 45
 20 Tyr Asn Ile Pro Ala Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr
 50 55 60
 Gly Ala Gly Ala Ser Thr Leu Ala Ser Val His Asn His Phe Gly
 65 70 75 80
 Ile Lys Cys His Lys Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp
 85 90 95
 25 Asp Ala Pro Asn Glu Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser
 100 105 110
 Tyr Glu Asp His Ser Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu
 115 120 125
 30 Phe Lys Leu Asp Arg Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln
 130 135 140
 Arg Cys Gly Tyr Ala Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys
 145 150 155 160
 35 Met Val Glu Leu Tyr Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro
 165 170 175
 Ser Trp Phe His Lys Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln
 180 185 190
 Thr Thr Lys Gln Lys Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser
 195 200 205
 40 Tyr Gly Leu Leu Tyr Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser
 210 215 220
 Leu Ala Glu Glu Phe Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn
 225 230 235 240
 45 Asp Ala Pro Val Asp Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu
 245 250 255
 Glu Lys Lys His Ala Cys Ser Ile Ser Lys His Thr Gln His Val Val
 260 265 270
 Arg Val Gly Asp Ser Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg
 275 280 285
 50 Met Lys Asn Leu Tyr Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro
 290 295 300
 Gln Glu Gly Asp Ile Leu Arg Leu Arg
 305 310
 55 (i) INFORMATION FOR SEQ ID NO:401
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 523 amino acids
 60 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 65 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 70 (B) LOCATION: 1...523
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401
 75 Met Asp Gly Arg Arg Tyr Ser Asp Gly Leu His Gln Ala Ile Glu Ala

336/ 490

1 Lys Glu His Val 5 Lys Val Glu Ala Ala 10 Thr Gln Thr Phe Ala Thr Ile
 20 Thr Leu Gln Asn Tyr Phe Arg Met Tyr His Lys Leu Ala Gly Met Thr
 35 Gly Thr Ala Glu Thr Glu Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu
 50 Asp Val Val Val Ile Pro Thr Asn Lys Pro Ile Ala Arg Lys Asp Met
 65 Asn Asp Arg Ile Tyr Lys Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile
 85 Glu Glu Ile Val Arg Leu Val Glu Glu Gly Arg Pro Val Leu Val Gly
 100 Thr Thr Ser Val Glu Ile Ser Glu Leu Leu Ser Arg Met Leu Arg Leu
 115 Arg Gly Ile Gln His Asn Val Leu Asn Ala Lys Leu His Gln Lys Glu
 130 Ala Glu Ile Val Ala Gln Ala Gly Gln Lys Gly Thr Val Thr Ile Ala
 145 Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Ser Ala Glu Val
 165 Lys Lys Ala Gly Glu Leu Ala Ile Ile Gly Thr Glu Arg His Glu Ser
 180 Arg Arg Val Asp Arg Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp
 195 Pro Gly Ser Ser Ile Phe Tyr Val Ser Leu Glu Asp His Leu Met Arg
 210 Leu Phe Ala Thr Glu Lys Ile Ala Ser Leu Met Asp Arg Leu Gly Phe
 225 Lys Glu Gly Glu Val Leu Glu Asn Asn Met Leu Ser Lys Ser Val Glu
 245 Arg Ala Gln Lys Lys Val Glu Glu Asn Asn Phe Gly Ile Arg Lys His
 260 Leu Leu Glu Tyr Asp Asp Val Met Asn Ser Gln Arg Glu Val Ile Tyr
 275 Thr Arg Arg Arg His Ala Leu Met Gly Glu Arg Ile Gly Met Asp Val
 290 Leu Asn Thr Ile Tyr Asp Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala
 305 Glu Ala Asn Asp Phe Glu Gly Phe Lys Glu Asp Leu Met Arg Ala Leu
 325 Ala Ile Glu Ser Pro Ile Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala
 340 Glu Glu Leu Thr Asp Met Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln
 355 Arg Lys Met Asp Leu Ile Ala Glu Val Ala His Pro Val Val His Gln
 370 Val Phe Glu Thr Gln Ala Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile
 385 Thr Asp Gly Lys Arg Val Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala
 405 Asp Glu Thr Gln Gly Lys Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile
 420 Val Leu His Thr Ile Asp Glu Ser Trp Lys Glu His Leu Arg Glu Met
 435 Asp Glu Leu Arg Asn Ser Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp
 450 Pro Leu Leu Ile Tyr Lys Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met
 465 Val Glu Ala Met Asn Arg Lys Thr Val Ala Ile Leu Met Arg Ala Arg
 485 Ile Pro Val Pro Glu Ala Pro Ser Gln Glu Glu Leu Glu His Arg Arg
 500 Gln Ile Glu Ile Arg His Ala Thr Gln Gln Arg
 515

(2) INFORMATION FOR SEQ ID NO:402

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

WO 99/29870

PCT/AU98/01023

338/ 490

(A) NAME/KEY: misc_feature
(B) LOCATION 1...362

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:403

5
Met Ile Tyr Leu Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu
1 5 10 15
Arg Ala Val Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg
20 25 30
Val Ser Leu Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln
35 40 45
Val Glu Lys Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly
50 55 60
Asn Ala Leu Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile
65 70 75 80
Lys Ala Leu Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn
85 90 95
Ile Phe Ile Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile
100 105 110
20 Phe Thr Ile Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile
115 120 125
Thr Lys Arg Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val
130 135 140
Ala Leu Thr Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly
145 150 155 160
25 Arg Ser Lys Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val
165 170 175
Gln Arg Asp Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu
180 185 190
30 Thr Tyr Gln Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val
195 200 205
Leu Arg Glu Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu
210 215 220
35 Asn Glu Ser Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser
225 230 235 240
Gln Ile Glu Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu
245 250 255
Ser Ser Ala Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met
260 265 270
40 Val Leu Leu Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp
275 280 285
Cys Pro Thr Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe
290 295 300
45 Leu Val Pro Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu
305 310 315 320
Leu Met Asp Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu
325 330 335
Leu Met Val Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys
340 345 350
50 Lys Leu Phe Val Glu Ile Gly Tyr Met Asn
355 360

(2) INFORMATION FOR SEQ ID NO:404

55 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 640 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
60 (11) MOLECULE TYPE: protein
(111) HYPOTHETICAL: YES
(71) ORIGINAL SOURCE:
65 (A) ORGANISM: Porphyromonas gingivalis
(12) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...640
70

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:404

Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val
1 5 10 15
75 Ser Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly

340/490

Pro Ser Asp Asp Lys Asn Val Thr Asp Val Arg Phe Glu Glu Val Lys
625 630 635 640

(2) INFORMATION FOR SEQ ID NO:405

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly Tyr Thr
1 5 10 15
Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Ile Glu
20 25 30
Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile Pro Thr
35 40 45
Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala Thr Ala
50 55 60
Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu Gly Lys
65 70 75 80
Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala Gly Ile
85 90 95
Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala Glu Ala
100 105 110
Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr Ala Gly
115 120 125
Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Leu Cys Thr Gly Ser Glu
130 135 140
Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr Trp Thr
145 150 155 160
Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu Val Ile
165 170 175
Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe Asn Gly
180 185 190
Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile Leu Asn
195 200 205
Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr Glu Lys
210 215 220
Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val Arg Asn
225 230 235 240
Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile Glu Gly
245 250 255
Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln Gly Phe
260 265 270
Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr Asn Glu
275 280 285
Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp Ile Thr
290 295 300
Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu Val Ala
305 310 315 320
Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr Arg Ala
325 330 335
Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val Gly Glu
340 345 350
Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val Arg Arg
355 360 365
Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu Gln Gly
370 375 380
Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu Ile Gly
385 390 395 400
Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr Ala Ala
405 410 415

WO 99/29870

PCT/AU98/01023

342/ 490

Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu Lys Arg Tyr Glu
 385 390 395 400
 Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn Ala Tyr Ala Asn
 405 410 415
 5 Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile Pro Gly Ile Glu
 420 425 430
 Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln Val Pro Leu Glu
 435 440 445
 Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro Val Lys Asn Ala
 10 450 455 460
 Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala Lys Ile Pro Ser
 465 470 475 480
 Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg Gln Gln Lys Val
 485 490 495
 15 Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu Met Glu Lys Ala
 500 505 510
 Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp Gln Lys Phe Gly
 515 520 525
 20 Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val Tyr Leu Lys Lys
 530 535 540
 Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala Leu Ser Pro Gly
 545 550 555 560
 Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser Val Met Asn Ser
 565 570 575
 25 Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala Ile Gln Leu Asp
 580 585 590
 Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro Ser Leu Ser Leu
 595 600 605
 30 Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu Asp Met Glu Thr
 610 615 620
 Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn Arg Lys Asp Pro
 625 630 635 640
 Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn Asn Leu Lys Asn
 645 650 655
 35 Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser Ile Arg His Thr
 660 665 670
 Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys Ala Ala Asp Val
 675 680 685
 40 Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr Asn Glu Arg Phe
 690 695 700
 Ala Asp Ala Gly Asp Phe Met Phe Phe Phe Ile Gly Asn Leu Asp Glu
 705 710 715 720
 Ala Lys Met Lys Pro Leu Ile Glu Thr Tyr Leu Ala Ser Leu Pro Asn
 725 730 735
 45 Leu Lys Arg Gly Asp Lys Met Asn Lys Ala Gln Val Pro Ala Ala Arg
 740 745 750
 Ser Gly Lys Ile Asp Cys Lys Phe Glu Lys Glu Met Asp Thr Pro Ser
 755 760 765
 50 Thr Thr Ile Phe Asp Val Val Ser Gly Asn Val Glu Tyr Thr Leu Lys
 770 775 780
 Asn Ser Leu Leu Leu Glu Val Phe Ser Ala Val Met Asp Gln Val Tyr
 785 790 795 800
 Thr Ala Thr Val Arg Glu Lys Glu Gly Glu Ala Tyr Ser Val Ala Ala
 805 810 815
 55 Phe Gly Gly Leu Glu Gln Tyr Pro Gln Pro Lys Ala Leu Met Gln Ile
 820 825 830
 Tyr Phe Pro Thr Asp Pro Ala Arg Ala Glu Glu Met Asn Ala Ile Val
 835 840 845
 60 Phe Ala Glu Leu Glu Lys Leu Ala Lys Glu Gly Pro Asn Val Glu Tyr
 850 855 860
 Phe Lys Lys Thr Ile Glu Asn Leu Asn Lys Gln His Lys Glu Ser Leu
 865 870 875 880
 Arg Glu Asn Arg Phe Trp Leu Glu Ala Met Lys Ala Ser Phe Phe Glu
 885 890 895
 65 Gly Asn Asp Phe Ile Thr Asp Tyr Glu Ser Val Leu Asn Gly Leu Thr
 900 905 910
 Pro Ala Glu Leu Gln Lys Phe Ala Ala Asp Leu Leu Lys Gln Gln Asn
 915 920 925
 70 Arg Val Val Val Met Met Ala Pro Val Ala Lys Ala Gln
 930 935 940

(2) INFORMATION FOR SEQ ID NO:407

75 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 684 amino acids

WO 99/29870

PCT/AU98/01023

343/ 490

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(a) NAME/KEY: misc feature
(B) LOCATION 1...664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

Met Ser Lys Lys Gly Thr Ile Gly Val Thr Ser Asp Asn Ile Phe Pro
1 5 10 15
Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu Arg Glu
20 20 25 30
Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr Leu Thr
35 40 45
Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val Thr Val
50 55 60
Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg Gly Val
65 70 75 80
Gly Met Thr Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile Ala Phe
85 90 95
Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys Ala Ala
100 105 110
Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met Val Ser
115 120 125
Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala Thr Ala
130 135 140
Val Lys Trp Ser Cys Asp Gly Ser Pro Glu Tyr Thr Leu Glu Pro Ala
145 150 155 160
Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp Glu Glu
165 170 175
Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu Gly Lys
180 185 190
Tyr Cys Lys Phe Leu Thr Val Pro Ile Ile Phe Gly Lys Lys Gln Glu
195 200 205
Trp Lys Asp Gly Lys Met Gln Asp Thr Asp Glu Asp Asn Gln Ile Asn
210 215 220
Asp Thr His Pro Ala Trp Thr Lys Lys Pro Ala Asp Leu Lys Asp Glu
225 230 235 240
Asp Tyr Lys Glu Phe Tyr Arg Ser Leu Tyr Pro Met Ser Glu Glu Pro
245 250 255
Leu Phe Trp Ile His Leu Asn Val Asp Tyr Pro Phe Asn Leu Thr Gly
260 265 270
Ile Leu Tyr Phe Pro Lys Ile Lys Asn Asn Leu Asp Leu Gln Arg Asn
275 280 285
Lys Ile Gln Leu Tyr Cys Asn Gln Val Tyr Val Thr Asp Glu Val Gln
290 295 300
Gly Ile Val Pro Asp Phe Leu Thr Leu Leu His Gly Val Ile Asp Ser
305 310 315 320
Pro Asp Ile Pro Leu Asn Val Ser Arg Ser Tyr Leu Gln Ser Asp Ala
325 330 335
Asn Val Lys Lys Ile Ser Ser His Ile Thr Lys Lys Val Ala Asp Arg
340 345 350
Leu Glu Glu Ile Phe Lys Asn Asp Arg Pro Thr Phe Glu Glu Lys Trp
355 360 365
Asp Ser Leu Lys Leu Phe Val Glu Tyr Gly Met Leu Thr Asp Glu Lys
370 375 380
Phe Tyr Glu Arg Ala Ala Lys Phe Phe Leu Phe Thr Asp Met Asp Gly
385 390 395 400
His Lys Tyr Thr Phe Asp Glu Tyr Arg Thr Leu Val Glu Gly Val Gln
405 410 415
Thr Asp Lys Asp Gly Gln Val Val Tyr Leu Tyr Ala Thr Asp Lys His
420 425 430
Gly Gln Tyr Ser His Val Lys Arg Ala Ser Asp Lys Gly Tyr Ser Val
435 440 445
Met Leu Leu Asp Gly Gln Leu Asp Pro His Ile Val Ser Leu Leu Glu
450 455 460
Gln Lys Leu Glu Lys Thr His Phe Val Arg Val Asp Ser Asp Thr Ile

WO 99/29870

PCT/AU98/01023

344/ 490

465 470 475 480
Asn Asn Leu Ile Arg Lys Glu Glu Arg Ala Glu Val Lys Leu Ser Asp
485 490 495
5 Thr Glu Arg Ala Thr Leu Val Lys Leu Phe Glu Ala Arg Leu Pro Arg
500 505 510
5 Asp Glu Lys Lys His Phe Asn Val Ala Phe Glu Ser Leu Gly Ala Glu
515 520 525
Gly Glu Ala Ile Leu Ile Thr Gln Ala Glu Phe Met Arg Arg Met Arg
530 535 540
10 Asp Met Ala Gln Leu Gln Pro Gly Met Ser Phe Tyr Gly Glu Leu Pro
545 550 555
Asp Ser Tyr Asn Leu Val Leu Asn Thr Asp His Pro Leu Ile Asp Arg
560 565 570 575
15 Val Leu Ser Gly Glu Lys Glu Ser Val Glu Pro Ser Leu Thr Glu Leu
580 585 590
Arg Ala Lys Ile Ala Glu Leu Lys Ala Glu Glu Ala Lys Leu Leu Asp
595 600 605
Glu Glu Lys Gly Lys Lys Pro Glu Glu Ile Pro Val Ala Thr Lys Glu
610 615 620
20 Ala Lys Glu Asn Asn Ala Val Glu Gln Ala Lys Thr Glu Gly Ser Ile
625 630 635 640
Asn Asp Glu Leu Thr Lys Tyr Ala Gln Asp Asn Glu Leu Ile Gly Gln
645 650 655
25 Leu Ile Asp Leu Ala Leu Leu Gly Ser Gly Leu Leu Thr Gly Glu Ala
660 665 670
Leu Ala Glu Phe Ile Arg Arg Ser Gln Arg Leu Leu
675 680

(2) INFORMATION FOR SEQ ID NO:408
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...464
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

Met Glu Lys Leu Ile Asp Ile Leu Val Val Asp Asp Asp Val Ala Val
1 5 10 15
50 Cys Ala Ala Leu Arg Leu Val Leu Lys Arg Ala Gly Tyr Asn Pro Val
20 25 30
Ile Ala Asn Ser Pro Asp Glu Ala Leu Ser Ile Met Arg Asn Pro Asp
35 40 45
55 Gly Gly Cys Lys Pro Ala Val Ile Leu Met Asp Met Asn Phe Ser Leu
50 55 60
Ser Thr Ser Gly Arg Glu Gly Leu Glu Leu Glu Lys Met Gln Ile
65 70 75 80
60 Phe Thr Ser Cys Pro Val Ile Leu Met Thr Ala Trp Ala Ser Ile Pro
85 90 95
Leu Ala Val Glu Gly Met Arg Leu Gly Ala Phe Asp Phe Ile Gly Lys
100 105 110
Pro Trp Asp Asn Asp Arg Leu Leu Arg Thr Ile Asp Thr Ala Leu His
115 120 125
65 Leu Ala Ala Pro Ser Ala Val Ala Asn Pro Ser Glu Gln Ser Asp Arg
130 135 140
Asp Thr Ala Arg Gln Pro Lys Ala Thr Val Gln Glu Asn Asp Pro Cys
145 150 155 160
70 Ala His Ile Ile Gly Arg Ser Asp Ala Ile Cys Lys Ile Lys Glu Arg
165 170 175
Ile Arg Arg Ile Ala Pro Thr His Ala Ser Val Leu Ile Thr Gly Glu
180 185 190
Ser Gly Thr Gly Lys Glu Leu Ile Ala Glu Ala Leu His Arg Gly Ser
195 200 205
75 Lys Arg Ala Ser Ala Pro Phe Val Lys Val Asn Leu Gly Gly Ile Pro

WO 99/29870

PCT/AU98/01023

345 / 490

210 215 220
Glu Ser Leu Phe Glu Ser Glu Leu Phe Gly His Lys Lys Gly Ala Phe
225 230 235 240
Thr Asn Ala Phe Ser Asp Arg Lys Gly Arg Phe Glu Leu Ala Asp Gly
5 Gly Thr Ile Phe Leu Asp Glu Ile Gly Glu Leu Pro Val Gly Asn Gln
245 250 255
Val Lys Leu Leu Arg Val Leu Gln Glu Gln Thr Phe Glu Pro Leu Gly
260 265 270
10 Glu Ser Val Ser His Arg Val Asp Ile Arg Val Val Ser Ala Thr Asn
275 280 285
Ala Ser Leu Glu Arg Met Val Ala Glu Gly Arg Phe Arg Glu Asp Leu
290 295 300
305 Tyr Tyr Arg Ile Asn Leu Ile His Leu His Leu Pro Pro Leu Arg Glu
15 310 315 320
325 330 335
Arg Gln Glu Asp Ile Gln Leu Leu Val Glu Ala Phe Ser Glu Ala Phe
340 345 350
Ala Gln Ser Asn Gly Leu Pro His Ala Val Trp Ser Ala Glu Ala Met
355 360 365
20 Arg Arg Ile Cys Ala Met Pro Leu Pro Gly Asn Val Arg Glu Leu Lys
370 375 380
Asn Val Val Glu Arg Thr Leu Leu Leu Ser Gly Ser Arg Glu Ile Ser
385 390 395
Ala Arg Asp Val Ala Asp Phe Gly Ser Gln Val Thr Ala Ala Asp His
25 400 405 410 415
Ser Asp Glu Arg Ala Leu Thr Asp Met Glu Glu Ala Ala Ile Arg Glu
420 425 430
Thr Leu Thr Lys Tyr Asn Gly Asn Val Ser Arg Ala Ala Arg Ala Leu
435 440 445
30 Gly Leu Ser Arg Ala Ala Leu Tyr Arg Arg Met Glu Lys Tyr Gly Leu
450 455 460

(2) INFORMATION FOR SEQ ID NO:409

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
40 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
45 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...250
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

Met Leu Lys Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile
1 5 10 15
55 Leu Lys Gly Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile
20 25 30
Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val
35 40 45
60 Gly His Pro Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly
50 55 60
Ile Asp Leu Leu Glu Leu Glu Pro Glu Glu Ala His Leu Gly Leu
65 70 75 80
Phe Leu Ser Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val
85 90 95
65 Asn Phe Met Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala
100 105 110
Glu Pro Val Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg
115 120 125
Ala Ile Val Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu
70 130 135 140
Gly Phe Ser Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala
145 150 155 160
Met Leu Glu Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu
165 170 175
75 Asp Ile Asp Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg

WO 99/29870

PCT/AU98/01023

346 / 490

180 185 190
 Ser Pro Glu Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu
 195 200 205
 Glu Tyr Ile Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile
 210 215 220
 Val Lys Ser Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly
 225 230 235 240
 Tyr Asp Trp Ile Lys Glu Glu Ile Gly Glu
 245 250
 (2) INFORMATION FOR SEQ ID NO:410
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...461
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410
 Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr Lys
 1 5 10 15
 Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn Cys
 20 25 30
 Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala Ala
 35 40 45
 Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu Gln
 50 55 60
 Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu Glu
 65 70 75 80
 Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val Leu
 85 90 95
 Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln Thr
 100 105 110
 Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu Glu
 115 120 125
 Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala Met
 130 135 140
 Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu Ser
 145 150 155 160
 Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile Gln
 165 170 175
 Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly Gln
 180 185 190
 Ile Arg Glu Cys Ala Ala Leu Leu Leu Lys Tyr Cys Lys Thr Thr Gly
 195 200 205
 Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile Ala
 210 215 220
 Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe Asp
 225 230 235 240
 Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn Arg
 245 250 255
 Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp Gly
 260 265 270
 Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn Arg
 275 280 285
 Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile Arg
 290 295 300
 Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr Ala
 305 310 315 320
 Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn Met
 325 330 335
 Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln Lys
 340 345 350
 Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro Ala

WO 99/29870

PCT/AU98/01023

348/ 490

(ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 10 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...417
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412
 15 Met Ser Thr Asn Ile Asp Val Gln Gln Ile Lys Gln Arg Phe Gly Ile
 1 5 10 15
 Ile Gly Ser Ser Pro Leu Met Glu His Ala Phe Arg Val Ala Ala Gln
 20 20 25 30
 Val Ala Pro Thr Asp Met Ser Val Leu Val Thr Gly Glu Ser Gly Ser
 35 40 45
 20 Gly Lys Glu Phe Phe Pro Gln Ile Ile His Tyr Tyr Ser Ala Arg Lys
 50 55 60
 His His Ser Tyr Ile Ala Val Asn Cys Gly Ala Ile Pro Glu Gly Thr
 65 70 75 80
 25 Ile Asp Ser Glu Leu Phe Gly His Arg Lys Gly Ser Phe Thr Gly Ala
 85 90 95
 Val Ser Asp Arg Lys Gly Tyr Phe Glu Glu Ala Ser Gly Gly Thr Ile
 100 105 110
 30 Phe Leu Asp Glu Val Gly Glu Leu Pro Leu Pro Thr Gln Ala Arg Leu
 115 120 125
 Leu Arg Val Leu Glu Thr Gly Glu Phe Ile Pro Val Gly Ala Ser Gln
 130 135 140
 Ser Gln Lys Thr Asp Val Arg Ile Val Ala Ala Asn Val Asn Leu
 145 150 155 160
 35 Lys Glu Ala Val Ala Asn Gly Lys Phe Arg Glu Asp Leu Phe Phe Arg
 165 170 175
 Leu Asn Thr Val Pro Ile Glu Val Pro Ala Leu Arg Met Arg Pro Asp
 180 185 190
 40 Asp Val Pro Leu Leu Phe Arg Arg Phe Ala Ala Asp Ser Ala Glu Lys
 195 200 205
 Tyr Arg Met Pro Pro Leu Arg Leu Ser Asp Glu Ala Arg Thr Ile Leu
 210 215 220
 Met Arg Tyr Arg Trp Pro Gly Asn Val Arg Glu Leu Arg Asn Ile Thr
 225 230 235 240
 45 Asp Arg Leu Ser Ile Leu Glu Glu Glu Arg Thr Val Ser Ala Glu Thr
 245 250 255
 Ile Thr Arg Tyr Leu Asp Ala Glu Gly Met Gln Asp Leu His Pro Val
 260 265 270
 Val Ile Arg Arg Asn Glu Thr Thr Glu Ala Asp Lys Gln Ile Pro His
 275 280 285
 50 Tyr Glu Arg Glu Ile Ile Tyr Gln Val Leu Tyr Asp Met Lys Lys Glu
 290 295 300
 Ile Ala Asp Leu Lys Gly Met Met Asn Arg Leu Ala His His Glu Gln
 305 310 315 320
 55 Pro Ser Trp Pro Val Gly Ser Asp Val Trp Gly Asn Asp Asp Lys Arg
 325 330 335
 Thr Ala Asp Pro Lys Trp Gly Val Ser Thr His Lys Ala Pro Ile Ala
 340 345 350
 60 Asn Ala Ala Glu Pro Val Glu Pro Ile Gln Glu Ala Ser Glu Tyr Thr
 355 360 365
 Glu Asp Pro Val Ser Leu Glu Glu Val Glu Lys Lys Met Ile Ser Leu
 370 375 380
 Ala Leu Glu Arg His Gly Gly Arg Arg Lys Gln Thr Ala Glu Glu Leu
 385 390 395 400
 65 Lys Ile Ser Glu Arg Thr Leu Tyr Arg Lys Ile Lys Glu Tyr Gly Leu
 405 410 415
 Glu
 70 (2) INFORMATION FOR SEQ ID NO:413
 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 602 amino acids
 (B) TYPE: amino acid
 75 (D) TOPOLOGY: linear

WO 99/29870

PCT/AU98/01023

349/490

(ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...602
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

15	Met	Ile	Leu	Leu	Phe	Gly	Gly	Thr	Thr	Glu	Gly	Arg	Ala	Ala	Ala	Arg
	1				5					10					15	
	Val	Leu	Asp	Glu	Ala	Gly	Ser	Pro	Phe	Phe	Tyr	Ser	Thr	Lys	Gly	Asn
					20					25				30		
20	Leu	Gln	Glu	Ile	Gln	Ser	Ser	His	Gly	His	Arg	Leu	Thr	Gly	Ala	Met
					35				40					45		
	Thr	Val	Ala	Asp	Met	Val	Ser	Phe	Cys	Arg	Lys	Glu	Glu	Ile	Arg	Leu
					50				55					60		
	Ile	Val	Asp	Ala	Ala	His	Pro	Phe	Ala	Glu	Glu	Leu	His	Ala	Ser	Val
					65				70					75		80
25	Ala	Glu	Ala	Ser	Glu	Gln	Thr	Gly	Ile	Pro	Val	Val	Arg	Tyr	Glu	Arg
					85				90					95		
	Gln	Tyr	Pro	Pro	Arg	Glu	Glu	Gly	Ile	Val	Trp	Cys	Ala	Asn	Tyr	Asp
					100				105					110		
	Thr	Ala	Ala	Glu	Arg	Met	Leu	Gly	Asp	Gly	Val	Gln	Arg	Leu	Leu	Met
					115				120					125		
30	Leu	Thr	Gly	Val	Asn	Thr	Ile	Pro	Lys	Leu	Ala	Ala	Phe	Trp	Lys	Glu
					130				135					140		
	Arg	Thr	Thr	Phe	Cys	Arg	Ile	Leu	Lys	Arg	Asp	Glu	Ser	Val	Ala	Leu
					145				150					155		160
35	Ala	Glu	Lys	Asn	Gly	Phe	Pro	Ala	Glu	Arg	Ile	Val	Phe	Phe	Glu	Pro
					165				170					175		
	His	Ala	Asp	Glu	Glu	Leu	Met	Gln	Ala	Val	Arg	Pro	Asp	Ala	Ile	Ile
					180				185					190		
	Thr	Lys	Glu	Ser	Gly	Glu	Ser	Gly	Tyr	Phe	Arg	Glu	Lys	Ile	Glu	Ala
					195				200					205		
40	Ala	Arg	Arg	Met	Gly	Ile	Arg	Ile	Tyr	Ala	Val	Val	Arg	Pro	Pro	Leu
					210				215					220		
	Pro	Pro	Ser	Phe	Ile	Pro	Val	Gly	Gly	Pro	Val	Gly	Leu	Arg	Arg	Ala
					225				230					235		240
45	Val	Glu	Arg	Leu	Val	Pro	Gly	Phe	Phe	Ser	Leu	Arg	Ser	Gly	Phe	Thr
					245				250					255		
	Thr	Gly	Thr	Thr	Ala	Thr	Ala	Ala	Val	Val	Ala	Ala	Met	Tyr	Arg	Leu
					260				265					270		
50	Met	Gly	Leu	Gly	Ser	Leu	Ala	Glu	Ala	Pro	Val	Glu	Leu	Pro	Ser	Gly
					275				280					285		
	Glu	Ile	Val	Ser	Leu	Pro	Ile	Ala	Glu	Ile	Arg	Glu	Glu	Glu	Asp	Ala
					290				295					300		
	Val	Val	Ser	Ala	Val	Leu	Lys	Asp	Ala	Gly	Asp	Asp	Pro	Asp	Val	Thr
					305				310					315		320
55	Asn	Gly	Met	Ala	Val	Cys	Ala	Thr	Ile	Arg	Leu	Asn	Pro	Glu	His	Glu
					325				330					335		
	Glu	Val	Arg	Phe	Leu	Gln	Gly	Glu	Gly	Val	Gly	Val	Val	Thr	Leu	Pro
					340				345					350		
60	Gly	Leu	Gly	Leu	Glu	Val	Gly	Gly	Pro	Ala	Ile	Asn	Leu	Val	Pro	Arg
					355				360					365		
	Arg	Met	Met	Thr	Ala	Glu	Val	Arg	Arg	Leu	Tyr	Ala	Gln	Gly	Gly	Val
					370				375					380		
	Asp	Ile	Thr	Ile	Ser	Val	Pro	Glu	Gly	Arg	Glu	Ala	Ala	Thr	Gln	Thr
					385				390					395		400
65	Phe	Asn	Pro	Arg	Leu	Gly	Ile	Arg	Asp	Gly	Ile	Ser	Ile	Ile	Gly	Thr
					405				410					415		
	Ser	Gly	Val	Val	Lys	Pro	Phe	Ser	Ala	Glu	Ala	Phe	Val	Gly	Ala	Ile
					420				425					430		
	Arg	Lys	Gln	Val	Gly	Ile	Ala	Thr	Ala	Leu	Gly	Ala	Asn	His	Ile	Val
					435				440					445		
70	Leu	Asn	Ser	Gly	Ala	Lys	Ser	Glu	Arg	Tyr	Val	Lys	Gly	Ala	Tyr	Pro
					450				455					460		
	Ala	Leu	Ile	Pro	Gln	Ala	Phe	Val	Gln	Tyr	Gly	Asn	Phe	Val	Gly	Glu
					465				470					475		480
75	Ser	Leu	Ser	Cys	Val	Ala	Ser	Phe	Pro	Ser	Val	Arg	Ser	Val	Thr	Val

WO 99/29870

PCT/AU98/01023

350/ 490

485 490 495
Gly Ile Met Leu Gly Lys Ala Val Lys Leu Ala Glu Gly Tyr Leu Asp
500 505 510
515 520 525
530 535 540
545 550 555 560
565 570 575 580 585 590
595 600

(2) INFORMATION FOR SEQ ID NO:414
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) SYNTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...443
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:414

Met Leu Arg Thr Phe Arg Ile Gly Gly Ile His Pro Pro Glu Asn Lys
1 5 10 15
Leu Ser Ala Gly Lys Pro Val Glu Val Leu Pro Ile Pro Ser Gln Val
20 25 30
Val Ile Pro Leu Gly Gln His Ile Gly Ala Pro Ala Thr Ala Thr Val
35 40 45
Lys Lys Gly Asp Glu Val Lys Val Gly Thr Ile Ile Ala Gln Ala Gly
50 55 60
Gly Phe Val Ser Ala Asn Ile His Ser Ser Val Ser Gly Lys Val Leu
65 70 75 80
Lys Ile Asp Asn Val Tyr Asp Ser Ser Gly Tyr Pro Lys Pro Ala Val
85 90 95
Phe Ile Ser Val Glu Gly Asp Glu Trp Glu Glu Gly Ile Asp Arg Ser
100 105 110
Pro Ala Ile Val Lys Glu Cys Asn Leu Asp Ala Lys Glu Ile Val Ala
115 120 125
Lys Ile Ser Ala Ala Gly Ile Val Gly Leu Gly Gly Ala Thr Phe Pro
130 135 140
Thr His Val Lys Leu Ser Pro Pro Gly Asn Lys Ala Glu Ile Leu
145 150 155 160
Ile Ile Asn Ala Val Glu Cys Glu Pro Tyr Leu Thr Ser Asp His Val
165 170 175
Leu Met Leu Glu His Gly Glu Glu Ile Met Ile Gly Val Ser Ile Leu
180 185 190
Met Lys Ala Ile Gln Val Asn Lys Ala Val Ile Gly Val Glu Asn Asn
195 200 205
Lys Lys Asp Ala Ile Ala His Leu Thr Lys Leu Ala Thr Ala Tyr Pro
210 215 220
Gly Ile Glu Val Met Pro Leu Lys Val Gln Tyr Pro Gln Gly Gly Glu
225 230 235 240
Lys Gln Leu Ile Asp Ala Val Ile Arg Lys Gln Val Lys Ser Gly Ala
245 250 255
Leu Pro Ile Ser Thr Gly Ala Val Val Gln Asn Val Gly Thr Val Phe
260 265 270
Ala Val Tyr Glu Ala Val Gln Lys Asn Lys Pro Leu Val Glu Arg Ile
275 280 285
Val Thr Val Thr Gly Lys Lys Leu Ser Arg Pro Ser Asn Leu Leu Val
290 295 300
Arg Ile Gly Thr Pro Ile Ala Ala Leu Ile Glu Ala Ala Gly Gly Leu

WO 99/29870

PCT/AU98/01023

352/ 490

290 295 300
 Leu Glu Ile Ile Asn Ser Asp Lys Tyr Ala Asp Asp Ala Arg Glu
 305 310 315 320
 Gln Ala Leu Lys Gln Leu Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile
 325 330 335
 Tyr Pro Asn Leu Arg Arg Asn Thr Ile Thr Met Gly Tyr Ile Val Arg
 340 345 350
 Asp Tyr Thr Leu Glu Glu Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys
 355 360 365
 Glu Leu Ser Glu Ala Glu Met Tyr Arg Val Ala Met Ser Tyr Pro Glu
 370 375 380
 Gly His Gln Glu Arg Leu Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe
 385 390 395 400
 Pro Glu Ser Val Thr Gly Arg Ile Asn Leu Ala Val Ala Ala Phe Asn
 405 410 415
 Gly Gly Asp Val Gln Gln Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr
 420 425 430
 Glu Lys Gly Val Ser Asn Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly
 435 440 445
 Asp Phe Ala Arg Ala Glu Thr Phe Phe Arg Lys Ala Val Ala Glu Gly
 450 455 460
 Asp Ala Asn Ala Gln Arg Asn Leu Asp Met Leu Leu Gly Lys Lys
 465 470 475

5
 10
 15
 20
 25 (2) INFORMATION FOR SEQ ID NO:416
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 35
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 40
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...383
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416
 45 Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys Asn
 1 5 10 15
 Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile Gln
 20 25 30
 Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His Phe
 35 40 45
 Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys Arg
 50 55 60
 Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala Gly
 65 70 75 80
 Gly Gly Phe Ser Gly Gly Gly Met Ser Met Glu Asp Ile Phe Ser Arg
 85 90 95
 Phe Gly Asp Leu Phe Gly Gly Phe Gly Gly Phe Gly Phe Ser Asp
 100 105 110
 Met Gly Gly Gly Ser Arg Arg Arg Val Arg Arg Gly Ser Asp Leu Arg
 115 120 125
 Val Arg Val Lys Leu Ser Leu Ala Asp Ile Ser Lys Gly Val Glu Lys
 130 135 140
 Lys Val Lys Val Lys Lys Gln Val Val Cys Ser Lys Cys Arg Gly Asp
 145 150 155 160
 Gly Thr Glu Glu Ala Asn Gly Lys Thr Thr Cys Gln Thr Cys His Gly
 165 170 175
 Thr Gly Val Val Thr Arg Val Ser Asn Thr Phe Leu Gly Ala Met Gln
 180 185 190
 Thr Gln Ser Thr Cys Pro Thr Cys His Gly Glu Gly Glu Ile Ile Thr
 195 200 205
 Lys Pro Cys Ser Lys Cys Lys Gly Glu Gly Val Glu Ile Gly Glu Glu
 210 215 220
 Val Ile Ser Phe His Ile Pro Ala Gly Val Ala Gly Met Gln Met
 225 230 235 240
 75 Ser Val Asn Gly Lys Gly Asn Ala Ala Pro Arg Gly Gly Val Asn Gly

353/ 490

245 250 255
 Asp Leu Ile Val Val Ile Ala Glu Glu Pro Asp Pro Asn Leu Ile Arg
 260 265 270
 Asn Gly Asn Asp Leu Ile Tyr Asn Leu Leu Ile Ser Val Pro Leu Ala
 275 280 285
 Ile Lys Gly Gly Ser Val Glu Val Pro Thr Ile Asp Gly Arg Ala Lys
 290 295 300
 Ile Arg Ile Glu Ala Gly Thr Gln Pro Gly Lys Met Leu Arg Leu Arg
 305 310 315
 Asn Lys Gly Leu Pro Ser Val Asn Gly Tyr Gly Met Gly Asp Gln Leu
 320 325 330 335
 Val Asn Val Asn Val Tyr Ile Pro Glu Ser Ile Asp Ala Lys Asp Glu
 340 345 350
 Gln Ala Ile Ala Ala Met Glu Asn Ser Asp Ser Phe Lys Pro Thr Asp
 355 360 365
 Ala Ala Arg Lys Asp Ile Asp Lys Lys Tyr Arg Glu Met Leu Asp
 370 375 380

(2) INFORMATION FOR SEQ ID NO:417
 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...293
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met
 1 5 10 15
 Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala
 20 25 30
 Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr
 35 40 45
 Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Ala Tyr Pro Asp Gln Arg
 50 55 60
 Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln
 65 70 75 80
 Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala
 85 90 95
 Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro
 100 105 110
 Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala
 115 120 125
 Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr
 130 135 140
 Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln
 145 150 155 160
 Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr
 165 170 175
 Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys
 180 185 190
 Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser
 195 200 205
 Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val
 210 215 220
 Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp
 225 230 235 240
 Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala
 245 250 255
 Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala
 260 265 270
 Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys
 275 280 285
 Ala Thr Ser Ala Arg

WO 99/29870

PCT/AU98/01023

354/ 490

290

(2) INFORMATION FOR SEQ ID NO:418

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...356
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

Met Thr Ser Val Ser His Leu Arg Thr Ile Ser Val Ala Gly Ile Leu
 1 5 10 15
 25 Ala Ala Leu Gly Gly Ala Val Leu Ile Leu Phe Gly Val Asn Leu Phe
 20 25 30
 Leu Gly Ser Val Ala Ile Pro Met Ser Glu Ile Phe Arg His Leu Phe
 35 40 45
 Ser Asp Arg Pro Glu Gly Gly Glu Ala Leu Val His Tyr Asn Ile Leu
 50 55 60
 30 Trp Lys Ser Arg Leu Pro Glu Ala Leu Thr Ala Ala Phe Ala Gly Ala
 65 70 75 80
 Gly Leu Ser Val Ser Gly Leu Gln Met Gln Thr Val Phe Arg Asn Pro
 85 90 95
 35 Leu Ala Gly Pro Ser Val Leu Gly Ile Ser Ser Gly Ala Ser Leu Gly
 100 105 110
 Val Ala Leu Val Val Leu Leu Ser Gly Ser Leu Gly Val Ala Leu
 115 120 125
 40 Ser Ser Leu Gly Tyr Met Gly Glu Val Ala Met Asn Ile Ala Ala Ala
 130 135 140
 Val Gly Ser Leu Ala Val Met Gly Leu Ile Val Phe Val Ser Thr Lys
 145 150 155 160
 Val Arg Ser His Val Thr Leu Leu Ile Ile Gly Val Met Ile Gly Tyr
 165 170 175
 45 Val Ala Thr Ala Val Ile Gly Val Phe Lys Phe Phe Ser Ile Glu Glu
 180 185 190
 Asp Ile Arg Ala Tyr Val Ile Trp Gly Leu Gly Ser Phe Ser Arg Ala
 195 200 205
 Thr Asp Ser Gln Leu Ser Phe Phe Ala Ile Leu Met Leu Ile Phe Ile
 210 215 220
 50 Pro Ala Gly Met Leu Leu Val Lys Gln Leu Asn Leu Leu Leu Gly
 225 230 235 240
 Glu Ser Tyr Ala Arg Asn Leu Gly Leu Asn Thr Arg Arg Ala Arg Leu
 245 250 255
 55 Leu Val Ile Ser Ser Ala Gly Leu Leu Ile Ala Thr Val Thr Ala Tyr
 260 265 270
 Cys Gly Pro Ile Gly Phe Leu Gly Met Ala Val Pro His Leu Ala Arg
 275 280 285
 60 Val Ile Phe His Thr Ser Asp His Arg Ile Leu Met Pro Ala Thr Cys
 290 295 300
 Leu Ile Gly Ser Ala Leu Ala Leu Phe Cys Asn Ile Ile Ala Arg Met
 305 310 315 320
 Pro Gly Phe Glu Gly Ala Leu Pro Val Asn Ser Val Thr Ala Leu Val
 325 330 335
 65 Gly Ala Pro Ile Ile Val Thr Val Leu Phe Arg Arg Arg Arg Phe Lys
 340 345 350
 Glu Glu Thr Asp
 355

70 (2) INFORMATION FOR SEQ ID NO:419

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 757 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 75

355/ 490

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

15	Met	Arg	Thr	Lys	Thr	Ile	Phe	Phe	Ala	Ile	Ile	Ser	Phe	Ile	Ala	Leu
	1			5					10					15		
	Leu	Ser	Ser	Ser	Leu	Ser	Ala	Gln	Ser	Lys	Ala	Val	Leu	Thr	Gly	Ser
				20					25					30		
20	Val	Ser	Asp	Ala	Glu	Thr	Gly	Glu	Pro	Leu	Ala	Gly	Ala	Arg	Ile	Glu
			35					40					45			
	Val	Ile	His	Thr	Asn	Ile	Val	Ala	Gly	Ala	Asp	Ala	Gly	Gly	His	Phe
			50				55				60					
	Glu	Ile	Lys	Asn	Leu	Pro	Ala	Gly	Gln	His	Thr	Ile	Ile	Cys	Ser	Leu
			65			70				75				80		
25	Gly	Gly	Tyr	Gly	Gln	Lys	Glu	Glu	Val	Val	Ala	Ile	Glu	Ala	Gly	Gln
				85					90					95		
	Thr	Lys	Thr	Ile	Ser	Phe	Ala	Leu	Arg	Leu	Arg	Thr	Asn	Asn	Leu	Glu
			100					105					110			
30	Glu	Val	Val	Val	Thr	Gly	Thr	Gly	Thr	Arg	Tyr	Arg	Leu	Val	Asp	Ala
			115					120					125			
	Pro	Val	Ala	Thr	Glu	Val	Leu	Thr	Ala	Lys	Asp	Ile	Ala	Ser	Phe	Ser
			130				135					140				
	Ala	Pro	Thr	Ser	Glu	Ala	Leu	Leu	Gln	Gly	Leu	Ser	Pro	Ser	Phe	Asp
			145			150					155				160	
35	Phe	Gly	Pro	Asn	Leu	Met	Gly	Ser	Phe	Met	Gln	Leu	Asn	Gly	Leu	Ser
			165						170					175		
	Ser	Lys	Tyr	Ile	Leu	Ile	Leu	Ile	Asp	Gly	Lys	Arg	Val	Tyr	Gly	Asp
			180						185					190		
40	Val	Gly	Gly	Gln	Ala	Asp	Leu	Ser	Arg	Ile	Ser	Pro	Asp	Gln	Ile	Glu
			195					200					205			
	Arg	Ile	Glu	Leu	Val	Lys	Gly	Ala	Ser	Ser	Ser	Leu	Tyr	Gly	Ser	Asp
			210				215					220				
	Ala	Ile	Ala	Gly	Val	Ile	Asn	Val	Ile	Thr	Lys	Lys	Asn	Thr	Asn	Arg
			225			230					235				240	
45	Leu	Ser	Ala	Tyr	Thr	Ser	His	Arg	Ile	Ser	Lys	Tyr	Asn	Asp	Arg	Gln
			245								250			255		
	Thr	Asn	Thr	Ser	Leu	Asp	Ile	Asn	Ile	Gly	Lys	Phe	Ser	Ser	Asn	Thr
			260					265					270			
50	Asn	Tyr	Phe	Phe	Tyr	His	Thr	Asp	Gly	Trp	Gln	Asn	Ser	Pro	Phe	Glu
			275					280					285			
	Ile	Lys	Lys	Lys	Lys	Gly	Ser	Gly	Glu	Pro	Val	Leu	Glu	Glu	Thr	Tyr
			290				295					300				
	Lys	Lys	Thr	Phe	Arg	Ala	Gln	Glu	Asn	Gln	Gly	Val	Ser	Gln	Ser	Leu
			305			310					315				320	
55	Ser	Tyr	Tyr	Ala	Thr	Asn	Asn	Leu	Ser	Phe	Ser	Gly	Asn	Val	Gln	Tyr
			325							330				335		
	Asn	Lys	Arg	Gln	Ile	Phe	Thr	Pro	Thr	Phe	Ser	Glu	Lys	Lys	Ala	Tyr
			340					345					350			
60	Asp	Met	Asp	Tyr	Arg	Ala	Leu	Thr	Ala	Ser	Leu	Gly	Thr	Asn	Tyr	Leu
			355				360						365			
	Phe	Pro	Asn	Gly	Leu	His	Thr	Leu	Ser	Phe	Asp	Ala	Val	Tyr	Asp	Arg
			370				375					380				
	Phe	Arg	Phe	Gly	Tyr	Leu	Tyr	His	Asp	Lys	Asp	Ser	Ser	Glu	Ser	Leu
			385			390				395				400		
65	Ile	Asn	Asn	Gln	Gly	Gln	Thr	Glu	Gln	Pro	Thr	Phe	Phe	Pro	Gly	Gln
			405							410				415		
	Leu	Arg	Asn	Lys	Asn	Asp	Gln	Ile	Arg	Tyr	Thr	Ala	Glu	Ala	Arg	Gly
			420					425					430			
70	Val	Phe	Thr	Leu	Pro	Tyr	Ala	Gln	Lys	Leu	Thr	Gly	Gly	Leu	Glu	Tyr
			435					440					445			
	Phe	Arg	Glu	Glu	Leu	Ile	Ser	Pro	Tyr	Asn	Leu	Ile	Thr	Asp	Lys	Ala
			450				455					460				
	Asp	Ala	Ser	Thr	Leu	Ser	Ala	Tyr	Val	Gln	Asp	Glu	Trp	Lys	Pro	Leu
			465			470				475				480		
75	Asp	Trp	Phe	Asn	Met	Thr	Ala	Gly	Phe	Arg	Leu	Val	His	His	Gln	Glu

356/ 490

485 490 495
 Phe Gly Thr Arg Met Thr Pro Lys Val Ser Ile Leu Ala Lys Tyr Gly
 500 505 510
 5 Pro Leu Asn Phe Arg Ala Thr Tyr Ala Asn Gly Tyr Lys Thr Pro Thr
 515 520 525
 Leu Lys Glu Leu Phe Ala Arg Asn Glu Leu Thr Thr Met Gly Ser His
 530 535 540
 Asn Leu Tyr Leu Gly Asn Ala Asp Leu Lys Pro Gln Met Ser Asp Tyr
 545 550 555 560
 10 Tyr Ala Leu Gly Leu Glu Tyr Asn Gln Gly Pro Ile Ser Phe Ser Ala
 565 570 575
 Thr Val Tyr Asp Asn Glu Leu Arg Asn Leu Ile Ser Phe Met Asp Ile
 580 585 590
 15 Pro Thr Ser Pro Glu His Glu Ala Gln Gly Ile Lys Lys Thr Lys Gln
 595 600 605
 Tyr Ala Asn Ile Gly Lys Ala Arg Ser Arg Gly Leu Asp Val Leu Cys
 610 615 620
 Asp Ala Ser Ile Gly Trp Gly Ile Lys Leu Gly Ala Gly Tyr Ser Leu
 625 630 635 640
 20 Val Glu Ala Lys Asn Leu Gln Thr Asp Glu Trp Leu Glu Gly Ala Ala
 645 650 655
 Arg His Arg Ala Asn Val His Ala Asp Trp Val His Tyr Trp Gly Gln
 660 665 670
 25 Tyr Arg Leu Gly Val Ser Leu Phe Gly Arg Ile Gln Ser Glu Arg Tyr
 675 680 685
 Tyr Lys Asp Gly Asn Ala Pro Asp Tyr Thr Leu Trp Arg Leu Ala Thr
 690 695 700
 Ser His Arg Phe Ala His Phe Arg His Ile Ile Leu Asp Gly Thr Leu
 705 710 715 720
 30 Gly Ile Asp Asn Leu Phe Asp Tyr Val Asp Asp Arg Pro Met Gly Val
 725 730 735
 Asn Tyr Ala Thr Val Thr Pro Gly Arg Thr Phe Phe Ala Gln Ile Ala
 740 745 750
 35 Ile Arg Phe Asn Asn
 755

(2) INFORMATION FOR SEQ ID NO:420

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 50 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...331
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe Leu Leu
 1 5 10 15
 60 Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe Met Leu
 20 25 30
 Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr Glu Tyr
 35 40 45
 Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg Val Ser
 50 55 60
 65 Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile Glu Ala
 65 70 75 80
 Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu Ala Ala
 85 90 95
 70 Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser Glu Gln
 100 105 110
 Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly Val Ala
 115 120 125
 Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp Gln Gly
 130 135 140
 75 Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg Asp Ala

WO 99/29870

PCT/AU98/01023

358/ 490

Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys
245 250 255
260 265

5 (2) INFORMATION FOR SEQ ID NO:422

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

Met Lys Lys Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr
1 5 10 15
Gly Ser Phe Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu
20 25 30
Thr Glu Glu Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val
35 40 45
Leu Ser Asn Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile
50 55 60
Ser Ile Lys His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly
65 70 75 80
Leu Asp Pro Tyr Thr Glu Tyr Ile Pro Tyr Glu Met Asp Glu Leu
85 90 95
Lys Leu Met Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser
100 105 110
Gln Arg Pro Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met
115 120 125
Pro Ala Asp Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile
130 135 140
Asp Gly Lys Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala
145 150 155 160
Leu Lys Gly Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr
165 170 175
Gly Glu Thr Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile
180 185 190
Met Asn Ser Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr
195 200 205
Ile Arg Leu Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr
210 215 220
Ala Leu Leu Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu
225 230 235 240
Asp Leu Arg Gly Asn Gly Gly Gly Leu Met Gln Ala Ala Ile Glu Ile
245 250 255
Val Asn Leu Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly
260 265 270
Arg Ile Ala Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile
275 280 285
Asp Thr Lys Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser
290 295 300
Ser Ser Glu Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val
305 310 315 320
Leu Met Gly Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg
325 330 335
Gln Leu Pro Tyr Asn Gly Val Ile Lys Leu Thr Thr Ala Lys Tyr Tyr
340 345 350
Ile Pro Ser Gly Arg Cys Ile Gln Arg Leu Asp Tyr Ser Arg Thr Asn
355 360 365
Arg Thr Gly Met Ala Thr Ala Ile Pro Asp Ser Leu His Lys Ile Phe
370 375 380
Tyr Thr Ala Ala Gly Arg Arg Val Glu Asp Ala Gly Gly Ile Leu Pro
385 390 395 400
75 Asp Ile Glu Val Lys Gln Asp Thr Ala Ala Thr Leu Leu Tyr Tyr Met

WO 99/29870

PCT/AU98/01023

360/ 490

				260						265					270		
		Ser	Ala	Ala	Val	Gln	Ala	Val	Ala	Asp	Ser	Ala	Thr	Val	Ala	Gln	Lys
				275					280					285			
5		Glu	Ala	Lys	Asp	Ala	Thr	Arg	Lys	Asp	Ala	Leu	Phe	Ser	Leu	Leu	Thr
				290				295					300				
		Pro	Val	Asn	Arg	Gly	Gly	Ala	Val	Val	Gly	Val	Ala	Arg	Arg	Ala	Asn
				305				310					315			320	
		Met	Ala	Gln	Ile	Ser	Glu	Met	Leu	Gln	Gln	Ala	His	Asp	Leu	Lys	Val
10					325								330			335	
		Thr	Arg	Glu	Asp	Val	Leu	Phe	Leu	Trp	Gly	Ala	Lys	Ala	Ile	Glu	Asp
					340										350		
		Pro	Glu	Thr	Lys	Lys	Glu	Thr	Asp	Leu	Tyr	Glu	Leu	Tyr	Ala	Ile	Arg
					355				360					365			
15		Thr	Asn	Arg	Thr	Gly	Asp	Pro	Asp	Leu	Gly	Gly	Asp	Val	Val	Thr	Ser
					370			375					380				
		Ala	Lys	Ser	Asp	Ile	Gln	Asn	Asp	Phe	Gly	Arg	Ser	Glu	Pro	Ile	Val
					385			390				395				400	
		Ser	Met	Thr	Met	Asn	Glu	Glu	Gly	Ala	Arg	Lys	Trp	Ala	Arg	Ile	Thr
20					405										415		
		Lys	Asp	Asn	Val	Gly	Arg	Ala	Ile	Ala	Ile	Val	Leu	Asp	Gly	Val	Val
					420					425					430		
		Tyr	Ser	Ala	Pro	Asn	Val	Asn	Asp	Glu	Ile	Thr	Gly	Gly	Arg	Ser	Gln
					435				440					445			
25		Ile	Ser	Gly	His	Phe	Thr	Val	Glu	Glu	Ala	Gly	Asp	Leu	Ala	Asn	Val
					450			455					460				
		Leu	Asn	Ser	Gly	Lys	Met	Asp	Ala	Thr	Val	Ser	Ile	Glu	Gln	Glu	Asn
					465			470					475			480	
		Val	Ile	Gly	Pro	Thr	Leu	Gly	Ala	Glu	Ser	Ile	Lys	Ala	Gly	Phe	Leu
30					485						490				495		
		Ser	Phe	Leu	Leu	Ala	Leu	Val	Ile	Leu	Met	Cys	Tyr	Met	Cys	Leu	Ala
					500					505					510		
		Tyr	Gly	Phe	Leu	Pro	Gly	Leu	Ile	Ala	Asn	Gly	Ala	Leu	Ile	Val	Asn
					515				520					525			
35		Ser	Phe	Phe	Thr	Leu	Gly	Val	Leu	Ala	Ser	Phe	His	Ala	Val	Leu	Thr
					530			535					540				
		Leu	Ser	Gly	Ile	Ala	Gly	Leu	Val	Leu	Thr	Leu	Gly	Met	Ala	Val	Asp
					545			550				555				560	
		Ala	Asn	Val	Leu	Ile	Phe	Glu	Arg	Ile	Lys	Glu	Glu	Leu	Arg	Ala	Gly
40					565						570				575		
		Lys	Thr	Pro	Ile	Arg	Ala	Val	Thr	Asp	Gly	Tyr	Gly	Asn	Ala	Phe	Ser
					580					585					590		
		Ala	Ile	Phe	Asp	Ser	Asn	Val	Thr	Thr	Ile	Ile	Thr	Gly	Ile	Ile	Leu
					595				600					605			
45		Phe	Leu	Tyr	Gly	Thr	Gly	Pro	Ile	Arg	Gly	Phe	Ala	Thr	Thr	Leu	Ile
					610			615					620				
		Ile	Gly	Leu	Ile	Ala	Ser	Phe	Ile	Thr	Ala	Val	Phe	Leu	Thr	Arg	Ile
					625			630				635				640	
		Val	Phe	Glu	Lys	Leu	Ala	Lys	Lys	Gly	Arg	Leu	Asp	Lys	Ile	Thr	Phe
50					645						650				655		
		Thr	Thr	Ser	Ile	Thr	Arg	Asn	Leu	Leu	Val	Asn	Pro	Ser	Tyr	Asn	Ile
					660					665					670		
		Leu	Gly	Lys	Arg	Lys	Thr	Gly	Phe	Ile	Ile	Pro	Val	Ile	Ile	Ile	Val
					675				680					685			
55		Leu	Gly	Leu	Ile	Ala	Ser	Phe	Thr	Ile	Gly	Leu	Asn	Arg	Gly	Ile	Glu
					690			695					700				
		Phe	Ser	Gly	Gly	Arg	Asn	Tyr	Val	Val	Lys	Phe	Asp	Gln	Pro	Val	Ser
					705			710				715				720	
		Ser	Glu	Ala	Val	Arg	Ser	Ala	Leu	Ser	Ser	Pro	Leu	Gln	Glu	Lys	Val
60					725						730				735		
		Leu	Val	Thr	Ser	Ile	Gly	Thr	Glu	Gly	Thr	Glu	Val	Arg	Ile	Ser	Thr
					740					745					750		
		Asn	Tyr	Lys	Ile	Gln	Glu	Glu	Ser	Glu	Glu	Thr	Glu	Ala	Glu	Ile	Thr
					755				760					765			
65		Asp	Lys	Leu	Tyr	Gln	Ser	Leu	Lys	Gly	Phe	Tyr	Thr	Gln	Gln	Pro	Thr
					770			775						780			
		Ala	Asp	Gln	Phe	Leu	Asp	Asn	Ile	Ile	Ser	Ser	Gln	Lys	Val	Ser	Pro
					785			790				795				800	
		Ser	Met	Ser	Ser	Asp	Ile	Thr	Arg	Gly	Ala	Ile	Trp	Ala	Val	Leu	Leu
70					805						810					815	
		Ser	Met	Ile	Phe	Met	Ala	Ile	Tyr	Ile	Leu	Ile	Arg	Phe	Arg	Asp	Ile
					820					825					830		
		Ser	Phe	Ser	Ala	Gly	Val	Phe	Val	Ser	Val	Ala	Ala	Thr	Thr	Phe	Cys
					835				840					845			
75		Ile	Ile	Ala	Leu	Tyr	Ala	Leu	Leu	Trp	Lys	Ile	Leu	Pro	Phe	Thr	Met
					850			855					860				

WO 99/29870

PCT/AU98/01023

362/490

	Glu	Tyr	Gly	Lys	Thr	Leu	Phe	Pro	Val	Asp	Phe	Asn	His	Asp	Ala	Asp
	305					310					315					320
	Trp	Leu	Lys	Ala	Leu	Phe	Lys	Thr	Ala	Pro	Thr	Ser	Gln	Gly	Asp	Ile
				325						330					335	
5	Ser	Phe	Ser	Gly	Gly	Ser	Gln	Gly	Thr	Ser	Tyr	Tyr	Ala	Ser	Ile	Gly
				340					345					350		
	Tyr	Phe	Asp	Gln	Glu	Gly	Met	Ala	Arg	Glu	Pro	Ala	Asn	Phe	Lys	Arg
			355				360						365			
10	Tyr	Ser	Gly	Arg	Leu	Asn	Phe	Glu	Ser	Arg	Ile	Asn	Glu	Trp	Leu	Lys
			370				375					380				
	Val	Gly	Ala	Asn	Leu	Ser	Gly	Ala	Ile	Ala	Asn	Arg	Arg	Ser	Ala	Asp
	385				390					395					400	
	Tyr	Phe	Gly	Lys	Tyr	Met	Gly	Ser	Gly	Thr	Phe	Gly	Val	Leu	Thr	
				405					410					415		
15	Met	Pro	Arg	Tyr	Tyr	Asn	Pro	Phe	Asp	Val	Asn	Gly	Asp	Leu	Ala	Asp
				420					425					430		
	Val	Tyr	Tyr	Met	Tyr	Gly	Ala	Thr	Arg	Pro	Ser	Met	Thr	Glu	Pro	Tyr
			435					440					445			
20	Phe	Ala	Lys	Met	Arg	Pro	Phe	Ser	Ser	Glu	Ser	His	Gln	Ala	Asn	Val
		450					455					460				
	Asn	Gly	Phe	Ala	Gln	Ile	Thr	Pro	Ile	Lys	Gly	Leu	Thr	Leu	Lys	Ala
	465				470					475					480	
	Gln	Ala	Gly	Val	Asp	Ile	Thr	Asn	Thr	Arg	Thr	Ser	Ser	Lys	Arg	Met
				485					490					495		
25	Pro	Asn	Asn	Pro	Tyr	Asp	Ser	Thr	Pro	Leu	Gly	Glu	Arg	Arg	Glu	Arg
				500					505					510		
	Ala	Tyr	Arg	Val	Ser	Lys	Ser	Phe	Thr	Asn	Thr	Ala	Glu	Tyr	Lys	
		515				520						525				
30	Phe	Ser	Ile	Asp	Glu	Lys	His	Asp	Leu	Thr	Ala	Leu	Met	Gly	His	Glu
		530				535						540				
	Tyr	Ile	Glu	Tyr	Glu	Gly	Asp	Val	Ile	Gly	Ala	Ser	Ser	Lys	Gly	Phe
	545				550					555					560	
	Glu	Ser	Asp	Lys	Leu	Met	Leu	Leu	Ser	Gln	Gly	Lys	Thr	Gly	Asn	Ser
				565						570				575		
35	Leu	Ser	Leu	Pro	Glu	His	Arg	Val	Ala	Glu	Tyr	Ala	Tyr	Leu	Ser	Phe
			580						585					590		
	Phe	Ser	Arg	Phe	Asn	Tyr	Gly	Phe	Asp	Lys	Trp	Met	Tyr	Ile	Asp	Phe
		595					600						605			
40	Ser	Val	Arg	Asn	Asp	Gln	Ser	Ser	Arg	Phe	Gly	Ser	Asn	Asn	Arg	Ser
		610					615						620			
	Ala	Trp	Phe	Tyr	Ser	Val	Gly	Gly	Met	Phe	Asp	Ile	Tyr	Asn	Lys	Phe
		625				630					635				640	
	Ile	Gln	Glu	Ser	Asn	Trp	Leu	Ser	Asp	Leu	Arg	Leu	Lys	Met	Ser	Tyr
				645						650				655		
45	Gly	Thr	Thr	Gly	Asn	Ser	Glu	Ile	Gly	Asn	Tyr	Asn	His	Gln	Ala	Leu
			660						665					670		
	Val	Thr	Val	Asn	Asn	Tyr	Thr	Glu	Asp	Ala	Met	Gly	Leu	Ser	Ile	Ser
		675					680						685			
50	Thr	Ala	Gly	Asn	Pro	Asp	Leu	Ser	Trp	Glu	Lys	Gln	Ser	Gln	Phe	Asn
		690				695						700				
	Phe	Gly	Leu	Ala	Ala	Gly	Ala	Phe	Asn	Asn	Arg	Leu	Ser	Ala	Glu	Val
		705				710					715				720	
	Asp	Phe	Tyr	Val	Arg	Thr	Thr	Asn	Asp	Met	Leu	Ile	Asp	Val	Pro	Met
				725					730					735		
55	Pro	Tyr	Ile	Ser	Gly	Phe	Phe	Ser	Gln	Tyr	Gln	Asn	Val	Gly	Ser	Met
			740						745					750		
	Lys	Asn	Thr	Gly	Val	Asp	Leu	Ser	Leu	Lys	Gly	Thr	Ile	Tyr	Gln	Asn
		755					760						765			
60	Lys	Asp	Trp	Asn	Val	Tyr	Ala	Ser	Ala	Asn	Phe	Asn	Tyr	Asn	Arg	Gln
		770					775						780			
	Glu	Ile	Thr	Lys	Leu	Phe	Phe	Gly	Leu	Asn	Lys	Tyr	Met	Leu	Pro	Asn
		785				790					795				800	
	Thr	Gly	Thr	Ile	Trp	Glu	Ile	Gly	Tyr	Pro	Asn	Ser	Phe	Tyr	Met	Ala
				805					810					815		
65	Glu	Tyr	Ala	Gly	Ile	Asp	Lys	Lys	Thr	Gly	Lys	Gln	Leu	Trp	Tyr	Val
			820						825					830		
	Pro	Gly	Gln	Val	Asp	Ala	Asp	Gly	Asn	Lys	Val	Thr	Thr	Ser	Gln	Tyr
		835					840						845			
70	Ser	Ala	Asp	Leu	Glu	Thr	Arg	Ile	Asp	Lys	Ser	Val	Thr	Pro	Pro	Ile
		850					855					860				
	Thr	Gly	Gly	Phe	Ser	Leu	Gly	Ala	Ser	Trp	Lys	Gly	Leu	Ser	Leu	Asp
		865				870					875				880	
	Ala	Asp	Phe	Ala	Tyr	Ile	Val	Gly	Lys	Trp	Met	Ile	Asn	Asn	Asp	Arg
				885					890					895		
75	Tyr	Phe	Thr	Glu	Asn	Ala	Gly	Gly	Leu	Met	Gln	Leu	Asn	Lys	Asp	Lys

WO 99/29870

PCT/AU98/01023

363/490

5 900 905 910
Met Leu Leu Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro
 915 920 925
Lys Leu Gly Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala
 930 935 940
Ser Phe Leu Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn
945 950 955 960
Ser Leu Phe Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu
 965 970 975
10 Met Ala Arg Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro
 980 985 990
Glu Ala Gly Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln
 995 1000 1005
15 Tyr Val Ala Gly Ile Gln Leu Ser Phe
 1010 1015
(2) INFORMATION FOR SEQ ID NO:425
20 (ii) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1014 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
25 (iii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
30 (vii) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1014
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425
Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met
1 5 10 15
Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn
40 20 25 30
Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile
 35 40 45
Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala
 50 55 60
45 Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu
 65 70 75 80
Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys
 85 90 95
50 Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu
 100 105 110
Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala
 115 120 125
Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala
 130 135 140
55 Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser
 145 150 155 160
Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu
 165 170 175
60 Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met
 180 185 190
Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala
 195 200 205
Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln
 210 215 220
65 Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala
 225 230 235 240
Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met
 245 250 255
70 Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala Gly Phe Trp
 260 265 270
Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile Leu Ala Gly
 275 280 285
Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp Glu Tyr Gly
 290 295 300
75 Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp Trp Leu Lys

WO 99/29870

PCT/AU98/01023

365 / 490

5 Asn Ala Trp Thr Glu Asp Asn Lys Glu Thr Asp Val Pro Lys Leu Gly
915 920 925
Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala Ser Phe Leu
930 935 940
Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn Ser Leu Phe
945 950 955 960
Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu Met Ala Arg
965 970 975
10 Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro Glu Ala Gly
980 985 990
Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln Tyr Val Ala
995 1000 1005
Gly Ile Gln Leu Ser Phe
1010

15 (2) INFORMATION FOR SEQ ID NO:426

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 amino acids
(P) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

30 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...821

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426

Met Lys Lys Lys Asn Phe Leu Leu Leu Gly Ile Phe Val Ala Leu Leu
1 5 10 15
Thr Phe Ile Gly Ser Met Gln Ala Gln Gln Ala Lys Asp Tyr Phe Asn
20 25 30
40 Phe Asp Glu Arg Gly Glu Ala Tyr Phe Ser Phe Lys Val Pro Asp Arg
35 40 45
Ala Val Leu Gln Glu Leu Ala Ile Met Ser Ile Asp Glu Phe Asp
50 55 60
45 Pro Val Thr Asn Glu Ala Ile Ala Tyr Ala Ser Glu Glu Glu Phe Glu
65 70 75 80
Ala Phe Leu Arg Tyr Gly Leu Lys Pro Thr Phe Leu Thr Pro Pro Ser
85 90 95
Met Gln Arg Ala Val Glu Met Phe Asp Tyr Arg Ser Gly Glu Lys Tyr
100 105 110
50 Glu Trp Asn Ala Tyr Pro Thr Tyr Glu Ala Tyr Ile Ser Met Met Glu
115 120 125
Glu Phe Gln Thr Lys Tyr Pro Ser Leu Cys Thr Thr Ser Val Ile Gly
130 135 140
55 Lys Ser Val Lys Asp Arg Lys Leu Met Ile Cys Lys Leu Thr Ser Ser
145 150 155 160
Ala Asn Thr Gly Lys Lys Pro Arg Val Leu Tyr Thr Ser Thr Met His
165 170 175
Gly Asp Glu Thr Thr Gly Tyr Val Val Leu Leu Arg Leu Ile Asp His
180 185 190
60 Leu Leu Ser Asn Tyr Glu Ser Asp Pro Arg Ile Lys Asn Ile Leu Asp
195 200 205
Lys Thr Gln Val Trp Ile Cys Pro Leu Thr Asn Pro Asp Gly Ala Tyr
210 215 220
65 Arg Ala Gly Asn His Thr Val Gln Gly Ala Thr Arg Tyr Asn Ala Asn
225 230 235 240
Asn Val Asp Leu Asn Arg Asn Phe Lys Asp Asp Val Ala Gly Asp His
245 250 255
Pro Asp Gly Lys Pro Trp Gln Pro Glu Ala Thr Ala Phe Met Asp Leu
260 265 270
70 Glu Gly Asn Thr Ser Phe Val Leu Gly Ala Asn Ile His Gly Gly Thr
275 280 285
Glu Val Val Asn Tyr Pro Trp Asp Asn Lys Lys Glu Arg His Ala Asp
290 295 300
75 Asp Glu Trp Tyr Lys Leu Ile Ser Arg Asn Tyr Ala Ala Ala Cys Gln
305 310 315 320

WO 99/29870

PCT/AU98/01023

366/ 490

5 Ser Ile Ser Ala Ser Tyr Met Thr Ser Glu Thr Asn Ser Gly Ile Ile
325 330 335
Asn Gly Ser Asp Trp Tyr Val Ile Arg Gly Ser Arg Gln Asp Asn Ala
340 345 350
5 Asn Tyr Phe His Arg Leu Arg Glu Ile Thr Leu Glu Ile Ser Asn Thr
355 360 365
Lys Leu Val Pro Ala Ser Gln Leu Pro Lys Tyr Trp Asn Leu Asn Lys
370 375 380
10 Glu Ser Leu Leu Ala Leu Ile Glu Glu Ser Leu Tyr Gly Ile His Gly
385 390 395 400
Thr Val Thr Ser Ala Ala Asn Gly Gln Pro Leu Lys Cys Gln Ile Leu
405 410 415
15 Ile Glu Asn His Asp Lys Arg Asn Ser Asp Val Tyr Ser Asp Ala Thr
420 425 430
Thr Gly Tyr Tyr Val Arg Pro Ile Lys Ala Gly Thr Tyr Thr Val Lys
435 440 445
Tyr Lys Ala Glu Gly Tyr Pro Glu Ala Thr Arg Thr Ile Thr Ile Lys
450 455 460
20 Asp Lys Glu Thr Val Ile Met Asp Ile Ala Leu Gly Asn Ser Val Pro
465 470 475 480
Leu Pro Val Pro Asp Phe Thr Ala Ser Pro Met Thr Ile Ser Val Gly
485 490 495
Glu Ser Val Gln Phe Gln Asp Gln Thr Thr Asn Asn Pro Thr Asn Trp
500 505 510
25 Glu Trp Thr Phe Glu Gly Gly Gln Pro Ala Met Ser Thr Glu Gln Asn
515 520 525
Pro Leu Val Ser Tyr Ser His Pro Gly Gln Tyr Asp Val Thr Leu Lys
530 535 540
30 Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile
545 550 555 560
Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr
565 570 575
Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn
580 585 590
35 Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser
595 600 605
Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp
610 615 620
40 Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys
625 630 635 640
Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala
645 650 655
Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr
660 665 670
45 Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe
675 680 685
Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr
690 700
50 Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu
705 710 715 720
Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu
725 730 735
Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg
740 745 750
55 Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile
755 760 765
Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr
770 775 780
60 Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu
785 790 795 800
Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu
805 810 815
Lys Ile His Ile Gly
820

65 (2) INFORMATION FOR SEQ ID NO:427

70 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

75 (111) HYPOTHETICAL: YES

WO 99/29870

PCT/AU98/01023

368/ 490

5 Glu Arg Ile Val Asn Arg Lys Val Ser Arg Ile Leu Phe Asp Lys Arg
275 280 285
Ile Ile Ser Leu Asp Leu Ala Gln Met Val Ala Gly Thr Lys Tyr Arg
290 295 300
5 Gly Gln Phe Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Leu Lys Lys
305 310 315 320
Asn Pro Gln Ile Ile Leu Phe Ile Asp Glu Ile His Thr Ile Val Gly
325 330 335
10 Ala Gly Ser Ala Ala Gly Ser Met Asp Thr Ala Asn Met Leu Lys Pro
340 345 350
Ala Leu Ala Arg Gly Gln Val Gln Cys Ile Gly Ala Thr Thr Leu Asp
355 360 365
15 Glu Tyr Arg Lys Asn Ile Glu Lys Asp Gly Ala Leu Glu Arg Arg Phe
370 375 380
Gln Lys Val Pro Ile Ala Pro Ser Thr Ala Glu Glu Thr Leu Thr Ile
385 390 395 400
Leu Gln Asn Ile Lys Glu Lys Tyr Glu Asp Tyr His Gly Val Arg Tyr
405 410 415
20 Thr Asp Glu Ala Ile Lys Ala Ala Val Glu Leu Thr Asp Arg Tyr Val
420 425 430
Ser Asp Arg Phe Phe Pro Asp Lys Ala Ile Asp Ala Met Asp Glu Ala
435 440 445
Gly Ala Ser Val His Ile Thr Asn Val Val Ala Pro Lys Glu Ile Glu
450 455 460
25 Ile Leu Glu Ala Glu Leu Ala Ser Val Arg Glu Asn Lys Leu Ser Ala
465 470 475 480
Val Lys Ala Gln Asn Tyr Glu Leu Ala Ala Ser Phe Arg Asp Gln Glu
485 490 495
30 Arg Arg Thr Gln Gln Gln Ile Ala Glu Glu Lys Lys Lys Trp Glu Glu
500 505 510
Gln Met Ser Lys His Arg Glu Thr Val Asp Glu Asn Val Val Ala His
515 520 525
Val Val Ala Leu Met Thr Gly Val Pro Ala Glu Arg Leu Ser Thr Gly
530 535 540
35 Glu Gly Glu Arg Leu Arg Thr Met Ala Asp Asp Leu Lys Thr Lys Val
545 550 555 560
Val Gly Gln Asp Thr Ala Ile Glu Lys Met Val His Ala Ile Gln Arg
565 570 575
40 Asn Arg Leu Gly Leu Arg Asn Glu Lys Lys Pro Ile Gly Ser Phe Leu
580 585 590
Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Tyr Leu Ala Lys Lys Leu
595 600 605
Ala Glu Tyr Leu Phe Glu Asp Glu Asn Ala Met Ile Arg Val Asp Met
610 615 620
45 Ser Glu Tyr Met Glu Lys Phe Ser Val Ser Arg Leu Val Gly Ala Pro
625 630 635 640
Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu Thr Glu Arg Val
645 650 655
50 Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu Ile Glu Lys Ala
660 665 670
His Ala Asp Val Phe Asn Leu Leu Leu Gln Val Met Asp Glu Gly Gln
675 680 685
Leu Thr Asp Ser Leu Gly Arg Arg Val Asn Phe Lys Asn Thr Val Ile
690 695 700
55 Ile Ile Thr Ser Asn Val Gly Thr Arg Gln Leu Lys Asp Phe Gly Gln
705 710 715 720
Gly Ile Gly Phe Arg Ser Glu Lys Asp Glu Ala Asn Lys Glu His
725 730 735
60 Ser Arg Ser Val Ile Gln Lys Ala Leu Asn Lys Thr Phe Ser Pro Glu
740 745 750
Phe Leu Asn Arg Leu Asp Asp Ile Ile Leu Phe Asp Gln Leu Gly Lys
755 760 765
Thr Glu Ile Arg Arg Met Val Asp Ile Glu Leu Lys Ala Val Leu Ala
770 775 780
65 Arg Ile His Arg Ala Gly Tyr Asp Leu Val Leu Thr Asp Glu Ala Lys
785 790 795 800
Asp Val Ile Ala Thr Lys Gly Tyr Asp Leu Gln Tyr Gly Ala Arg Pro
805 810 815
70 Leu Lys Arg Thr Leu Gln Asn Glu Val Glu Asp Arg Leu Thr Asp Leu
820 825 830
Ile Leu Ser Gly Gln Ile Glu Lys Gly Gln Thr Leu Thr Leu Ser Ala
835 840 845
Arg Asp Gly Glu Ile Ile Val Gln Glu Gln Ala
850 855
75

370/ 490

(2) INFORMATION FOR SEQ ID NO:430

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...293
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

Met Lys Gln Asn Tyr Phe Lys Arg Val Cys Ser Leu Leu Trp Leu Val
 1 5 10 15
 Leu Pro Met Leu Ile Met Pro Leu Glu Val Ala Ala Gln Glu Ile Ile
 20 25 30
 Pro Asn Glu Glu Val Leu Glu Ser Leu Thr Phe Val Ala Pro Val Glu
 35 40 45
 Glu Thr Asp Ala Ile Glu Ala Glu Val Glu Ala Leu Gln Glu Ile Val
 50 55 60
 Ala Thr Glu Glu Ile Ala Glu Gln Ala Val Arg Ser Tyr Thr Tyr Thr
 65 70 75 80
 Val Tyr Arg Asp Gly Val Lys Ile Ala Ser Gly Leu Thr Glu Pro Thr
 85 90 95
 Phe Leu Asp Glu Asp Val Pro Ala Gly Glu His Thr Tyr Cys Val Glu
 100 105 110
 Val Gln Tyr Gln Gly Gly Val Ser Asp Lys Val Cys Val Asp Val Glu
 115 120 125
 Val Lys Asp Phe Lys Pro Val Thr Asn Leu Thr Gly Thr Ala Ser Asn
 130 135 140
 Asp Glu Val Ser Leu Asp Trp Asp Gly Val Glu Glu Lys Ala Glu Glu
 145 150 155
 Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn Val Tyr Lys Asn Gly Thr
 160 165 170 175
 Leu Ile Gly Asn Thr Ala Glu Thr His Tyr Val Glu Thr Gly Val Ala
 180 185 190
 Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val Lys Tyr Pro Asp Gly Val
 195 200 205
 Ser Pro Lys Val Ala Val Thr Val Thr Val Thr Asn Ser Ser Leu Ser
 210 215 220
 Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu Arg Val Glu Gly Lys Lys
 225 230 235 240
 Ile Ile Ala Glu Ala His Gly Met Ile Thr Leu Tyr Asp Ile Asn Gly
 245 250 255
 Arg Thr Val Ala Val Ala Pro Asn Arg Leu Glu Tyr Met Ala Gln Thr
 260 265 270
 Gly Phe Tyr Ala Val Arg Phe Asp Val Gly Asn Lys His His Val Ser
 275 280 285
 Lys Ile Gln Val Arg
 290

(2) INFORMATION FOR SEQ ID NO:431

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature

WO 99/29870

PCT/AU98/01023

371/ 490

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```

5 Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile Trp
  1      5      10      15
Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu Thr
  20      25      30
10 Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr Ile
  35      40      45
Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro Glu
  50      55      60
Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Tyr Trp Val Cys
  65      70      75
15 Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser Ser
  85      90      95
Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu Glu
  100      105      110
Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly Asn
  115      120      125
20 Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn Asp
  130      135      140
Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe Trp
  145      150      155
25 Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg Arg
  165      170      175
Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg Arg
  180      185      190
30 Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp Thr
  195      200      205
Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr Leu
  210      215      220
Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn Ser
  225      230      235
35 Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val Gly
  245      250      255
Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr Asp
  260      265      270
40 Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr Lys
  275      280      285
Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr Val
  290      295      300
Tyr Thr Glu Lys Ile Gln Ile Gln
  305      310

```

(2) INFORMATION FOR SEQ ID NO:432

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 843 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

```

65 Met Lys Lys Ser Phe Leu Leu Ala Ile Val Met Leu Phe Gly Ile Ala
  1      5      10      15
Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu
  20      25      30
70 Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala
  35      40      45
Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala
  50      55      60
75 Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr
  65      70      75      80

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WO 99/29870

PCT/AU98/01023

372/ 490

Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr Ala Leu Val Ala Ala Asp
 85 90 95
 Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser Pro Ile Gly Arg Phe Asp
 100 105 110
 5 Met Asp Ser Met Pro Asp Asn Leu Arg Met Trp Leu Gln Ile Tyr Asp
 115 120 125
 Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys Ala Gln Leu Asn Glu Glu
 130 135 140
 10 Ile Leu Arg Thr Glu Gly Val Pro Ala Glu Val His Ala Leu Met Asp
 145 150 155 160
 Asn Gly His Phe Ala Asn Asp Pro Met Arg Trp Asn Gln Gly Tyr Pro
 165 170 175
 Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn Gly Asn His Ala Tyr Thr
 180 185 190
 15 Gly Cys Val Ala Thr Ala Ala Ala Gln Ile Met Arg Tyr His Ser Trp
 195 200 205
 Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr His Ala Gly Ser Leu Val
 210 215 220
 20 Gly Asn Trp Ser Gly Thr Phe Gly Glu Met Tyr Asp Trp Ile Asn Met
 225 230 235 240
 Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr Gln Ser Gln Val Asp Ala
 245 250 255
 Tyr Ala Thr Leu Met Arg Asp Val Ser Ala Ser Val Ser Met Ser Phe
 260 265 270
 25 Tyr Glu Asn Gly Ser Gly Thr Tyr Ser Val Tyr Val Val Gly Ala Leu
 275 280 285
 Arg Asn Asn Phe Arg Tyr Lys Arg Ser Leu Gln Leu His Val Arg Ala
 290 295 300
 30 Leu Tyr Thr Ser Gln Glu Trp His Asp Met Ile Arg Gly Glu Leu Ala
 305 310 315 320
 Ser Gly Arg Pro Val Tyr Tyr Ala Gly Asn Asn Gln Ser Ile Gly His
 325 330 335
 Ala Phe Val Cys Asp Gly Tyr Ala Ser Asp Gly Thr Phe His Phe Asn
 340 345 350
 35 Trp Gly Trp Gly Gly Val Ser Asn Gly Phe Tyr Lys Leu Thr Leu Leu
 355 360 365
 Ser Pro Thr Ser Leu Gly Ile Gly Gly Glu Gly Ile Gly Phe Thr Ile
 370 375 380
 40 Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro Ala Lys Thr Pro Ala Glu
 385 390 395 400
 Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala Leu Lys Asp Ile Glu Ala
 405 410 415
 Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val Gly Tyr Ser Ile Tyr Asn
 420 425 430
 45 Thr Gly Glu Glu Gln Ser Asn Leu Asp Leu Gly Tyr Arg Leu Asn Lys
 435 440 445
 Ala Asp Gly Glu Val Ile Glu Val Lys Thr Ser Ser Ile Asn Ile Ser
 450 455 460
 50 Trp Tyr Gly Tyr Gly Glu His Pro Glu Ser Phe Ser Leu Ala Pro Asn
 465 470 475 480
 Gln Leu Ser Gln Gly Ile Asn Thr Ile Thr Leu Leu Tyr Arg Arg Thr
 485 490 495
 Gly Thr Glu Gln Trp Glu Pro Val Arg His Ala Gln Gly Gly Tyr Val
 500 505 510
 55 Asn Ser Ile Lys Val Asn Thr Thr Asp Pro Asn Asn Val Val Val Thr
 515 520 525
 Val Asp Asn Asn Glu Gly Lys Leu Ser Ile Val Pro Asn Ser Phe Val
 530 535 540
 60 Ala Asp Leu Asn Ser Tyr Glu His Ser Thr Ile Thr Val Gln Phe Asn
 545 550 555 560
 Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro Val Ala Phe Ala Leu Ser
 565 570 575
 Thr Gly Ala Thr Ala Asp Asp Val Ile Ser Leu Gly Trp Val Met Ala
 580 585 590
 65 Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro Val Val Trp Ser Lys Asp
 595 600 605
 Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr Leu Trp Tyr Arg Phe Ser
 610 615 620
 70 Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys Ile Gly Ser Val Ser Val
 625 630 635 640
 Lys Thr Pro Thr Glu Tyr Thr His Pro Leu Phe Glu Val Gly His Asn
 645 650 655
 Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala His Asn Arg Val Leu Pro
 660 665 670
 75 Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro Phe Asn Gly Glu Leu Val

WO 99/29870

PCT/AU98/01023

373/490

675 680 685
Val Val Phe Arg Gln Thr Gln Ser Ser Ser Gly Ser Leu Trp Ala Ala
690 695 700
5 Gln Glu Thr Val His Ile Lys Gln Gly Glu Thr Phe Val Tyr Lys Pro
705 710 715
Val Val Glu Gly Pro Ile Pro Asp Gly Ser Tyr Arg Ala Thr Leu His
720 725 730 735
Ala Phe Val Asn Gly Gln Gln Gln Leu Tyr Leu Lys Gly Lys Arg Asn
740 745 750
10 Tyr Thr Val Lys Ile Val Asn Gly Thr Ala Val Glu Ala Ile Glu Ser
755 760 765
Ser Glu Glu Ile Arg Val Phe Pro Asn Pro Ala Arg Asp Tyr Val Glu
770 775 780
15 Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr Ser Ile Ile Leu Phe Asp
785 790 795 800
Leu Ser Gly Lys Ile Val Met Lys Asn Ser Leu Ser Ala Gly His Gly
805 810 815
Arg Met Asp Val Ser Arg Leu Pro Asn Gly Ala Tyr Ile Leu Lys Val
820 825 830
20 Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val His
835 840

(2) INFORMATION FOR SEQ ID NO:433

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

35 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...290

40 (iii) SEQUENCE DESCRIPTION: SEQ ID NO:433

Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu Val Met Val Phe Ala
1 5 10 15
45 Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln Thr Leu Leu Pro Ala
20 25 30
Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp Asn Pro Ser Glu Ile
35 40 45
50 Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val Leu Ala Glu Glu Phe
50 55 60
Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly His Arg Lys Leu Ala
65 70 75 80
Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr Val Val Gly Ile His
85 90 95
55 Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe Arg Thr Glu Ala Gly
100 105 110
Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr Pro Leu Pro Ala Leu
115 120 125
60 Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr Val Tyr Asp Lys Ser
130 135 140
Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln Met Glu Gln Lys Ala
145 150 155 160
Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr Asp Thr Gln Lys Ile
165 170 175
65 Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly Asn Thr Leu Pro Lys
180 185 190
Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys Leu Ile Ala Pro Gln
195 200 205
70 Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu His Asn His Val Leu
210 215 220
Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu Phe Val Asn Leu Lys
225 230 235 240
Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu Ser Gly Met Ser Phe
245 250 255
75 Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val Tyr Asp Val Gln Thr

375/490

```

Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys Ser Leu Cys Phe Ile
1      5      10      15
Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn Val Arg Asn Ser Gln
20      25      30
5 Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys Pro Ser Asp Ser Val
35      40      45
Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu Glu Phe Arg Asn Lys
50      55      60
10 Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu Tyr Glu Asn Arg Leu
65      70      75      80
Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp Leu Tyr Gly Glu Asp
85      90      95
Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly Ala Gly Thr Asp Val
100      105      110
15 Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser Ser Phe Val Met Pro
115      120      125
Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly Tyr Arg Arg Arg Phe
130      135      140
20 Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val Asn Arg Gly Asp Thr
145      150      155      160
Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val Arg Ser Tyr Glu Ala
165      170      175
Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His Pro Asn Gly Leu Glu
180      185      190
25 Thr Val Tyr Gly His Met Ser Arg Gln Leu Val Asp Glu Asn Gln Ile
195      200      205
Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly Ser Thr Gly Arg Ser
210      215      220
30 Thr Gly Pro His Leu His Phe Glu Thr Arg Phe Met Gly Ile Pro Ile
225      230      235      240
Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly Val Pro Leu Arg Asp
245      250      255
Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg Tyr Ala Lys Ala Ser
260      265      270
35 Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys Lys Gly Arg Gln Ala
275      280      285
Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly Asp Thr Leu Glu Thr
290      295      300
40 Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys Leu Cys Ala Thr Asn
305      310      315      320
Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly Lys Ala Leu Arg Ile
325      330      335
Lys

```

- 45 (2) INFORMATION FOR SEQ ID NO:436
- 50 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 55 (11) MOLECULE TYPE: protein
- (11) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- 60 (1x) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...151
- 65 (x1) SEQUENCE DESCRIPTION: SEQ ID NO:436

```

Met Ala Lys Ile Asn Phe Tyr Ala Glu Gly Val Ser Leu Pro Arg Ile
1      5      10      15
Arg Arg Arg Ile Val Gly Lys Trp Ile Ala Glu Val Cys Ser Arg Tyr
20      25      30
70 Gly Lys Ala Val Gly Glu Ile Ser Tyr Leu Phe Cys Asp Asp Glu Tyr
35      40      45
Ile Leu Lys Ala Asn Gln Glu Phe Leu Asp His Asp Tyr Tyr Thr Asp
50      55      60
75 Ile Ile Thr Phe Asp Ser Cys Glu Ala Asp Thr Val Asn Gly Asp Leu
65      70      75      80

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376/490

Leu Ile Ser Leu Asp Thr Val Arg Ser Asn Ala Arg Ala Leu Asp Leu
 85 90 95
 Arg Tyr Glu Asp Glu Leu His Arg Val Ile Ile His Gly Ile Leu His
 100 105 110
 5 Leu Cys Gly Leu Lys Asp Lys Ser Lys Lys Asp Glu Ala Gln Met Arg
 115 120 125
 Ala Ala Glu Glu Lys Ala Leu Val Met Leu Arg Glu Thr Ile Gly Ser
 130 135 140
 10 Glu Leu Ser Leu Leu His Thr
 145 150

(2) INFORMATION FOR SEQ ID NO:437

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...391
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly Ala Ile Ala Leu
 1 5 10 15
 35 Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr Gly Gln Leu Pro
 20 25 30
 Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly Ser Asn Trp Phe
 35 40 45
 Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu Asn Asp Asn Asn
 50 55 60
 40 Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly Ser Leu Ser Val
 65 70 75 80
 Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu Gln Ile Asn Gly
 85 90 95
 45 Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu Gln Glu Ile Asn
 100 105 110
 Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe Asp Val Val Asn
 115 120 125
 Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His Leu Ile Pro Trp
 130 135 140
 50 Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser Glu Trp Ser Lys
 145 150 155 160
 Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val Met Met Ala Phe
 165 170 175
 55 Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala Gln Ala His
 180 185 190
 Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys Lys Thr Pro Val
 195 200 205
 Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe Gln Gly Met Ala
 210 215 220
 60 Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly Phe Asn Ala Ile
 225 230 235 240
 Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn Gly Gln Ile Asn
 245 250 255
 65 Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg Pro Val Ser Cys
 260 265 270
 Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr Glu Asn Ile Leu
 275 280 285
 Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His Val Val Asp Lys
 290 295 300
 70 Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe Val Lys Glu Thr
 305 310 315 320
 Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro Thr Gly Asn Thr
 325 330 335
 75 Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Val Asp
 340 345 350

WO 99/29870

PCT/AU98/01023

377/ 490

Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu Ile Ser Val Glu
355 360 365
Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys Ala Trp Asn Arg
370 375 380
5 Val Val Ile Val Arg Ser Lys
385 390

(2) INFORMATION FOR SEQ ID NO:438

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(iii) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...385

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

30 Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala Leu Ala
1 5 10 15
Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr Thr Gln
20 25 30
Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala Ser Asp
35 40 45
His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu Ser Gly
50 55 60
Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val Pro Thr
65 70 75 80
Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg Leu Gln
85 90 95
40 Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys Glu Arg
100 105 110
Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe Asp Leu
115 120 125
45 Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His Ile Ile
130 135 140
Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe Ser Glu Asn Ala
145 150 155 160
Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr Val Asn
165 170 175
50 Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp Phe Asn
180 185 190
Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly Thr Lys
195 200 205
55 Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu Thr Phe
210 215 220
Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp Tyr Ala
225 230 235 240
Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly Gln Val
245 250 255
60 Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro Glu Pro
260 265 270
Thr Gln Pro Thr Val Thr Arg Val Val Asp Asn Val Val Tyr Phe
275 280 285
65 Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn Val Tyr
290 295 300
Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys Val Val
305 310 315 320
Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met Lys Leu
325 330 335
70 Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys Tyr Gly
340 345 350
Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser Glu Gln
355 360 365
75 Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr Ala Ala
370 375 380

WO 99/29870

PCT/AU98/01023

378/490

Glu
385

5 (2) INFORMATION FOR SEQ ID NO:439

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1...190

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

25 Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val
1 5 10 15
Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys
20 25 30
Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu
35 40 45
Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp
50 55 60
Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile
65 70 75 80
Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro
85 90 95
Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn
100 105 110
Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr
115 120 125
Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr
130 135 140
Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr
145 150 155 160
Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala
165 170 175
Glu Ile Leu Ala Met Ala Phe Met Gly Phe Ser Gly Ile Ala
180 185 190

50 (2) INFORMATION FOR SEQ ID NO:440

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

60 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...186

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

70 Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val Val Leu Ser Gln
1 5 10 15
Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys Lys Val Asp Thr
20 25 30
Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu Ala Leu Ala Thr
35 40 45
Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp Arg Phe Gly Leu
75

WO 99/29870

PCT/AU98/01023

379/ 490

50 55 60
Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile Ala Ala Leu Val
65 70 75 80
Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro Pro Leu Tyr Gln
85 90 95
Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn Cys Cys Val Leu
100 105 110
Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr Leu Leu Gln Ser
115 120 125
10 Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr Leu Ala Met Val
130 135 140
Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr Asn Leu Pro Lys
145 150 155 160
Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala Gly Ile Leu Ala
15 165 170 175
Met Ala Phe Met Gly Phe Ser Gly Ile Ala
180 185

(2) INFORMATION FOR SEQ ID NO:441

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

40 Met Lys Gln Leu Asn Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu
1 5 10 15
Gly Thr Ser Ala Ser Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr
20 25 30
Val Val Asp Lys Ser Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe
35 40 45
45 Val Lys Gly Thr Thr Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr
50 55 60
Ser Ile Lys Gly Ile Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu
65 70 75 80
50 Met Gly Tyr Ser Thr Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly
85 90 95
Ser Arg His Val Asp Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp
100 105 110
Gly Val Val Val Ser Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala
115 120 125
55 Pro Ser Leu Val Thr Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn
130 135 140
Ser Thr Asn Leu Ser Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val
145 150 155 160
60 Glu Asp Asn Cys Gln Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly
165 170 175
Leu Glu Gly Ala Tyr Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe
180 185 190
Ser Ser Leu Ala Gly Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met
195 200 205
65 Ile Glu Arg Val Glu Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly
210 215 220
Ser Asn Ala Val Gly Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu
225 230 235 240
70 Arg Asn Ser Ala Glu Ile Ser His Ser Thr Met Thr Phe Asp His Ala
245 250 255
Lys Gly Trp Gly Ser Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met
260 265 270
Leu Thr Glu Asp Arg Lys Ala Gly Val Met Val Phe Gly Gln His Asn
275 280 285
75 Tyr Arg Pro Gly Gln Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

380/ 490

290 295 300
 Asn Leu Arg Asn Arg Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly
 305 310 315 320
 5 Leu Tyr Ser Lys Ala Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg
 325 330 335
 Arg Gly Gly Asp Arg Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala
 340 345 350
 Glu Tyr Leu Gln His Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln
 355 360 365
 10 Gly Phe Ser Gly Gly Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln
 370 375 380
 Asp Val Gln Arg Arg Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn
 385 390 395 400
 15 Leu Leu Asn Gly Ala Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr
 405 410 415
 Asn Asp Ala Phe Thr Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe
 420 425 430
 Asp Leu Gln Gly Gly Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp
 435 440 445
 20 Asp Phe Thr Gly Gly Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg
 450 455 460
 Ser Gly Tyr Arg Pro Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser
 465 470 475 480
 25 Gln Tyr Asp Gln Leu Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile
 485 490 495
 Gly Ala Arg Ile Asp Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr
 500 505 510
 Ile Asp Pro Leu Phe Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn
 515 520 525
 30 Pro Asn Lys Asn Leu Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg
 530 535 540
 Ala Pro Gln Tyr Phe Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly
 545 550 555 560
 35 Thr Pro Ile Ser Arg Val Leu Ser Pro Asn Leu Lys Glu Glu Arg Ser
 565 570 575
 Arg Ser Ile Ser Ala Ser Phe Asp Tyr Tyr His Arg Ala Asp Glu Trp
 580 585 590
 Gln Phe Asn Ile Met Gly Glu Ala Phe Ser Thr Phe Ile Ser Asn Gln
 595 600 605
 40 Phe Lys Pro Ser Asp Lys Val Glu Thr Thr Ser Asp Gly Lys Glu Trp
 610 615 620
 Ile Ile Arg Thr Ile Tyr Asn Asp Lys Asp Gly Val Ser Lys Val Tyr
 625 630 635 640
 45 Gly Val Asn Leu Glu Gly Arg Ile Ala Tyr Asn Lys Ser Phe Asp Leu
 645 650 655
 Gln Leu Gly Gly Thr Trp Gln Arg Ser Arg Tyr Gly Ser Ile Tyr Thr
 660 665 670
 Ala Val Glu Ala Asp Lys Thr Thr Gly Gln Ala Glu Ile Ser Val Lys
 675 680 685
 50 Asp Tyr Val Arg Thr Pro Asn Leu Tyr Gly Tyr Phe Val Ala Thr Val
 690 695 700
 Arg Pro Thr Glu His Phe Ala Ile Asn Leu Ser Gly Thr Phe Thr Gly
 705 710 715 720
 55 Lys Met Asp Val Val His Glu Ala Tyr Glu Gly Asp Ile Pro Ala Glu
 725 730 735
 His Ile Ala Pro Asp Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln
 740 745 750
 Phe Lys Gly Leu Ala Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala
 755 760 765
 60 Phe Ala Asp Ile Asp Leu Lys Leu Ser His Asp Phe His Leu Ala Ser
 770 775 780
 Thr Met Thr Leu Glu Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser
 785 790 795 800
 65 Tyr Gln Lys Asp Thr Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val
 805 810 815
 Tyr Gly Pro Met Gln Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn
 820 825 830
 Phe

70

(2) INFORMATION FOR SEQ ID NO:442

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 amino acids

(B) TYPE: amino acid

75

WO 99/29870

PCT/AU98/01023

381/ 490

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

15 Met Tyr Lys Lys Ile Ile Ala Val Ala Ala Leu Phe Cys Ala Ser Ile
1 5 10 15
Gly Ile Leu Lys Gly Gln Ser Ser Asp Leu Thr Pro Gln Asp Thr Ile
20 25 30
Tyr Ser Pro Glu Ile Ser Tyr Ala Lys Pro Ile His Lys Thr Ile Ala
35 40 45
Ser Ile Glu Ile Glu Gly Met Arg Ser Phe Asp Asp Phe Val Leu Arg
50 55 60
Asn Leu Ser Gly Leu Ala Val Gly Asp Glu Val Leu Ile Pro Gly Asp
25 65 70 75 80
Ala Met Ser Ala Ala Val Asn Arg Ile Met Arg Gln Gly Tyr Phe Ser
85 90 95
Asn Val Arg Ile Ile Ala Asp Lys Tyr Val Gly Asn Lys Val Tyr Leu
100 105 110
30 Lys Ile Ile Val Thr Glu Arg Pro Arg Ile Ser Lys Val Thr Phe Ser
115 120 125
Gly Val Lys Lys Ser Glu Arg Glu Asp Leu Glu Met Lys Ile Gly Leu
130 135 140
35 Arg Glu Gly Ile Gln Met Thr Arg Asn Asn Glu Asp Lys Val Arg Gln
145 150 155 160
Ile Val Gln Lys Tyr Phe Ser Glu Lys Gly Tyr Arg Asp Ala Ser Ile
165 170 175
Arg Ile Thr Gln Glu Pro Asp Leu Ser Lys Asp Gly Phe Val Asn Val
180 185 190
40 Leu Ile Ser Ile Glu Lys Lys Ser Lys Thr Lys Val Asn Glu Ile Tyr
195 200 205
Phe Ser Gly Asn Lys Ala Leu Ser Asn His Lys Leu Arg Met Ala Met
210 215 220
45 Lys Asn Thr Asn Ala Lys Phe Ser Leu Arg Lys His Ile Arg Ser Ser
225 230 235 240
Phe Leu Lys Leu Phe Ser Thr His Lys Phe Val Glu Glu Ser Tyr Arg
245 250 255
Glu Asp Leu Val Arg Leu Ile Glu Lys Tyr Gln Glu Tyr Gly Tyr Arg
260 265 270
50 Asp Ala Glu Ile Leu Thr Asp Ser Val Val Lys Ala Pro Asp Gly Lys
275 280 285
Arg Val Asp Ile Tyr Leu Asn Ile Glu Glu Gly Gln Lys Tyr Tyr Ile
290 295 300
55 Lys Asp Val Asn Phe Val Gly Asn Ser Gln Tyr Pro Ser Glu Tyr Leu
305 310 315 320
Glu Arg Val Leu Gly Ile Lys Ser Gly Asp Val Tyr Asn Gln Arg Arg
325 330 335
Leu Ala Lys Arg Leu Asn Glu Asp Glu Asp Ala Val Gly Asn Leu Tyr
340 345 350
60 Tyr Asn Asn Gly Tyr Ile Phe Ala Trp Val Asp Pro Val Glu Thr Asn
355 360 365
Val Val Gly Asp Ser Val Ser Leu Asp Ile Arg Ile Ala Glu Gly Lys
370 375 380
65 Gln Ala Asn Ile Asn Lys Val Ile Ile Lys Gly Asn Thr Val Val Tyr
385 390 395 400
Glu Asp Val Val Arg Arg Glu Leu Tyr Thr Lys Pro Gly Gln Leu Phe
405 410 415
Ser Arg Glu Asp Ile Ile Asn Ser Ile Arg Leu Ile Asn Gln Leu Gly
420 425 430
70 His Phe Asp Ala Glu Lys Ser Ile Pro Arg Pro Ile Pro Asn Pro Glu
435 440 445
Thr Gly Thr Val Asp Ile Glu Tyr Asp Leu Val Pro Arg Ser Ser Asp
450 455 460
75 Gln Leu Glu Leu Ser Val Gly Trp Ser Gln Ser Gly Leu Leu Phe Arg
465 470 475 480

WO 99/29870

PCT/AU98/01023

382/490

5 Gly Ala Ile Lys Phe Thr Asn Phe Ser Val Gly Asn Leu Leu His Pro
485 490 495
Ser Met Tyr Lys Lys Gly Ile Ile Pro Gln Gly Asp Gly Gln Thr Leu
500 505 510
10 Ser Leu Ser Ala Gln Thr Asn Gly Lys Tyr Tyr Gln Gln Tyr Ser Val
515 520 525
Thr Phe Met Asp Pro Trp Phe Gly Gly Lys Arg Pro Asp Met Phe Ser
530 535 540
Phe Ser Ala Phe Tyr Ser Lys Thr Thr Ala Ile Asp Ser Lys Phe Tyr
545 550 555 560
15 Asn Ser Asn Ala Gly Asn Tyr Tyr Asn Ala Tyr Tyr Asn Ser Tyr Tyr
565 570 575
Asn Asn Tyr Asn Ser Tyr Tyr Asn Gly Met Ser Asn Tyr Thr Gly Asp
580 585 590
Leu Tyr Thr Gln Ala Ser Asp Pro Asp Arg Ser Leu Gln Met Leu Gly
595 600 605
20 Thr Ser Ile Gly Tyr Gly Lys Arg Leu Thr Trp Pro Asp Asn Trp Phe
610 615 620
Gln Ile Tyr Thr Ser Leu Asn Tyr Thr Tyr Arg Leu Arg Asn Trp
625 630 635 640
Ser Tyr Asn Thr Phe Gln Asn Phe His His Gly Ser Ala Asn Asp Leu
645 650 655
25 Asn Leu Glu Leu Arg Leu Ser Arg Thr Ser Ile Asp Asn Pro Ile Tyr
660 665 670
Thr Arg Ser Gly Ser Asp Phe Met Val Ser Val Ala Ala Thr Leu Pro
675 680 685
Tyr Ser Leu Trp Asp Asn His Asp Tyr Ala Ser Gln Asn Leu Ser Val
690 695 700
30 Ser Asp Arg Tyr Arg Phe Ile Glu Tyr His Lys Trp Lys Phe Arg Gly
705 710 715 720
Arg Val Phe Thr Pro Leu Leu Asn Pro Ala Thr His Lys Tyr Thr Pro
725 730 735
Val Leu Met Ser Arg Val Glu Gly Ala Val Leu Gly Ser Tyr Asn Ser
740 745 750
35 Asn Lys Lys Ser Pro Phe Gly Thr Phe Tyr Met Gly Gly Asp Gly Met
755 760 765
Ser Ser Tyr Tyr Gly Gly Tyr Met Asn Glu Thr Ile Gly Leu Arg Gly
770 775 780
40 Tyr Lys Asn Gly Ser Ile Ala Gly Asn Asn Tyr Asp Tyr Ala Tyr Ala
785 790 795 800
Tyr Met Arg Leu Thr Met Glu Leu Arg Phe Pro Ile Leu Phe Glu Asn
805 810 815
Ser Phe Asn Ala Trp Leu Leu Ala Phe Ala Glu Ala Gly Asn Ala Trp
820 825 830
45 Arg Ser Ile Asp Asn Tyr Asn Pro Phe Asn Leu Lys Arg Ser Ala Gly
835 840 845
Val Gly Leu Arg Val Thr Leu Pro Met Val Gly Met Leu Gly Ile Asp
850 855 860
50 Trp Gly Tyr Gly Phe Asp Arg Pro Asp Asn Ser Leu Gln Arg Gly Gly
865 870 875 880
Ser Asn Val His Phe Val Leu Gly Gln Glu Phe
885 890

(2) INFORMATION FOR SEQ ID NO:443

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu
1 5 10 15

383/ 490

Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met
 20 25 30
 Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln
 35 40 45
 5 Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu
 50 55 60
 Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe
 65 70 75 80
 10 Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys
 85 90 95
 Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly
 100 105 110
 Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu
 115 120 125
 15 Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met
 130 135 140
 Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile
 145 150 155 160
 20 Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:444

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...170
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu Ala Val Ala Phe
 1 5 10 15
 45 Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met Glu Tyr Ile Leu
 20 25 30
 Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln Leu Glu Gln Val
 35 40 45
 Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu Asn Glu Ala Gln
 50 55 60
 Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe Leu Ser Ala Ala
 65 70 75 80
 Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys Glu Gln Gln Ala
 85 90 95
 55 Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly Glu Leu Tyr Lys
 100 105 110
 Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu Ile Trp Asn Ala
 115 120 125
 Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met Val Leu Asp Arg
 130 135 140
 60 Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile Asp Ile Ser Asp
 145 150 155 160
 Leu Val Leu Ser Lys Met Gly Phe Ser Lys
 165 170

65 (2) INFORMATION FOR SEQ ID NO:445

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

384/ 490

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

10 Met Lys Lys Phe Phe Leu Met Leu Leu Met Ala Leu Pro Leu Ser Leu
1 5 10 15
Leu Ala Gln Lys Val Ala Val Val Asn Thr Glu Glu Ile Ile Ser Lys
20 25 30
Met Pro Glu Gln Val Ala Ala Thr Lys Gln Leu Asn Glu Leu Ala Glu
15 35 40 45
Lys Tyr Arg Leu Asp Leu Lys Ser Met Asp Asp Glu Phe Ala Lys Lys
50 55 60
Thr Glu Glu Phe Val Lys Glu Lys Asp Ser Leu Glu Asn Ile Arg
65 70 75 80
20 Asn Arg Arg Gln Gln Glu Leu Gln Asp Ile Gln Thr Arg Tyr Gln Gln
85 90 95
Ser Tyr Gln Thr Met Gln Glu Asp Leu Gln Lys Arg Gln Gln Gln Leu
100 105 110
Phe Ala Pro Ile Gln Gln Lys Val Ala Asp Ala Ile Lys Lys Val Gly
115 120 125
25 Asp Glu Glu Asn Cys Ala Tyr Ile Met Glu Ala Gly Met Met Leu Tyr
130 135 140
Thr Gly Ala Thr Ala Ile Asp Leu Thr Ala Lys Val Lys Ala Lys Leu
145 150 155 160
30 Gly Ile Lys

(2) INFORMATION FOR SEQ ID NO:446

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(v1) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...827

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn Gly
1 5 10 15
55 Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser Gln
20 25 30
Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp Arg
35 40 45
60 Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr Gly
50 55 60
Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met Lys
65 70 75 80
Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr Gln
85 90 95
65 Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu Asn
100 105 110
Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val Gln
115 120 125
70 Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg Asp
130 135 140
Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile Ser
145 150 155 160
Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr Ser
165 170 175
75 Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly Val

WO 99/29870

PCT/AU98/01023

387/ 490

5 Gln Pro Val Asn Ser Ser Ala Asp Asp Phe Gly Leu Ala Val Glu Pro
385 390 395 400
Lys Gly Lys Asn Lys Glu Glu Ala Leu Pro Asp Asn Gly Val Lys Gly
405 410 415
Val Phe Cys Ser Asn Arg Gly Asp Ala Arg Gly Trp Pro His Leu Phe
420 425 430
His Phe Glu Leu Pro Ala Ile Tyr Thr Glu Ile Gln Gly Tyr Val Met
435 440 445
10 Asp Arg Glu Glu Asn Pro Ile Ala Gly Ala Thr Val Arg Ile Val Gly
450 455 460
Glu Arg Gly Pro Val Gly Gln Gly Phe Val Thr Thr Arg Asp Asp Gly
465 470 475 480
Ser Tyr Lys Met Ser Val Gln Gly Asp Thr Arg Tyr Val Met Leu Ala
485 490 495
15 Gly Ala Ser Gly Tyr Leu Asn Gln Tyr Val Glu Leu Lys Trp Asp Thr
500 505 510
Ala Lys Gln Ser Glu Thr Tyr Tyr Val Asp Phe Phe Leu Ala Ser Arg
515 520 525
20 Glu Lys Ala Glu Gly Leu Gln Asn Ile Phe Tyr Asp Phe Asp Lys Ala
530 535 540
Thr Leu Arg Pro Glu Ser Met Lys Ser Leu Asp Glu Leu Ile Arg Ile
545 550 555 560
Leu Thr Asp Asn Pro Asp Ile Arg Ile Glu Leu Gly Ser His Ala Asp
565 570 575
25 Arg Lys Gly Pro Asp Ala Tyr Asn Leu Gly Leu Ser Asp Arg Arg Ala
580 585 590
Lys Ser Val Val Asp Tyr Leu Thr Ser Arg Gly Ile Ala Ala Asp Arg
595 600 605
30 Leu Thr Trp Lys Gly Tyr Gly Lys Ser Val Pro Lys Thr Val Thr Ala
610 615 620
Lys Ile Ala Glu Arg His Asp Phe Leu Lys Glu Gly Asp Val Leu Thr
625 630 635 640
Glu Glu Phe Val Ala Pro Leu Thr Glu Glu Gln Gln Ser Val Cys Asp
645 650 655
35 Gln Leu Asn Arg Arg Thr Glu Phe Arg Val Ile Glu Glu Glu Leu Arg
660 665 670

(2) INFORMATION FOR SEQ ID NO:448

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 708 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
50 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
55 (B) LOCATION 1...708
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln
1 5 10 15
60 Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His
20 25 30
Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu
35 40 45
65 Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys
50 55 60
Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser
65 70 75 80
Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg
85 90 95
70 Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile
100 105 110
Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu
115 120 125
75 Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn
130 135 140

WO 99/29870

PCT/AU98/01023

388/490

Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys
145 150 155 160
Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala
165 170 175
5 Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp
180 185 190
Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser
195 200 205
10 Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val
210 215 220
Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala
225 230 235 240
Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu
245 250 255
15 Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly
260 265 270
Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser
275 280 285
20 Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln
290 295 300
Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala
305 310 315 320
Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly
325 330 335
25 Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu
340 345 350
Gly Val Asp Ser Arg Asn Met Thr Met Glu Ser Glu Arg Phe Glu Gln
355 360 365
30 Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr Asn Asn
370 375 380
Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp Ala Leu
385 390 395 400
Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Phe Asp Leu Lys
405 410 415
35 Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val
420 425 430
Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr
435 440 445
40 Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln
450 455 460
Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro
465 470 475 480
Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr
485 490 495
45 Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe
500 505 510
His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn
515 520 525
50 Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile
530 535 540
Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe
545 550 555 560
Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met
565 570 575
55 Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg
580 585 590
Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu
595 600 605
60 Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn
610 615 620
Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu
625 630 635 640
Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro
645 650 655
65 Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr
660 665 670
Leu Thr Phe Gly Val Asn Leu Asn Asn Ile Leu Asp Glu Leu Tyr Thr
675 680 685
70 Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val
690 695 700
Met Val Asn Phe
705

(2) INFORMATION FOR SEQ ID NO:449

75

WO 99/29870

PCT/AU98/01023

389/490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...462

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

20 Met Asn Arg Phe Ser Asn His Trp Pro Cys Ile Leu Val Gly Phe Val
 1 5 10 15
 Leu Trp Phe Val Ser Ala Ser Arg Thr Val Ala Gln Asn Ala Ser Glu
 20 25 30
 Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala Val Leu Ser Glu Ala Asp
 35 40 45
 25 Val Leu Arg Ile Ala Leu Ser Glu Asn Ala Thr Val Lys Val Ala Asp
 50 55 60
 Met Asp Val Arg Lys Gln Glu Tyr Ala Arg Arg Ala Ala Arg Ala Asp
 65 70 75 80
 30 Leu Phe Pro Lys Val Asp Leu Asn Gly Val Tyr Ser His Thr Leu Lys
 85 90 95
 Lys Gln Val Leu Tyr Ile Asp Met Pro Gly Phe Ser Ser Ser Glu Gly
 100 105 110
 Ile Glu Met Gly Arg Thr His Asn Thr Gln Gly Gly Val Asn Val Ser
 115 120 125
 35 Met Pro Leu Val Ser Ala Gln Leu Trp Lys Ser Ile Ala Met Thr Gly
 130 135 140
 Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala Arg Ser Ser Arg Ile Asp
 145 150 155 160
 40 Leu Val Ala Glu Val Lys Lys Ala Tyr Leu Ser Val Leu Leu Ala Glu
 165 170 175
 Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr Asp Asn Ala Leu Ala Asn
 180 185 190
 Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg Gly Leu Val Ala Glu Tyr
 195 200 205
 45 Asp Lys Ile Arg Ala Asn Val Gln Val Arg Asn Ile Glu Pro Asn Leu
 210 215 220
 Leu Gln Ala Gln Asn Ser Val Ala Leu Ala Leu Trp Gln Leu Lys Val
 225 230 235 240
 50 Leu Met Ser Met Glu Val Glu Thr Pro Ile Arg Leu Ser Gly Ser Leu
 245 250 255
 Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly Tyr Phe Ala Ala Asp Thr
 260 265 270
 Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln Leu Asp Ile Gln Arg Arg
 275 280 285
 55 Leu Ala Val Ser Ala Asp Lys Leu Asn Lys Tyr Ser Phe Leu Pro Thr
 290 295 300
 Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser Leu Asn Ser Asn Asp Ile
 305 310 315 320
 60 Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr Pro Phe Ser Thr Ile Ser
 325 330 335
 Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly Gly Lys Arg Leu Tyr Asn
 340 345 350
 Val Lys Gln Ser Ala Leu Ser Ile Arg Gln Ile Asp Leu Gln Arg Arg
 355 360 365
 65 His Ile Glu Gln Ser Ile Arg Met Gly Ile Lys Asn Gln Asn Asp Arg
 370 375 380
 Leu Arg Thr Cys Met Gln Arg Phe Val Ala Ser Glu Glu Ala Val Arg
 385 390 395 400
 70 Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu Lys Arg-Tyr Gln Thr Gly
 405 410 415
 Glu Gly Thr Leu Val Glu Leu Asn Asp Ala Asp Val Ala Leu Leu Gln
 420 425 430
 Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe Asp Phe Met Thr Ala Lys
 435 440 445
 75 Ala Glu Leu Asp Lys Met Asn Gly Met Gly Ile Pro Glu Gln

WO 99/29870

PCT/AU98/01023

390/ 490

450 455 460

(2) INFORMATION FOR SEQ ID NO:450

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...492

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg Arg Thr
1 5 10 15
25 Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln
20 25 30
Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr
35 40 45
30 Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro
50 55 60
Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu
65 70 75 80
Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe
85 90 95
35 Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser
100 105 110
Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro
115 120 125
40 Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly
130 135 140
Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg
145 150 155 160
Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala
165 170 175
45 Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile
180 185 190
Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg
195 200 205
50 Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala
210 215 220
Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly
225 230 235 240
Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile
245 250 255
55 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile
260 265 270
Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg
275 280 285
60 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser
290 295 300
Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr
305 310 315 320
Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp
325 330 335
65 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser
340 345 350
Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg
355 360 365
70 Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu
370 375 380
Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys
385 390 395 400
Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu
405 410 415
75 His Ser Leu Pro Leu Gly Pro Asp Gly Arg Arg Asp Gly Ala Val Tyr

WO 99/29870

PCT/AU98/01023

391/490

5 Leu Phe Asp 420 His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn
435 440 445
Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr
450 455 460
Ile Glu Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile
465 470 475 480
Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln
485 490

10 (2) INFORMATION FOR SEQ ID NO:451

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

25 (ix) FEATURE:
(A) NAME/KEY: msc_feature
(B) LOCATION 1...245

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe
1 5 10 15
Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg
20 25 30
35 Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys
35 40 45
Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp
50 55 60
40 Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
65 70 75 80
Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
85 90 95
Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln
100 105 110
45 Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
115 120 125
Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
130 135 140
50 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
145 150 155 160
Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
165 170 175
Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
180 185 190
55 Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
195 200 205
Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
210 215 220
60 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
225 230 235 240
Ser Phe Ala Leu Lys
245

65 (2) INFORMATION FOR SEQ ID NO:452

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

70 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

75 (vi) ORIGINAL SOURCE:

392/490

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu Leu Ala Leu Gly
1 5 10 15
Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala Val Ser Glu Lys
20 25 30
Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly Gln Asp Phe Ala
35 40 45
15 Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro Ile Asp Ser Val
50 55 60
Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr Thr Arg Phe Ser
65 70 75 80
Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala Arg Gln Leu Ala
85 90 95
20 His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala Met Arg Ala Ala
100 105 110
Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro Ala Asp Ala Gln
115 120 125
25 Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg Glu Asn Asn Met
130 135 140
Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu Tyr Ile Asp Thr
145 150 155 160
Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr Gly Leu Ala Tyr
165 170 175
30 Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser Leu Ala Asp Thr
180 185 190
Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly Lys Glu Phe Asp
195 200 205
35 Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly Val Ile Lys Gly
210 215 220
Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln Lys Val Arg Val
225 230 235 240
Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly Asn Tyr Thr Ile
245 250 255
40 Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu Ile Gly Ile Lys
260 265 270
Pro Gly Lys Lys
275

(2) INFORMATION FOR SEQ ID NO:453

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

Met Lys Val Leu Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu
1 5 10 15
Thr Gly Ala Cys Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu
20 25 30
70 Tyr Ile Gly Met Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His
35 40 45
Ala Gly Gln Gln Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr
50 55 60
Pro Asn Gly Ala Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile
65 70 75 80

WO 99/29870

PCT/AU98/01023

393/490

	Pro	Phe	Gly	Leu	Trp	Leu	Tyr	Asn	Ser	Phe	Val	Gly	Asp	Ser	Thr	Val
				85						90						95
	Ile	Ser	Lys	Trp	Ile	Phe	Asp	Lys	Phe	Ala	Ala	Lys	Pro	Val	Phe	Ile
				100					105							110
5	Ser	Gln	Val	Gln	Ser	Asp	Ser	Arg	Ala	Lys	Val	Ala	Thr	Asn	Ile	Leu
				115					120							125
	Arg	Glu	His	Gly	Tyr	Phe	Asp	Ala	Lys	Val	Lys	Ser	Ser	Val	Thr	Thr
				130					135							140
10	Leu	Lys	Lys	Asp	Ser	Leu	Lys	Ala	Lys	Ile	Ser	Tyr	Thr	Val	Asp	Met
				145					150							155
	Ala	Ser	Pro	Tyr	His	Tyr	Asp	Ser	Ile	Ile	Pro	Leu	Pro	Ile	Ser	Thr
				165												170
	Phe	Pro	Asp	Ser	Ile	Leu	Ala	Tyr	Arg	Gln	Thr	Pro	Ser	Leu	Ile	Arg
				180												185
15	Lys	Gly	Asp	Gln	Phe	Asn	Leu	Ala	Lys	Leu	His	Glu	Glu	Arg	Gln	Thr
				195												200
	Ile	Ser	Ala	Leu	Leu	Arg	Asp	Asn	Gly	Tyr	Tyr	Tyr	Phe	Arg	Pro	Gln
				210												215
20	Asp	Ile	Ile	Tyr	Glu	Ala	Asp	Thr	Leu	Leu	Val	Arg	Gly	Ala	Val	Cys
				225												230
	Leu	Arg	Ala	Lys	Leu	Ser	Glu	Asp	Thr	Pro	Pro	Gln	Ala	Met	Arg	Pro
				245												250
	Trp	Arg	Ile	Gly	Lys	Arg	Thr	Ala	Val	Leu	Leu	Gly	Met	Asn	Gly	Glu
				260												265
25	Ser	Pro	Thr	Asp	Ser	Leu	Glu	Val	Glu	Asp	Met	Lys	Val	Leu	Tyr	Tyr
				275												280
	Arg	Lys	Met	Pro	Val	Arg	Pro	Lys	Ile	Leu	Ala	Lys	Arg	Phe	Arg	Phe
				290												295
30	Phe	Ser	Gly	Asn	Leu	Tyr	Arg	Gln	Lys	Asp	Asp	Glu	Thr	Thr	Arg	Lys
				305												310
	Ser	Leu	Ala	Arg	Leu	Gly	Ala	Phe	Ser	Val	Ile	Asp	Leu	Asn	Phe	Leu
				325												330
	Gln	Arg	Asp	Ser	Ile	Ser	Gly	Leu	Leu	Asp	Val	Arg	Leu	Leu	Thr	Thr
				340												345
35	Leu	Asp	Lys	Pro	Trp	Asp	Ala	Ser	Leu	Glu	Thr	Leu	Phe	Thr	Ser	Lys
				355												360
	Ser	Asn	Asp	Phe	Ile	Gly	Pro	Gly	Leu	Asn	Phe	Ala	Leu	Ala	Arg	Arg
				370												375
40	Asn	Val	Phe	Gly	Gly	Gly	Gly	Asn	Leu	Ser	Trp	Asn	Ile	Gly	Gly	Ser
				385												390
	Tyr	Glu	Trp	Glu	Thr	Gly	Asn	Arg	Pro	Glu	Asn	Ser	Ser	Asn	Arg	Leu
				405												410
	Ile	Asp	Ile	Asn	Ser	Tyr	Asn	Met	Asn	Thr	Ala	Val	Asn	Leu	Ser	Phe
				420												425
45	Pro	Ser	Ile	Val	Phe	Pro	Gly	Leu	Leu	Asp	Lys	Tyr	Tyr	Tyr	Tyr	Pro
				435												440
	Thr	Thr	Thr	Thr	Phe	Gln	Ala	Ser	Ala	Thr	Ala	Leu	Asn	Arg	Ala	His
				450												455
50	Tyr	Phe	Ser	Met	Tyr	Ser	Phe	Gly	Phe	Ser	Thr	Thr	Tyr	Glu	Phe	Gln
				465												470
	Pro	Ser	Lys	Glu	His	Arg	His	Ala	Ile	Phe	Pro	Leu	Lys	Leu	Asn	Tyr
				485												490
	Asn	Leu	Leu	Gly	His	Gln	Thr	Glu	Thr	Phe	Gln	Ala	Ile	Thr	Ala	Asn
				500												505
55	Asn	Pro	Pro	Leu	Leu	Ser	Leu	Gln	Ser	Gln	Phe	Leu	Ala	Gln	Met	
				515												520
	Gly	Tyr	Ile	Tyr	Thr	Phe	Asn	Lys	Ser	Val	Ser	Glu	Lys	Ser	Pro	His
				530												535
60	His	Leu	Trp	Met	Gln	Phe	Gly	Leu	Ser	Glu	Ala	Gly	Asn	Leu	Leu	Asn
				545												550
	Leu	Ile	Tyr	Leu	Ala	Ala	Gly	Lys	Lys	Tyr	Ser	Asp	Thr	Lys	Asn	Phe
				565												570
	Val	Gly	Val	Pro	Phe	Ser	Gln	Phe	Ile	Lys	Ala	Thr	Gly	Glu	Leu	Arg
				580												585
65	Tyr	Ser	Tyr	Thr	Ile	Asp	Arg	Asn	Gln	Ser	Leu	Ala	Thr	Arg	Phe	Gly
				595												600
	Thr	Gly	Val	Ile	Tyr	Ser	Tyr	Gly	Asn	Met	Arg	Val	Ala	Pro	Tyr	Ser
				610												615
70	Glu	Gln	Phe	Tyr	Val	Gly	Gly	Ala	Asn	Ser	Ile	Arg	Ala	Phe	Thr	Val
				625												630
	Arg	Ser	Ile	Gly	Pro	Gly	Arg	Phe	Asn	Pro	Asp	Ser	Asp	Asn	Gln	Tyr
				645												650
	Ser	Tyr	Leu	Asp	Gln	Val	Gly	Glu	Phe	Lys	Leu	Glu	Ala	Asn	Val	Glu
				660												665
75	Tyr	Arg	Gly	Lys	Leu	Phe	Gly	Asp	Leu	His	Ala	Ala	Val	Phe	Leu	Asp

394/ 490

675
 Ala Gly Asn Val Trp Leu Leu 680
 690 695 700
 5 Ala Leu Ser Glu Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala
 705 710 715 720
 Leu Gly Thr Gly Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val
 725 730 735
 Arg Val Asp Val Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys
 740 745 750
 10 Lys Gly Tyr Tyr Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His
 755 760 765
 Leu Ala Val Gly Tyr Pro Phe
 770 775

15 (2) INFORMATION FOR SEQ ID NO:451
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 774 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 20
 (ii) MOLECULE TYPE: protein
 25 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 30 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...774
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454
 35 Met Ser Ser His Ser Val Arg Tyr Leu Ile Gl, Ile Ala Gly Cys Leu
 1 5 10 15
 Leu Leu Met Leu Ala Ser Ser Cys Ser Val Thr Arg Tyr Val Pro Asp
 20 25 30
 40 Gly Ser Arg Leu Leu Asp Arg Val Thr Ile Ala Ser Glu Thr Gly Ser
 35 40 45
 Ile Ala Leu Pro Glu Asp Ile Arg Asp Tyr Thr Leu Gln Gln Pro Asn
 50 55 60
 Tyr Arg Leu Phe Gly Met Thr Arg Trp Leu Leu Arg Val Tyr Ser Ser
 65 70 75 80
 45 Ser Asn Pro Asn Ser Asn Ser Trp Trp Asn Arg Ser Leu Arg Lys Met
 85 90 95
 Gly Glu Pro Pro Val Leu Ile Asp Ser Val Leu Thr Asp Arg Thr Ala
 100 105 110
 50 Asn Arg Leu Ala Lys Ala Met Ala Gly Asp Gly Phe Leu Asp Ala Thr
 115 120 125
 Ala Arg Ala Val Val Asp Thr Gly Leu Tyr Lys Lys Ala Arg Ile Thr
 130 135 140
 Tyr Leu Ile Gln Pro Gly Ser Arg Tyr Tyr Ile Arg Asn Met Ala Leu
 145 150 155 160
 55 Asp Val Lys Asn Pro Leu Leu Pro Pro Val Ala Leu Gly Asn Ser Leu
 165 170 175
 Pro Ser Ala Tyr Lys Val Gly Ile Ser Glu Gly Ser Pro Leu Ser Pro
 180 185 190
 60 Ile Val Leu Asp Glu Glu Arg Lys Ala Ile Ala Arg His Met Arg Asn
 195 200 205
 Asn Gly Phe Trp Lys Phe Ser Ala Glu Asp Val Tyr Tyr Glu Ala Asp
 210 215 220
 Thr Thr Val Ser Gly Gly Ser Gly Thr Lys Ser Ala Asp Leu Lys Leu
 225 230 235 240
 65 Val Val Asn Gly Ile Gly Arg Tyr Pro Tyr Arg Ile Gly Arg Val Phe
 245 250 255
 Phe His Ala Asp Tyr Asp Pro Leu Glu Ser Asp Phe Arg Val Gln Glu
 260 265 270
 70 Leu Pro Arg Ile Asp Ser Ile Ser Arg Gly Asp Tyr Thr Val Tyr Tyr
 275 280 285
 Gly Ser Arg Gly Arg Tyr Ile Arg Ala Ser Ala Leu Thr Arg Ser Val
 290 295 300
 Ser Val Thr Pro Gly Ala Phe Phe Cys Glu Asp Asp Val Glu Arg Ser
 305 310 315 320
 75 Tyr Ile Lys Leu Acn Ala Leu Pro Ile Val Arg Asn Val Asn Ile Arg

WO 99/29870

PCT/AU98/01023

395 / 490

5 Phe Val Glu His 325 Asn Gly Lys Asp Glu Ile Ala Leu Ala 335 Asp Ser Ser
 Arg Leu Val Asp 340 Cys Tyr Ile Leu Thr Val Pro Ala Lys Ser Lys Ser
 Phe Glu Ala Glu Val Leu Gly Thr Asn Ser Ala Gly Asp Phe Gly Ala
 10 Ala Leu Ser Leu Gly Phe Thr Asp Arg Asn Leu Phe Arg Gly Ala Glu
 Met Phe Asn Ile Lys 390 Leu Lys Gly Ala Tyr Glu Ala Ile Arg Lys Gly
 Ser His Ser Phe Met Glu Tyr Gly Val Glu Ser Ser Leu Arg Phe Pro
 15 Arg Leu Leu Phe Pro Phe Ile Ser Asp Glu Thr Arg Arg Arg Leu Arg
 Ala Ser Thr Glu Trp Lys Ile Gly Tyr Asn Tyr Gln Thr Arg Pro Glu
 Phe Asp Arg Val Ile Leu Ser Ala Gln Leu Asn Tyr Ser Trp Gln Thr
 20 Tyr Leu His Asn Arg Leu Arg His Thr Ile Arg Leu Leu Asp Val Asp
 Tyr Leu His Leu Pro Tyr Ile Asp Pro Asp Phe Ala Gln Ser Leu Pro
 25 Pro Thr Thr Ala Leu Tyr Asn Tyr Thr Thr Glu Gln Phe Ile Leu Gly Ser
 Ala Tyr Ile Leu Asn Tyr Thr Thr Ala Ser Ser Met Glu Arg Thr Val
 Ser Asn Pro Phe Thr Ala Arg Phe Ser Ile Gln Thr Ala Gly Asn Leu
 30 Leu Gln Ala Ile Ser Tyr Leu Thr Asp Ser Pro Lys Asp Glu His Gly
 Leu Tyr Lys Met Phe Gly Leu His Tyr Ala Gln Phe Val Lys Leu Asp
 Leu Asp Leu Ala Lys Thr Val Leu Leu Glu Lys Asp Asn Thr Leu Ala
 35 Leu His Leu Gly Phe Gly Leu Ala Phe Pro Tyr Gly Ser Asn Ser Val Arg
 Ile Pro Phe Glu Leu Arg Tyr Phe Ala Gly Gly Ser Asn Ser Val Arg
 40 Gly Trp Ser Val Arg Thr Leu Gly Pro Gly Ser Met Lys Met Thr Pro
 Asp Lys Thr Phe Phe Asp Gln Met Gly Asp Ile Arg Leu Asp Leu Asn
 Val Glu Tyr Arg Thr Lys Leu Phe Trp Lys Phe Arg Ala Ala Ala Phe
 45 Val Asp Ala Gly Asn Val Trp Thr Ile Lys Glu Tyr Glu Asn Gln Glu
 Asp Gly Leu Phe Arg Phe Asp Arg Phe Tyr Lys Glu Ile Ala Leu Ala
 50 Tyr Gly Leu Gly Leu Arg Leu Asp Phe Asp Tyr Phe Leu Val Arg Leu
 Asp Ala Gly Leu Lys Ala Tyr Asp Pro Gln Gln Thr Gly Arg Tyr Lys
 55 Trp Ala Ile Thr Arg Pro Asn Leu Ser Ser Asn Phe Ala Trp His Ile
 Ala Val Gly Tyr Pro Phe 770

60 (2) INFORMATION FOR SEQ ID NO:455
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 867 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 65 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 70 (i) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ii) FEATURE:
 (A) NAME/KEY: misc_feature
 75 (B) LOCATION 1...867

WO 99/29870

PCT/AU98/01023

396/ 490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:455

5	Met	Arg	Lys	Arg	Ile	Leu	Gln	Leu	Phe	Leu	Thr	Ala	Leu	Leu	Leu	Ala
	1				5					10					15	
	Leu	Gly	Ser	Ser	Leu	Ala	Ile	Ala	Gln	Thr	Val	Val	Thr	Gly	Lys	Val
				20					25					30		
	Ile	Asp	Ser	Glu	Thr	Ser	Glu	Pro	Leu	Ile	Gly	Val	Ser	Val	Ser	Thr
			35					40					45			
10	Gly	Gln	Gly	Ala	Ser	Leu	Arg	Gly	Val	Thr	Thr	Asp	Met	Asp	Gly	Gly
	50						55					60				
	Phe	Arg	Phe	Glu	Val	Pro	Ala	Lys	Ser	Val	Leu	Thr	Phe	Arg	Cys	Val
					70					75					80	
	Gly	Tyr	Ala	Thr	Val	Thr	Arg	Ser	Ile	Gly	Arg	Gly	Ser	Gln	Glu	Asp
				85						90				95		
15	Leu	Gly	Thr	Ile	Leu	Asp	Pro	Gln	Ala	Ile	Gly	Leu	Asp	Glu	Ile	
				100				105					110			
	Gln	Val	Ile	Ala	Ser	Val	Val	Pro	Lys	Asp	Arg	Met	Thr	Pro	Val	Pro
			115					120					125			
20	Val	Ser	Asn	Ile	Arg	Val	Ala	Asp	Ile	Gln	Ala	Ala	Ser	Leu	Asn	Val
						135						140				
	Glu	Phe	Pro	Glu	Leu	Val	Lys	Ser	Thr	Pro	Ser	Thr	Tyr	Thr	Thr	Lys
					150					155					160	
	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Gly	Arg	Thr	Asn	Val	Arg	Gly	Phe	Asp
				165						170				175		
25	Thr	Tyr	Asn	Phe	Gly	Val	Leu	Ile	Asn	Gly	Val	Pro	Val	Asn	Gly	Met
								185						190		
	Glu	Asp	Gly	Lys	Val	Tyr	Trp	Ser	Asn	Trp	Ser	Gly	Leu	Met	Asn	Gln
			195					200					205			
30	Ala	Ser	Thr	Ile	Gln	Ile	Gln	Arg	Gly	Leu	Gly	Ala	Ser	Lys	Leu	Gly
			210					215				220				
	Ile	Ser	Ser	Val	Gly	Gly	Thr	Met	Asn	Ile	Ile	Thr	Lys	Thr	Thr	Asp
					230					235					240	
	Ala	Asn	Thr	Gly	Gly	Ser	Ala	Tyr	Val	Gly	Met	Gly	Asn	Asp	Gly	Leu
				245						250				255		
35	His	Lys	Glu	Ser	Phe	Ser	Ile	Ser	Thr	Gly	Met	Asn	Asp	Gly	Trp	Ala
				260					265					270		
	Ile	Phe	Ile	Ala	Gly	Ser	His	Met	Thr	Gly	Leu	Gly	Tyr	Val	Lys	Gly
				275					280					285		
40	Leu	Lys	Gly	Arg	Ala	Phe	Ser	Tyr	Phe	Phe	Asn	Val	Ser	Lys	Lys	Phe
				290				295				300				
	Asn	Glu	Arg	His	Thr	Leu	Ser	Leu	Thr	Gly	Phe	Gly	Ala	Pro	Gln	Trp
				305				310			315				320	
	His	Asn	Gln	Arg	Ser	Ser	Lys	Tyr	Ser	Val	Ala	Asp	Tyr	Asp	Lys	Tyr
				325						330				335		
45	Gly	Ile	Arg	His	Asn	Gln	Ser	Phe	Gly	Tyr	Leu	Arg	Gly	Glu	Leu	Thr
				340					345					350		
	Pro	Thr	Ala	Tyr	Ala	Tyr	Asn	Thr	Tyr	His	Lys	Pro	Gln	Phe	Ser	Leu
				355				360					365			
50	Asn	His	Phe	Trp	Lys	Met	Asp	Glu	Asn	Thr	Ser	Leu	Tyr	Thr	Ala	Unk
				370			375					380				
	Tyr	Ala	Ser	Leu	Ala	Thr	Gly	Gly	Gly	Arg	Arg	Ala	Tyr	Gly	Lys	Asn
				385			390			395					400	
	Ser	Lys	Trp	Val	Leu	Ile	Asn	Tyr	Asn	Thr	Gly	Gln	Pro	Tyr	Glu	Gln
				405						410				415		
55	Thr	Lys	Val	Thr	Pro	Asp	Gly	Leu	Ile	Asp	Tyr	Asp	Ala	Val	Leu	Ala
				420						425				430		
	Ala	Asn	Ala	Ala	Ala	Ser	Asn	Gly	Ser	Glu	Ala	Ile	Phe	Ala	Leu	Gly
				435				440					445			
60	Ser	Asn	Ser	His	Lys	Trp	Phe	Gly	Leu	Leu	Ser	Ser	Phe	Lys	Lys	Lys
				450			455					460				
	Leu	Asn	Ser	Ser	Leu	Thr	Leu	Thr	Ala	Gly	Tyr	Asp	Gly	Arg	Tyr	Tyr
				465			470				475				480	
	Arg	Gly	Asp	His	Tyr	Asp	Lys	Ile	Thr	Asp	Leu	Leu	Gly	Gly	Ser	Tyr
				485						490				495		
65	Tyr	Ile	Glu	Asp	Pro	Lys	Thr	Lys	Leu	Ala	Tyr	His	Ala	Glu	Gly	Gln
				500					505					510		
	Gln	Leu	Lys	Val	Gly	Asp	Ile	Val	Asn	Arg	Asp	Tyr	Thr	Gly	Glu	Ile
				515				520					525			
70	Met	Trp	His	Gly	Leu	Phe	Ala	Gln	Met	Glu	His	Ser	Ser	Glu	Trp	Ile
				530			535					540				
	Asp	Ala	Phe	Val	Ser	Gly	Ser	Ile	Asn	Tyr	Glu	Leu	Tyr	Arg	Asn	His
				545			550			555					560	
75	Asn	Tyr	Gly	Gly	Ser	Lys	Ser	Thr	Gly	Tyr	Leu	Pro	Gly	Val	Ser	Pro
				565					570					575		

WO 99/29870

PCT/AU98/01023

402/ 490

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

5 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

10 Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu Thr Leu Ile Gly
1 5 10 15
Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln Ser Leu Phe Ser
20 25 30
15 Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu Tyr Gly Glu Ser
35 40 45
Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu Ser Ala Phe Pro
50 55 60
20 Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe Leu Gly Lys Pro
65 70 75 80
Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp Cys Ser Gly Tyr
85 90 95
Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu Pro Arg Gly Ala
100 105 110
25 Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg Glu Asp Val Arg
115 120 125
Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala Arg Ser Asn Arg
130 135 140
30 Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu Asp Asp Ile Thr
145 150 155 160
Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile Glu Lys Leu Asn
165 170 175
Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr Gly Arg Val Pro
180 185 190
35 Gly Ala Lys Arg Val Ile Pro Arg Lys Ser
195 200

(2) INFORMATION FOR SEQ ID NO:461

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES

50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...455

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

60 Met Lys Arg Thr Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu
1 5 10 15
Ser Leu Leu Arg Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met
20 25 30
Ser Gly Leu Ser Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn
35 40 45
65 Leu Asn Leu Arg Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser
50 55 60
Leu Asp Ala Ala Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile
65 70 75 80
Gly His Asn Tyr Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr
85 90 95
70 Val Asp Arg Ser Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val
100 105 110
Glu Val Phe Ser Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys
115 120 125
75 Tyr Asn Val Glu Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp
130 135 140

WO 99/29870

PCT/AU98/01023

403/ 490

Leu Ser Leu Gln Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln
145 150 155 160
Glu Met Thr Arg Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln
165 170 175
5 Arq Asn Arg Thr Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly
180 185 190
Lys Leu Leu Asp Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu
195 200 205
10 Val Gln Tyr Arq Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln
210 215 220
Ala Leu Glu Leu Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp
225 230 235 240
Thr Asp Val Leu Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu
245 250 255
15 Glu Ile Tyr Arg Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser
260 265 270
Glu Leu Gln Ile Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala
275 280 285
20 Ala Tyr Phe Pro Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr
290 295 300
Phe Arg Asp Leu Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser
305 310 315 320
Glu Gln Trp Lys Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn
325 330 335
25 Ile Pro Ile Phe Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser
340 345 350
Arg Leu Gln Ile Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys
355 360 365
30 Ala Leu Tyr Lys Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala
370 375 380
Asp Lys Ala Ile Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys
385 390 395 400
Ala Tyr Glu Tyr Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala
405 410 415
35 Tyr Glu Tyr Ala Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu
420 425 430
Glu Leu Arg Ala Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp
435 440 445
40 Phe Tyr Gln Gly Lys Asp Phe 455
450

(2) INFORMATION FOR SEQ ID NO:462

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
50 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...444

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

Met Arg Phe Gln His Tyr Leu Ile Cys Thr Ala Ala Val Ala Ala Leu
1 5 10 15
65 Ala Ala Asn Pro Leu Thr Gly Gln Ser Asn Met Thr Leu Glu Glu Cys
20 25 30
Ile Asp Tyr Ala Arg Arg His Ser Ser Ala Val Ala Leu Ser Ala Ala
35 40 45
Glu Leu Glu Gln Ser Lys Ala Asp Tyr Leu Gln Ala Val Gly Asn Phe
50 55 60
70 Leu Pro Arg Val Ser Ala Gly Thr Gly Ala Ser Trp Asn Phe Gly Arg
65 70 75 80
Gly Leu Asp Ala Glu Thr Asn Thr Tyr Thr Asp Ile Asn Ser Phe Asn
85 90 95
75 Asn Ser Tyr Ser Ile His Ala Thr Met Thr Leu Phe Asp Gly Leu Gln
100 105 110

WO 99/29870

PCT/AU98/01023

405 / 490

	Ser	His	Ile	Ser	Ser	Ile	Gly	Asp	Val	Asp	Val	Tyr	Arg	Leu	Gln	Phe	
				100					105						110		
	Lys	Leu	Glu	Gly	Ala	Lys	Ala	Ile	Thr	Leu	Tyr	Tyr	Asp	Ala	Phe	Asn	
				115					120					125			
5	Ile	Pro	Glu	Gly	Gly	Arg	Leu	Tyr	Ile	Tyr	Thr	Pro	Asp	His	Glu	Ile	
				130					135					140			
	Val	Leu	Gly	Ala	Tyr	Thr	Asn	Ala	Thr	His	Arg	Arg	Asn	Gly	Ala	Phe	
				145					150					155			160
10	Ala	Thr	Glu	Pro	Val	Pro	Gly	Ser	Glu	Leu	Ile	Met	Asp	Tyr	Glu	Val	
									165						175		
	Ser	Arg	Gly	Gly	Thr	Leu	Pro	Asp	Ile	Lys	Ile	Ser	Gly	Ala	Gly	Tyr	
									180						190		
	Ile	Phe	Asp	Lys	Val	Gly	Gly	Arg	Pro	Val	Thr	Asp	Asn	His	Tyr	Gly	
				195					200					205			
15	Ile	Gly	Glu	Asp	Asp	Ser	Asp	Ser	Asp	Cys	Glu	Ile	Asn	Ile	Asn	Cys	
				210					215					220			
	Pro	Glu	Gly	Ala	Asp	Trp	Gln	Ala	Glu	Lys	Asn	Gly	Val	Val	Gln	Met	
									230					235			240
20	Ile	Met	Val	Lys	Gly	Gln	Tyr	Ile	Ser	Met	Cys	Ser	Gly	Asn	Leu	Leu	
									245					250			255
	Asn	Asn	Thr	Lys	Gly	Asp	Phe	Thr	Pro	Leu	Ile	Ile	Ser	Ala	Gly	His	
									260					265			270
	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val	Thr	Gln	Ser	Glu	Leu	Asp	
				275					280					285			
25	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys	Arg	Gly	Cys	Ser	Asn	Gly	
									290					300			
	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile	Ile	Gly	Ala	Ser	Met	Lys	
									305					310			320
30	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp	Gly	Leu	Leu	Leu	Gln	Leu	
									325					330			335
	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val	Tyr	Tyr	Asn	Gly	Trp	Asp	
									340					345			350
	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala	Gly	Ile	His	His	Pro	Ala	
									355					360			365
35	Gly	Asp	Ala	Met	Lys	Ile	Ser	Ile	Leu	Lys	Lys	Thr	Pro	Ala	Leu	Asn	
									370					375			
	Thr	Trp	Ile	Ser	Ser	Ser	Gly	Ser	Gly	Gly	Thr	Asp	His	Phe	Tyr		
									385					390			400
40	Phe	Lys	Tyr	Asp	Gln	Gly	Gly	Thr	Glu	Gly	Gly	Ser	Ser	Gly	Ser	Ser	
									405					410			415
	Leu	Phe	Asn	Gln	Asn	Lys	His	Val	Val	Gly	Thr	Leu	Thr	Gly	Gly	Ala	
									420					425			430
	Gly	Asn	Cys	Gly	Gly	Thr	Glu	Phe	Tyr	Gly	Arg	Leu	Asn	Ser	His	Trp	
									435					440			445
45	Asn	Glu	Tyr	Ala	Ser	Asp	Gly	Asn	Thr	Ser	Arg	Met	Asp	Ile	Tyr	Leu	
									450					455			460
	Asp	Pro	Gln	Asn	Asn	Gly	Gln	Thr	Thr	Ile	Leu	Asn	Gly	Thr	Tyr	Arg	
									465					470			475
50	Asp	Gly	Tyr	Lys	Pro	Leu	Pro	Ser	Val	Pro	Arg	Leu	Leu	Leu	Gln	Ser	
									485					490			495
	Thr	Gly	Asp	Gln	Val	Glu	Leu	Asn	Trp	Thr	Ala	Val	Pro	Ala	Asp	Gln	
									500					505			510
	Tyr	Pro	Ser	Ser	Tyr	Gln	Val	Glu	Tyr	His	Ile	Phe	Arg	Asn	Gly	Lys	
									515					520			525
55	Glu	Ile	Ala	Thr	Thr	Lys	Glu	Leu	Ser	Tyr	Ser	Asp	Ala	Ile	Asp	Glu	
									530					535			540
	Ser	Ile	Ile	Gly	Ser	Gly	Ile	Ile	Arg	Tyr	Glu	Val	Ser	Ala	Arg	Phe	
									545					550			555
60	Ile	Tyr	Pro	Ser	Pro	Leu	Asp	Gly	Val	Glu	Ser	Tyr	Lys	Asp	Thr	Asp	
									565					570			575
	Lys	Thr	Ser	Ala	Asp	Leu	Ala	Ile	Gly	Asp	Ile	Gln	Thr	Lys	Leu	Lys	
									580					585			590
	Pro	Asp	Val	Thr	Pro	Leu	Pro	Gly	Gly	Gly	Val	Ser	Leu	Ser	Trp	Lys	
									595					600			605
65	Val	Pro	Phe	Leu	Ser	Gln	Leu	Val	Ser	Arg	Phe	Gly	Glu	Ser	Pro	Asn	
									610					615			620
	Pro	Val	Phe	Lys	Thr	Phe	Glu	Val	Pro	Tyr	Val	Ser	Ala	Ala	Ala	Ala	
									625					630			635
70	Gln	Thr	Pro	Asn	Pro	Pro	Val	Gly	Val	Val	Ile	Ala	Asp	Lys	Phe	Met	
									645					650			655
	Ala	Gly	Thr	Tyr	Pro	Glu	Lys	Ala	Ala	Ile	Ala	Ala	Val	Tyr	Val	Met	
									660					665			670
	Pro	Ser	Ala	Pro	Asp	Ser	Thr	Phe	His	Leu	Phe	Leu	Lys	Ser	Asn	Thr	
									675					680			685
75	Asn	Arg	Arg	Leu	Gln	Lys	Val	Thr	Thr	Pro	Ser	Asp	Trp	Gln	Ala	Gly	

WO 99/29870

PCT/AU98/01023

406/ 490

690 695 700
 Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro Phe Pro Val Asn Asn Asp
 705 710 715 720
 His Met Leu Phe Ala Gly Ile Arg Met Pro Asn Lys Tyr Lys Leu Asn
 725 730 735
 Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp Asn Leu Phe Ser Ile Thr
 740 745 750
 Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val Ser Phe Glu Gly Tyr Gly
 755 760 765
 10 Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile Lys Tyr Leu Val Val Asn
 770 775 780
 Thr Asp Ala Pro Lys Ile Asp Met Ser Leu Val Gln Glu Pro Tyr Ala
 785 790 795 800
 Lys Gly Thr Asn Val Ala Pro Phe Pro Glu Leu Val Gly Ile Tyr Val
 805 810 815
 15 Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln Asp Pro Ser Val Thr Thr
 820 825 830
 Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp Glu Tyr Glu Ile Lys Leu
 835 840 845
 20 Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly Val Ala Gln Ile Glu Asn
 850 855 860
 Asn Asn Ala Val Val Ala Tyr Pro Ser Val Val Thr Asp Arg Phe Ser
 865 870 875 880
 Ile Lys Asn Ala His Met Val His Ala Ala Leu Tyr Ser Leu Asp
 885 890 895
 25 Gly Lys Gln Val Arg Ser Trp Asn Asn Leu Arg Asn Gly Val Thr Phe
 900 905 910
 Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr Met Leu Val Met Gln Thr
 915 920 925
 30 Ala Asn Gly Pro Val Ser Gln Lys Ile Val Lys Gln
 930 935 940

(2) INFORMATION FOR SEQ ID NO:464

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 670 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...670
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

Met Lys Tyr Leu Ile Arg Leu Phe Leu Ser Leu Met Leu Leu Ser Leu
 1 5 10 15
 55 Trp Thr Gly Cys Thr His Glu Glu Leu Ser Ile Cys Asp Gly Glu Asn
 20 25 30
 Thr Leu Val Leu Arg Val Glu Thr Gly Lys Ala Pro Asn Ala Arg Ala
 35 40 45
 60 Thr Glu Pro Gly Gln Gly Ile Tyr Asn Glu Asn Lys Val Gly Ser Ile
 50 55 60
 Ser Val Leu Phe Tyr Leu Glu Gly Gln Leu Arg Trp Gln Val Lys Ser
 65 70 75 80
 Thr Arg Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu
 85 90 95
 65 Gln Met Arg Pro Leu Phe Asn Gly Asn Asn Phe Ser Ile Tyr Val
 100 105 110
 Val Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser
 115 120 125
 70 Gln Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro
 130 135 140
 Ala Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala
 145 150 155 160
 Thr Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala
 165 170 175
 75 Ala Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu

407 / 490

180 185 190
 Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly
 195 200 205
 Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys
 210 215 220
 Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile
 225 230 235 240
 His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys
 245 250 255
 10 Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro
 260 265 270
 Asp Asn Thr Ala Lys Pro Tyr Tyr Arg Val Pro Leu Glu Ser Gln
 275 280 285
 15 Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile
 290 295 300
 Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly
 305 310 315 320
 Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu
 325 330 335
 20 Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn
 340 345 350
 Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile
 355 360 365
 25 Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly
 370 375 380
 Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr
 385 390 395 400
 Ile Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val
 405 410 415
 30 Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala
 420 425 430
 Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile
 435 440 445
 35 Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu
 450 455 460
 Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val
 465 470 475 480
 Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr
 485 490 495
 40 Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr
 500 505 510
 Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr
 515 520 525
 45 Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala
 530 535 540
 Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu
 545 550 555 560
 Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn
 565 570 575
 50 Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys
 580 585 590
 Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp
 595 600 605
 55 Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly
 610 615 620
 Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln
 625 630 635 640
 Gly Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val
 645 650 655
 60 Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys
 660 665 670

(2) INFORMATION FOR SEQ ID NO:465

65

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1282 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

70

- (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES

75

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

WO 99/29870

PCT/AU98/01023

408/490

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...1202

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

	Met	Arg	Lys	Ile	Leu	Ser	Phe	Leu	Met	Met	Cys	Ser	Leu	His	Leu	Gly
	1			5						10				15		
10	Leu	Gln	Ser	Gln	Thr	Trp	His	Gly	Asp	Pro	Asp	Ser	Val	Ala	Ala	Leu
		20						25					30			
	Pro	Ser	Ile	Gly	Ile	Gln	Glu	Ser	Ser	Cys	Thr	Arg	Ile	Thr	Phe	Glu
		35						40					45			
15	Val	Val	Phe	Pro	Gly	Phe	Tyr	Ser	Val	Glu	Lys	Arg	Glu	Gly	Asn	Gln
		50						55				60				
	Val	Phe	Gln	Arg	Ile	Ser	Met	Pro	Gly	Cys	Gly	Ser	Phe	Gly	Asn	Leu
		65				70				75					80	
	Gly	Glu	Ala	Glu	Leu	Pro	Val	Leu	Lys	Lys	Met	Ile	Ala	Val	Pro	Glu
					85					90					95	
20	Phe	Ser	Thr	Ala	Asn	Val	Ala	Val	Lys	Ile	Lys	Glu	Thr	Glu	Thr	Phe
				100					105					110		
	Asp	Asn	Tyr	Asn	Ile	Tyr	Pro	Asn	Pro	Thr	Tyr	Val	Val	Glu	Glu	Leu
				115				120					125			
25	Pro	Glu	Gly	Gly	Thr	Tyr	Leu	Val	Glu	Ala	Phe	Ala	Ile	Asn	Asn	Asp
		130					135					140				
	Tyr	Tyr	Ser	Gln	Asu	Val	Ser	Leu	Pro	Ser	Thr	His	Tyr	Val	Tyr	Ser
		145				150					155				160	
	Gln	Asp	Gly	Tyr	Phe	Arg	Ser	Gln	Arg	Phe	Ile	Glu	Val	Thr	Leu	Tyr
					165					170					175	
30	Pro	Phe	Arg	Tyr	Asn	Pro	Val	Arg	Gln	Glu	Ile	Leu	Phe	Ala	Lys	Lys
				180					185					190		
	Ile	Glu	Val	Thr	Ile	Thr	Phe	Asp	Asn	Pro	Gln	Pro	Pro	Leu	Gln	Lys
				195				200					205			
35	Asn	Thr	Gly	Ile	Phe	Asn	Lys	Val	Ala	Ser	Ser	Ala	Phe	Ile	Asn	Tyr
		210					215					220				
	Glu	Ala	Asp	Gly	Lys	Ser	Ala	Ile	Glu	Asn	Asp	Met	Val	Phe	Ser	Arg
					225					230		235			240	
	Gly	Thr	Thr	Thr	Tyr	Ile	Ser	Gly	Asn	Val	Ala	Ser	Asn	Leu	Pro	Gln
					245					250					255	
40	Asn	Cys	Asp	Tyr	Leu	Val	Ile	Tyr	Asp	Asp	Met	Phe	Asn	Val	Asn	Gln
				260					265					270		
	Gln	Pro	His	Asp	Glu	Ile	Lys	Arg	Leu	Cys	Glu	His	Arg	Ala	Phe	Tyr
				275				280					285			
45	Asn	Gly	Phe	Asp	Val	Ala	Ala	Val	Ser	Ile	Lys	Asp	Val	Leu	Asn	Ser
		290					295					300				
	Phe	Pro	Ser	Asn	Ala	Thr	Ser	Tyr	Ile	Asn	Glu	Thr	Lys	Leu	Lys	Asn
					305			310			315				320	
	Phe	Ile	Arg	Ser	Val	Tyr	Asn	Gln	Ser	Asn	Ala	Lys	Arg	Thr	Leu	Asp
					325					330					335	
50	Gly	Lys	Leu	Gly	Tyr	Val	Leu	Leu	Ile	Gly	Lys	Pro	Leu	Ser	Lys	Tyr
				340					345					350		
	Leu	Ala	Asp	Thr	Asp	Asn	Thr	Lys	Val	Pro	Thr	Ser	Phe	Ile	His	Asn
				355				360					365			
55	Val	Ser	Leu	Ile	Pro	Ser	His	Pro	Thr	Phe	Gly	Ser	Ile	Cys	Ala	Ser
				370			375					380				
	Asp	Tyr	Phe	Phe	Ser	Cys	Val	Ser	Pro	Leu	Asp	Thr	Val	Gly	Asp	Leu
					385		390				395				400	
	Phe	Ile	Gly	Arg	Phe	Ser	Val	Thr	Asn	Ala	His	Glu	Leu	His	Asn	Leu
					405					410					415	
60	Ile	Glu	Lys	Thr	Ile	Asn	Lys	Glu	Ile	Ser	Tyr	Asn	Pro	Ile	Ala	His
				420					425					430		
	Lys	Asn	Ile	Leu	Tyr	Ala	Glu	Gly	Lys	Gly	Cys	Asp	Ala	Pro	Ile	Leu
				435				440					445			
65	Arg	Leu	Phe	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Tyr	Thr	Val	Asn	Ser	Ile
		450					455					460				
	Leu	Lys	Ser	Asn	Gln	Val	Ser	Ala	Ile	Asp	Ser	Ile	Phe	Asp	Cys	Leu
				465			470				475				480	
	Asn	Asn	Gly	Ser	His	His	Phe	Tyr	Phe	Asn	Thr	His	Gly	Met	Pro	Thr
					485					490					495	
70	Val	Trp	Gly	Ile	Gly	Gln	Gly	Leu	Asp	Val	Asn	Thr	Leu	Thr	Ala	Arg
				500					505					510		
	Leu	Asn	Asn	Thr	Ser	Ser	Gln	Gly	Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser
				515				520					525			
75	Ser	Ala	Val	Ala	Asp	Ser	Thr	Ile	Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr
				530			535					540				

WO 99/29870

PCT/AU98/01023

409/490

	Thr	Tyr	Ala	Pro	Asn	Lys	Gly	Phe	Ser	Ala	Phe	Leu	Gly	Gly	Ser	Arg	
	545					550					555					560	
	Ala	Thr	Gln	Tyr	Ala	Val	Tyr	Leu	Glu	Gly	Pro	Cys	Pro	Pro	Ser	Glu	
					565					570						575	
5	Phe	Tyr	Glu	Tyr	Leu	Pro	Tyr	Ser	Leu	Tyr	His	Asn	Leu	Ser	Thr	Val	
				580					585						590		
	Val	Gly	Glu	Met	Leu	Leu	Ser	Ser	Ile	Ile	Asn	Thr	Asn	Ser	Val	Asp	
			595					600					605				
10	Thr	Tyr	Ser	Lys	Phe	Asn	Phe	Asn	Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn	
	610						615					620					
	Ile	Met	Ala	His	Gly	Met	Glu	Val	Ser	Asn	Cys	Ile	Thr	Leu	Pro	Asn	
	625					630					635					640	
	Asn	Thr	Ile	Ile	Ser	Ser	Pro	Ile	Thr	Ile	Lys	Asn	Gly	Gly	Cys	Leu	
					645					650					655		
15	Lys	Ile	Pro	Glu	Lys	Gly	Val	Leu	His	Phe	Thr	Asn	Asn	Gly	Ser	Ile	
				660					665					670			
	Gln	Val	Met	Ser	Gly	Gly	Thr	Leu	Glu	Ile	Gly	Asn	Gln	Ala	Lys	Ile	
			675					680					685				
20	Ser	Gly	Glu	Thr	Gly	Ala	Asn	Pro	Thr	Phe	Ile	Thr	Val	Tyr	Gly	Asp	
	690						695					700					
	Gly	Leu	Ala	Ile	Asn	Lys	Gln	Val	Glu	Ile	Asp	Asn	Ile	Asp	Arg	Leu	
	705					710					715				720		
	Asn	Leu	Phe	Ser	Thr	His	Ser	Val	Met	Pro	Lys	Phe	His	Phe	Asp	Ser	
					725					730					735		
25	Val	Lys	Phe	Asn	Ser	Ala	Pro	Leu	Tyr	Thr	Thr	Asn	Cys	Ile	Val	Glu	
			740						745					750			
	Ile	Ser	Asn	Cys	Glu	Phe	Thr	Asn	Arg	Ser	Asp	Ile	Ile	Ser	Lys	Asn	
			755					760				765					
30	Cys	Asp	Leu	Ser	Val	Glu	Asn	Ser	Met	Phe	Ser	Ser	Ser	Gly	Ile	Thr	
	770						775					780					
	Val	Phe	Lys	Pro	Met	Ala	Thr	Ser	Ser	Ile	Thr	Gly	Leu	Ser	Thr	Lys	
	785					790					795					800	
	Ala	Lys	Ile	Thr	Asp	Asn	Thr	Phe	Phe	Ala	Thr	Gly	Asn	Phe	Ala	Tyr	
					805					810					815		
35	His	Ile	Thr	Asn	Thr	Pro	Gly	Leu	Thr	Ala	Thr	Ser	Asn	Ala	Ala	Ile	
			820						825					830			
	Lys	Leu	Asp	Asn	Ile	Pro	Glu	Tyr	Tyr	Ile	Ser	Gly	Asn	Lys	Ile	Val	
			835					840					845				
40	Asn	Cys	Asp	Glu	Ala	Leu	Val	Leu	Asn	Asn	Ser	Gly	Asn	Arg	Thr	Asn	
	850						855					860					
	Arg	Leu	His	Asn	Ile	Thr	Arg	Asn	Val	Ile	Lys	Asn	Cys	Arg	Ile	Gly	
	865					870					875					880	
	Ser	Thr	Leu	Tyr	Asn	Ser	Tyr	Gly	Ile	Tyr	Asn	Arg	Asn	Lys	Ile	Ser	
					885					890					895		
45	Asn	Asn	His	Ile	Gly	Val	Arg	Leu	Leu	Asn	Asn	Ser	Cys	Phe	Tyr	Phe	
			900						905					910			
	Asp	Asn	Ala	Pro	Val	Ile	Asn	Glu	Glu	Asp	Lys	Gln	Thr	Phe	Ile	Ser	
			915					920					925				
50	Asn	Arg	Thr	Trp	Gln	Leu	Tyr	Ser	Ser	Asn	Gly	Thr	Phe	Pro	Leu	Asn	
	930						935					940					
	Phe	His	Tyr	Asn	Ser	Leu	Gln	Gly	Gly	Asp	Thr	Asp	Thr	Trp	Ile	Tyr	
	945					950					955					960	
	Asn	Asp	Thr	Tyr	Thr	Asn	Arg	Tyr	Ile	Asp	Val	Ser	Asn	Asn	His	Trp	
					965					970					975		
55	Gly	Asn	Asn	Asp	Leu	Phe	Asp	Pro	Asn	Gln	Val	Phe	Asn	Thr	Pro	Asp	
				980					985					990			
	Leu	Phe	Ile	Trp	Ile	Pro	Phe	Trp	Asp	Gly	Leu	Pro	Asn	Gly	Arg	Ser	
			995					1000					1005				
60	Gly	Asn	Ser	Ser	Ala	Glu	Ala	Val	Glu	Phe	Gln	Thr	Ala	Leu	Asp	Cys	
	1010						1015					1020					
	Ile	Gly	Asn	Ser	Asp	Tyr	Leu	Ser	Ala	Lys	Val	Ala	Leu	Lys	Met	Met	
	1025					1030					1035					1040	
	Val	Glu	Thr	Tyr	Pro	Glu	Ser	Asp	Phe	Ala	Ile	Ala	Ala	Leu	Lys	Glu	
				1045						1050					1055		
65	Leu	Phe	Arg	Ile	Glu	Lys	Met	Ser	Gly	Asn	Asp	Tyr	Glu	Gly	Leu	Lys	
				1060						1065					1070		
	Asp	Tyr	Phe	Arg	Ser	Asn	Pro	Thr	Ile	Ile	Ser	Ser	Gln	Asn	Leu	Phe	
				1075					1080				1085				
	Pro	Thr	Ala	Asp	Phe	Leu	Ser	Ala	Arg	Cys	Asp	Ile	Val	Cys	Glu	Asn	
				1090				1095				1100					
70	Tyr	Gln	Ser	Ala	Ile	Asp	Trp	Tyr	Glu	Asn	Arg	Leu	Asn	Ser	Glu	Ile	
	1105					1110					1115					1120	
	Ser	Tyr	Gln	Asp	Ser	Val	Phe	Ala	Val	Ile	Asp	Leu	Gly	Asp	Ile	Tyr	
					1125					1130					1135		
75	Trp	Asn	Met	Gln	Leu	Asp	Ser	Leu	Arg	Gly	Thr	Gly	Ile	Asp	Leu	Asn	

WO 99/29870

PCT/AU98/01023

412/490

Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn His Ile Gly Val Arg Leu
 885 890 895
 Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn Ala Pro Val Ile Asn Glu
 900 905 910
 5 Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg Thr Trp Gln Leu Tyr Ser
 915 920 925
 Ser Asn Gly Thr Phe Pro Leu Asn Phe His Tyr Asn Ser Leu Gln Gly
 930 935 940
 10 Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp Thr Tyr Thr Asn Arg Tyr
 945 950 955 960
 Ile Asp Val Ser Asn Asn His Trp Gly Asn Asn Asp Leu Phe Asp Pro
 965 970 975
 Asn Gln Val Phe Asn Thr Pro Asp Leu Phe Ile Trp Ile Pro Phe Trp
 980 985 990
 15 Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn Ser Ser Ala Glu Ala Val
 995 1000 1005
 Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly Asn Ser Asp Tyr Leu Ser
 1010 1015 1020
 20 Ala Lys Val Ala Leu Lys Met Met Val Glu Thr Tyr Pro Glu Ser Asp
 1025 1030 1035 1040
 Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe Arg Ile Glu Lys Met Ser
 1045 1050 1055
 Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr Phe Arg Ser Asn Pro Thr
 1060 1065 1070
 25 Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr Ala Asp Phe Leu Ser Ala
 1075 1080 1085
 Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln Ser Ala Ile Asp Trp Tyr
 1090 1095 1100
 30 Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr Gln Asp Ser Val Phe Ala
 1105 1110 1115 1120
 Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn Met Gln Leu Asp Ser Leu
 1125 1130 1135
 Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu Ser Cys Glu Gln Arg Lys
 1140 1145 1150
 35 Ser Leu Glu Ser His Gln Asn Val Lys Asn Tyr Leu Leu Ser Thr Leu
 1155 1160 1165
 Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro Leu Glu Cys Asn Lys Ser
 1170 1175 1180
 40 Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile Ser Pro Asn Pro Ala Lys
 1185 1190 1195 1200
 Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp Asn Pro Ser Cys Ser Val
 1205 1210 1215
 Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser Ala Asp Ile Thr Gly Leu
 1220 1225 1230
 45 Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser Ile Gln Phe Asn Thr Ser
 1235 1240 1245
 Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr Leu Asn Val Asp Gln Lys
 1250 1255 1260
 50 Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys
 1265 1270

(2) INFORMATION FOR SEQ ID NO:467

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 925 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- 65 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...925
- 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

Met Ala Ile Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile
 1 5 10 15
 75 Leu Leu Ser Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser
 20 25 30

WO 99/29870

PCT/AU98/01023

413/490

Gly Met Asn Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile
 35 40 45
 Leu Tyr Glu Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu
 50 55 60
 5 Ile Asp Ala Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser
 65 70 75 80
 Phe Ser Val Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile
 85 90 95
 10 Arg Ser Gly Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile
 100 105 110
 Glu Gly Ala Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr
 115 120 125
 Asn Pro Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile
 130 135 140
 15 Glu Asp Phe Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr
 145 150 155 160
 Pro Leu Val Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys
 165 170 175
 20 Tyr Ile Ala Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe
 180 185 190
 Leu Lys Leu Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu
 195 200 205
 Pro Ala Thr Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg
 210 215 220
 25 Leu Thr Trp Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn
 225 230 235 240
 Glu Glu Leu Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu
 245 250 255
 30 Leu Ala Gln Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr
 260 265 270
 Tyr Ser Leu Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala
 275 280 285
 Val Tyr Asp Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His
 290 295 300
 35 Tyr Ala Thr Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val
 305 310 315 320
 Pro Asn Gly Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp
 325 330 335
 40 Gly His Tyr Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly
 340 345 350
 His Cys Ser Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr
 355 360 365
 Pro Asp Asn Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val
 370 375 380
 45 Lys Tyr Trp Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr
 385 390 395 400
 Ala Val Met Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile
 405 410 415
 50 Leu Phe Glu Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu
 420 425 430
 Arg Thr Ile Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His
 435 440 445
 Tyr Asn Cys Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val
 450 455 460
 55 Phe Gly Thr Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val
 465 470 475 480
 Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn
 485 490 495
 60 Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala
 500 505 510
 Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp
 515 520 525
 Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp
 530 535 540
 65 Gln Val Glu Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile
 545 550 555 560
 Glu Ser Gln Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp
 565 570 575
 70 Ile Ile Leu Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp
 580 585 590
 Leu Leu Ile Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro
 595 600 605
 Trp Thr Met Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser
 610 615 620
 75 Tyr Leu Pro Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr

WO 99/29870

PCT/AU98/01023

414/ 490

625 630 635 640
Pro Arg Leu Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln
645 650 655
5 Asp Ala Val Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr
660 665 670
Gly Thr Ala Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr
675 680 685
Ala Lys Ala Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala
690 695 700
10 Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe
705 710 715 720
Phe Leu Leu Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val
725 730 735
15 Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys
740 745 750
Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr
755 760 765
Asp Asp Lys Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn
770 775 780
20 Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile
785 790 795 800
Asp Glu Thr Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys
805 810 815
Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp
820 825 830
25 Lys Leu Asn Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr
835 840 845
Ser Leu Lys Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu
850 855 860
30 Gly Leu Ser Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly
865 870 875 880
Ile Cys Ile Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp
885 890 895
35 Val Ser Arg Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly
900 905 910
Asn Lys Thr Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
915 920 925

40 (2) INFORMATION FOR SEQ ID NO:468
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 922 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
55 (B) LOCATION 1...922
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468

60 Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
1 5 10 15
Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
20 25 30
Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
35 40 45
65 Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
50 55 60
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
65 70 75 80
70 Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His-Ile Arg Ser Gly
85 90 95
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
100 105 110
Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
115 120 125
75 His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe

WO 99/29870

PCT/AU98/01023

416/ 490

Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu
 740 745 750
 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys
 755 760 765
 5 Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu
 770 775 780
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr
 785 790 795 800
 10 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala
 805 810 815
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn
 820 825 830
 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys
 835 840 845
 15 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser
 850 855 860
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile
 865 870 875 880
 20 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg
 885 890 895
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr
 900 905 910
 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
 915 920

(2) INFORMATION FOR SEQ ID NO:469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 921 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature
 (B) LOCATION 1...921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469

Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser Trp
 1 5 10 15
 Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn Ala
 20 25 30
 50 Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu Ser
 35 40 45
 Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala Asp
 50 55 60
 Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val Pro
 65 70 75 80
 Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly Ile
 85 90 95
 Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala Lys
 100 105 110
 60 Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu His
 115 120 125
 Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe Val
 130 135 140
 65 Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val Trp
 145 150 155 160
 Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp
 165 170 175
 Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu Asp
 180 185 190
 70 Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr Asp
 195 200 205
 Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp Asn
 210 215 220
 75 Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu Gln
 225 230 235 240

WO 99/29870

PCT/AU98/01023

417 / 490

	Leu	Ser	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Thr	Leu	Leu	Ala	Gln	Ile
					245					250					255	
	Lys	Asp	Val	Ser	Ile	Leu	Glu	Tyr	Val	Asp	Ser	Thr	Tyr	Ser	Leu	Arg
				260					265					270		
5	Asp	Asn	Pro	Leu	Gln	Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asp	Glu
			275					280					285			
	Ser	Ile	Glu	Ser	Ser	Thr	Val	Cys	Gly	Thr	Leu	His	Tyr	Ala	Thr	Asp
		290					295					300				
10	Ala	Ile	Leu	Tyr	Glu	Asn	Phe	Glu	Asn	Gly	Pro	Val	Pro	Asn	Gly	Trp
	305					310					315					320
	Leu	Val	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Phe	Ser	Trp	Gly	His	Tyr	Leu
				325						330					335	
	Asn	Ala	Tyr	Asp	Ala	Phe	Pro	Gly	His	Asn	Gly	Gly	His	Cys	Ser	Leu
				340					345					350		
15	Ser	Ala	Ser	Tyr	Val	Pro	Gly	Ile	Gly	Pro	Val	Thr	Pro	Asp	Asn	Tyr
			355					360					365			
	Leu	Ile	Thr	Pro	Lys	Val	Glu	Gly	Ala	Lys	Arg	Val	Lys	Tyr	Trp	Val
		370					375					380				
20	Ser	Thr	Gln	Asp	Ala	Asn	Trp	Ala	Ala	Glu	His	Tyr	Ala	Val	Met	Ala
	385					390					395					400
	Ser	Thr	Thr	Gly	Thr	Ala	Val	Gly	Asp	Phe	Val	Ile	Leu	Phe	Glu	Glu
					405					410					415	
	Thr	Met	Thr	Ala	Lys	Pro	Thr	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Asn
				420					425					430		
25	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	Trp	Arg	His	Tyr	Asn	Cys	Thr
		435						440					445			
	Asp	Ile	Tyr	Phe	Leu	Lys	Leu	Asp	Asp	Ile	Thr	Val	Phe	Gly	Thr	Pro
		450					455					460				
30	Ala	Ser	Glu	Pro	Glu	Pro	Val	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu
	465					470					475					480
	Asn	Asn	Lys	Gly	Arg	Leu	Lys	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro
					485					490				495		
	Asp	Lys	Thr	Asp	Asp	Lys	Asp	Pro	Leu	Gln	Leu	Ala	Gly	Tyr	Asn	Ile
				500					505					510		
35	Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu
			515						520					525		
	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp	Gln	Val	Glu	Val
		530					535					540				
40	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser
	545					550					555					560
	Val	Cys	Asp	Lys	Leu	Ile	Tyr	Asp	Ser	Gln	Ser	Asp	Ile	Ile	Leu	Tyr
					565					570					575	
	Glu	Gly	Phe	Glu	Ala	Gly	Ser	Ile	Pro	Glu	Gly	Trp	Leu	Leu	Ile	Asp
				580					585					590		
45	Ala	Asp	Gly	Asp	Asn	Val	Asn	Trp	Asp	Tyr	Tyr	Pro	Trp	Thr	Met	Tyr
			595					600					605			
	Gly	His	Asp	Ser	Glu	Lys	Cys	Ile	Ala	Ser	Pro	Ser	Tyr	Leu	Pro	Met
		610					615						620			
50	Ile	Gly	Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Val	Thr	Pro	Arg	Leu	Glu
	625					630					635					640
	Gly	Ala	Lys	Leu	Val	Lys	Tyr	Trp	Val	Ser	Ala	Gln	Asp	Ala	Val	Tyr
					645					650					655	
	Ser	Ala	Glu	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala	Val
				660					665					670		
55	Glu	Asp	Phe	Val	Leu	Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Ala	Asn
				675					680					685		
	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Thr	Leu	Pro	Ala	Gly	Thr	Lys	Tyr
						695						700				
60	Ile	Ala	Trp	Arg	His	Tyr	Asp	Cys	Thr	Asp	Met	Phe	Phe	Leu	Leu	Leu
	705					710					715					720
	Asp	Asp	Ile	Thr	Val	Tyr	Arg	Ser	Thr	Glu	Thr	Val	Pro	Glu	Pro	Val
					725					730					735	
	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys
				740					745					750		
65	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro	Asp	Lys	Thr	Asp	Asp	Lys	Lys
				755				760						765		
	Pro	Leu	Gln	Leu	Thr	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu
					775							780				
70	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr
	785					790					795					800
	Ser	Ser	Arg	Asp	Gly	Gln	Val	Glu	Met	Glu	Tyr	Cys	Val	Thr	Ala	Val
					805					810					815	
	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser	Val	Cys	Asp	Lys	Leu	Asn	Tyr
				820					825					830		
75	Thr	Ile	Thr	Ser	Leu	Asp	Asn	Ile	Gln	Ser	Asp	Thr	Ser	Leu	Lys	Ile

WO 99/29870

PCT/AU98/01023

418 / 490

5 Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser Arg
835 840 845
850 855 860
Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile Leu
865 870 875 880
Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg Leu
885 890 895
Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr Thr
900 910
10 Thr Glu Lys Val Glu Ile Lys Arg Pro
915 920

(2) INFORMATION FOR SEQ ID NO:470

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 593 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 20 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
- 25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) LOCATION 1...593
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Met Asn Ser Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala
1 5 10 15
35 Leu Ser Val Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr
20 25 30
Lys Arg Pro Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln
35 40 45
40 Thr Val Glu Met Glu His Ala Asp Pro Leu Pro Ala Tyr Lys Ala
50 55 60
Ile Glu Pro Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr
65 70 75 80
Phe Gly Phe Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro
85 90 95
45 Asn Ile Leu Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn
100 105 110
Ile Gly Ile Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg
115 120 125
50 Leu Ile Asp Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg
130 135 140
Gly Met Lys Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys
145 150 155 160
Asp Arg Arg Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser
165 170 175
55 Phe Val Leu Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn
180 185 190
Tyr Gly Arg Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser
195 200 205
60 Thr Pro Val Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val
210 215 220
Tyr Leu Gly Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg
225 230 235 240
Phe Phe Arg Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu
245 250 255
65 Thr Glu His Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser
260 265 270
Asp Asp Ile Lys Leu Gly Val Glu Val Arg Thr Gly Gly Lys Phe Phe
275 280 285
70 Ala Lys Asn Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp
290 295 300
Arg Asn Leu Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly
305 310 315 320
Asp Ser Asp Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser
325 330 335
75 Ser His Phe Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp

WO 99/29870

PCT/AU98/01023

419/ 490

340 345 350
 Ala Ser Leu Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe
 355 360 365
 Gly Gly Val Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met
 370 375 380
 5 Pro Tyr Leu Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu
 385 390 395 400
 Thr Ala Gln Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met
 405 410 415
 10 Glu Val Tyr Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr
 420 425 430
 Pro Thr Leu Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val
 435 440 445
 15 Ser Phe Leu Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly
 450 455 460
 Lys Leu Glu Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala
 465 470 475 480
 Ser Tyr Gly Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln
 485 490 495
 20 Pro Asp Leu Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro
 500 505 510
 Leu Asp Val Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr
 515 520 525
 25 Ser Phe Gly Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His
 530 535 540
 Leu Leu Ser Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu
 545 550 555 560
 Tyr Leu Lys Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly
 565 570 575
 30 Tyr Tyr Pro Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr
 580 585 590
 Phe

 35 (2) INFORMATION FOR SEQ ID NO:471
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 589 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40
 (ii) MOLECULE TYPE: protein
 45 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 50 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...589
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471
 55 Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val Ser
 1 5 10 15
 Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro Asp
 20 25 30
 60 Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu Met
 35 40 45
 Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro Arg
 50 55 60
 Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe Val
 65 70 75 80
 Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu Pro
 85 90 95
 Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile Gly
 100 105 110
 70 His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp Ala
 115 120 125
 Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys Ser
 130 135 140
 Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Lys Asp Arg Arg Met
 145 150 155 160
 75 Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu Ala

WO 99/29870

PCT/AU98/01023

420/ 490

5 Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg Gly
 180 185 190
 Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val Thr
 195 200 205
 Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly Ala
 210 215 220
 Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg Ser
 225 230 235 240
 10 Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His Thr
 245 250 255
 Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile Lys
 260 265 270
 15 Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn Ser
 275 280 285
 Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu Tyr
 290 295 300
 Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp Asn
 305 310 315 320
 20 Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe Gly
 325 330 335
 Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu Ser
 340 345 350
 25 Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val Ile
 355 360 365
 Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu Met
 370 375 380
 Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln Leu
 385 390 395 400
 30 Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr Gly
 405 410 415
 Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu Pro
 420 425 430
 35 Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu Pro
 435 440 445
 Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu Tyr
 450 455 460
 Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly Lys
 465 470 475 480
 40 Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu Ile
 485 490 495
 Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val Arg
 500 505 510
 45 Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly Ser
 515 520 525
 Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser Ala
 530 535 540
 Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys Ile
 545 550 555 560
 50 Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro Met
 565 570 575
 Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe
 580 585

55 (2) INFORMATION FOR SEQ ID NO:472
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 60 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 65 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...346
 70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472
 75 Met Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe

WO 99/29870

PCT/AU98/01023

421/ 490

1 Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
20 25 30
5 Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
35 40 45
Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
50 55 60
Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
65 70 75 80
10 Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
85 90 95
Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
100 105 110
15 Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
115 120 125
Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
130 135 140
Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
145 150 155 160
20 Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
165 170 175
Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
180 185 190
25 Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
195 200 205
Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
210 215 220
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
225 230 235
30 Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
240 245 250 255
Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
260 265 270
35 Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
275 280 285
Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
290 295 300
Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
305 310 315 320
40 Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
325 330 335
Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
340 345

45 (2) INFORMATION FOR SEQ ID NO:473

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 amino acids
(B) TYPE: amino acid
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

65 Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met
1 5 10 15
Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe
20 25 30
70 Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His-Phe Leu Asn Leu
35 40 45
Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile
50 55 60
Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly
65 70 75 80
75 Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser

WO 99/29870

PCT/AU98/01023

422/ 490

5 Gly Ser His Met 85 Gly Asn Ala Cys Tyr 90 Ala Ser Ser Val Gly Glu Arg
100 105 110
115 120 125
130 135 140
145 150 155 160
10 Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser
165 170 175
180 185 190
15 Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu
195 200 205
210 215 220
225 230 235 240
20 Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp
245 250 255
260 265 270
25 Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln
275 280 285
290 295 300
30 Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser
305 310 315 320
325 330 335
340 345
35 (2) INFORMATION FOR SEQ ID NO:474
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
40 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
45 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...330
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474
55 Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
1 5 10 15
Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
20 25 30
60 Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
35 40 45
Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
50 55 60
Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
65 70 75 80
Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
85 90 95
Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
100 105 110
70 Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
115 120 125
Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
130 135 140
Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
145 150 155 160
75 Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp

WO 99/29870

PCT/AU98/01023

423/ 490

165 170 175
Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
180 185 190
5 Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
195 200 205
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
210 215 220
Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
225 230 235 240
10 Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
245 250 255
Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
260 265 270
15 Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
275 280 285
Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
290 295 300
Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
305 310 315 320
20 Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
325 330

(2) INFORMATION FOR SEQ ID NO:475

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
35 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...324
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

Met Cys Leu Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu
1 5 10 15
45 Gln Glu Leu Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly
20 25 30
Asn Glu Ile Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys
35 40 45
50 Glu Val Gly Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Gly
50 55 60
Thr Gly Lys Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser
65 70 75 80
Tyr Lys Gln Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly
85 90 95
55 Gly Tyr Arg Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly
100 105 110
Lys Pro Leu Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe
115 120 125
60 Leu His Asp Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val
130 135 140
Ser Leu Gln Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val
145 150 155 160
Leu Asp Asn Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro
165 170 175
65 Glu Ala Leu Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp
180 185 190
Arg Arg Ala Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser
195 200 205
70 Asp Pro Glu Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile
210 215 220
Ser Ala Glu Asp Glu Ala Leu Phe Ser Ser Asp Phe Asp Thr Asn
225 230 235 240
Tyr Lys Thr Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro
245 250 255
75 Pro Leu Val Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe

SUBSTITUTE SHEET (Rule 26) (RO/AU)

424/ 490

260 265 270
 Gly Thr Ala Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile
 275 280 285
 Phe Ile Ala Val Gly Lys Ile Leu Glu Glu Lys Lys Gln Arg His Ile
 290 295 300
 Glu Ser Phe Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser
 305 310 315 320
 Asn Gly Arg Ser

10 (2) INFORMATION FOR SEQ ID NO:476
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 547 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION: 1...547
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala Leu Phe Phe
 1 5 10 15
 Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln Met Leu Asn
 20 25 30
 Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro Thr Glu Arg
 35 40 45
 Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg Gly Ala Asp
 50 55 60
 Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr Val Arg Phe
 40 65 70 75 80
 Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro Tyr Asn Gly
 85 90 95
 Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg Ile Ser Val
 100 105 110
 Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser Arg Gly Met
 115 120 125
 His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu Ala Tyr Tyr
 130 135 140
 Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His Phe Glu Asp
 145 150 155 160
 Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg Leu Pro Leu
 165 170 175
 Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg Leu Thr Asp
 180 185 190
 Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser Cys Ala Thr
 195 200 205
 Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser Ala Ala Tyr
 210 215 220
 Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg Pro Gly Gln
 225 230 235 240
 Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val Asp Val Ser
 245 250 255
 Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr Val Asn Gly
 260 265 270
 Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp Ala Ile Gly
 275 280 285
 Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg Ser Ser Ile
 290 295 300
 Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr Gly Ser Trp
 305 310 315 320
 His Leu Ser Asp Phe Asp Phe Ser Phe Ala Asp Tyr Ala Leu Arg
 325 330 335
 Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp Asp Asn Tyr
 340 345 350
 His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp Tyr Met Leu

WO 99/29870

PCT/AU98/01023

425/ 490

355 360 365
Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile Arg Thr Asp
370 375 380
5 Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe Tyr Gly Tyr
385 390 395 400
Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser Gly Met Leu
405 410 415
Pro Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser Lys Leu Asp
420 425 430
10 Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu Thr His Ser
435 440 445
Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr Gln Leu Ala
450 455 460
15 Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu Val Arg Ser
465 470 475 480
Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg Leu Met Thr
485 490 495
Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp Gly Ile Ala
500 505 510
20 Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser Asp Pro Gln
515 520 525
Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys Asn Ile Ser
530 535 540
25 Tyr Leu Phe
545

(2) INFORMATION FOR SEQ ID NO:477

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
35 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
40 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...750
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

Met Lys Lys Leu His Met Ile Ala Ala Leu Ala Val Leu Pro Phe Cys
1 5 10 15
50 Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu Ile Asp Ser Leu Ser
20 25 30
Asn Val Gln Leu Gln Thr Val Gln Val Val Ala Thr Arg Ala Thr Ala
35 40 45
Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys Ala Glu Leu Ser Lys
50 55 60
55 Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu Met Leu Thr Pro Ser
65 70 75 80
Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile Gly Tyr Ser Gly Phe
85 90 95
60 Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn Ile Thr Thr Asn Gly
100 105 110
Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val Phe Trp Val Asn Met
115 120 125
Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln Val Gln Arg Gly Val
130 135 140
65 Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly Ala Ser Val Asn Met
145 150 155 160
Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly Arg Val Asp Leu Ser
165 170 175
70 Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val Lys Leu Gly Ser Gly
180 185 190
Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg Leu Ser Lys Ile Gly
195 200 205
Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp Leu Lys Ser Tyr Phe
210 215 220
75 Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala Leu Arg Phe Ile Thr

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

426/490

225 230 235 240
Phe Gly Gly Lys Glu Val Thr Gly Ile Ala Trp Asn Gly Leu Ser Lys
245 250 255
5 Glu Asp Glu Ala Lys Tyr Gly Arg Arg Tyr Asn Ser Ala Gly Leu Met
260 265 270
Tyr Val Asp Ala Gln Gly Val Pro His Tyr Tyr His Asn Thr Asp Asn
275 280 285
Tyr Glu Gln Arg His Tyr His Ala Ile Met Thr His Ser Phe Ser Pro
290 295 300
10 Ser Val Ile Leu Asn Leu Thr Ala His Tyr Thr Ala Gly Tyr Gly Tyr
305 310 315 320
Thr Asp Glu Tyr Arg Thr Gly Arg Lys Leu Lys Glu Tyr Ala Leu Gln
325 330 335
15 Pro Tyr Val Glu Asn Ser Val Thr Val Lys Lys Thr Asp Leu Ile Arg
340 345 350
Gln Lys Tyr Leu Asp Asn Asp Phe Gly Gly Leu Ile Gly Ser Leu Asn
355 360 365
Trp His Thr Gly Ala Trp Asp Leu Gln Phe Gly Ala Ser Gly Asn Ile
370 375 380
20 Tyr Lys Gly Asp His Phe Gly Arg Ile Thr Tyr Ile Lys Lys Tyr Asn
385 390 395 400
Gln Pro Leu Ala Pro Asp Phe Glu Tyr Tyr Arg Asn Arg Ala Asp Lys
405 410 415
25 Arg Glu Gly Ala Ala Phe Ala Lys Ala Asn Trp Gln Ile Thr Pro Glu
420 425 430
Leu Asn Met Tyr Ala Asp Leu Gln Tyr Arg Thr Ile Gly Tyr Thr Ile
435 440 445
Asn Gly Ile Thr Asp Glu Tyr Asp Glu Val Gln Gly Ser Met Gln His
450 455 460
30 Ile Asp Leu Asp Lys Thr Phe Arg Phe Leu Asn Pro Lys Ala Gly Leu
465 470 475 480
Thr Tyr Ser Phe Asp Ala His Thr Ala Tyr Ala Ser Val Ala Val
485 490 495
35 Ala His Arg Glu Pro Asn Arg Thr Asn Tyr Thr Glu Ala Gly Ile Gly
500 505 510
Gln Tyr Pro Thr Pro Glu Arg Leu Ile Asp Tyr Glu Leu Gly Tyr Arg
515 520 525
Tyr Ala Ser Pro Leu Leu Ser Ala Gly Val Gly Leu Tyr Tyr Met Gln
530 535 540
40 Tyr Lys Asp Gln Leu Val Leu Asp Gly Arg Leu Ser Asp Val Gly Gln
545 550 555 560
Met Leu Thr Ser Asn Val Pro Asp Ser Tyr Arg Met Gly Leu Glu Leu
565 570 575
45 Thr Leu Gly Trp Gln Ile Leu Pro Arg Leu Leu Arg Trp Asp Ala Ser
580 585 590
Phe Thr Met Ser Arg Asn Lys Ile Asp Arg Tyr Val Gln Tyr Thr Ser
595 600 605
Val Tyr Asp Ala Asp Tyr Asn Trp Leu Glu Leu Lys Glu Glu Thr Leu
610 615 620
50 Glu Ser Thr Asp Ile Ala Tyr Ser Pro Asn Val Ile Ala Gly Ser Met
625 630 635 640
Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala Trp Thr Ser Arg Phe
645 650 655
55 Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg Ser Asp Arg Met Leu
660 665 670
Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly Tyr Val Leu Pro Val
675 680 685
His Phe Val Lys Arg Val Ala Leu Gly Val Gln Leu Asn Asn Leu Phe
690 695 700
60 Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr Asp Ala Gly Tyr Val
705 710 715 720
Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp Leu Arg Tyr Tyr Pro
725 730 735
65 Gln Ala Gly Phe Asn Ala Leu Gly Ser Leu Thr Ile Asp Phe
740 745 750

(2) INFORMATION FOR SEQ ID NO:478

70 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

75 (1) MOLECULE TYPE: protein

WO 99/29870

PCT/AU98/01023

427/490

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

Met Lys Arg Arg Phe Leu Ser Leu Leu Leu Tyr Ile Leu Ser Ser
1 5 10 15
Ile Ser Leu Ser Ala Gln Arg Phe Pro Met Val Gln Gly Ile Glu Leu
20 25 30
Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys Arg Pro Trp Arg Ala Ile
35 40 45
Gly Lys Thr Ile Gly Val Asn Leu Ala Val Trp Gly Phe Asp His Phe
50 55 60
Ile Met Asn Glu Asp Phe Ala Asp Ile Ser Trp Gln Thr Ile Lys Ser
65 70 75 80
Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn Asp Lys Phe Val Thr Asn
85 90 95
Leu Phe Ala His Pro Tyr His Gly Ser Leu Tyr Phe Asn Ala Ala Arg
100 105 110
Ser Asn Gly Leu Ser Phe Arg His Ser Ala Pro Phe Ala Phe Phe Gly
115 120 125
Ser Leu Met Trp Glu Leu Leu Met Glu Asn Glu Pro Pro Ser Ile Asn
130 135 140
Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile Ala Leu Gly Glu Met Gly
145 150 155 160
His Arg Leu Ser Asp Leu Leu Ile Asp Asn Arg Thr Thr Gly Trp Glu
165 170 175
Arg Met Gly Arg Glu Val Ala Ile Ala Leu Ile Asn Pro Met Arg Phe
180 185 190
Leu Asn Arg Leu Thr Ala Gly Glu Val Thr Ser Val Gly Ser Arg Ser
195 200 205
Gly Gln Ile Phe Gln Ser Val Pro Ile Asn Ile Val Val Asp Ala Gly
210 215 220
Phe Arg Phe Leu Ala Asp Lys Arg His Ala Arg Thr Gly Ala Thr Ala
225 230 235 240
Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly Asp Pro Phe Arg Ser Glu
245 250 255
Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe Lys Ala Gly Leu Ser Phe
260 265 270
Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile Asn Leu Ile Gly Ile Leu
275 280 285
Ser Gly Cys Gln Leu Leu Ala His Glu Arg Thr Val Leu Val Gly Gly
290 295 300
Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser Glu Lys Arg Ile Ser Lys
305 310 315 320
Asn Ser Glu Glu Val Leu Val Thr Pro Tyr Arg Ile Ser Gln Val Ala
325 330 335
Ala Leu Gly Gly Gly Leu Ile Phe Gln His His Gly Lys Phe Arg Arg
340 345 350
Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr Leu Asn Val Val Pro Met
355 360 365
Gly Ala Ser Leu Ser Asp His Tyr Asn Val Asp Asn Arg Asp Tyr Asn
370 375 380
Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr Leu Gly Ala Thr Tyr Asn
385 390 395 400
Asp Leu Trp Ser Trp Leu Leu Gly Val Glu Ser Tyr Arg Leu Tyr Thr
405 410 415
Trp Ile Gly Tyr Glu Glu Pro His Gln Lys Asn Thr Asp Val Ser Ser
420 425 430
Phe Met Val Gln Gly Asp Glu Ser Lys Ala Arg Leu Leu Val Thr Ser
435 440 445
Ser Glu Phe Ala Phe His Pro Gly Pro Trp His Val Ala Ile Val Ala
450 455 460
Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln Phe Tyr Pro Asn Val Ser
465 470 475 480
Phe Asp Thr Gly Asp Ile Gln Leu Arg Val Gly Phe His Phe
485 490

(2) INFORMATION FOR SEQ ID NO:479

WO 99/29870

PCT/AU98/01023

428/ 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 294 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...294

(x.i) SEQUENCE DESCRIPTION: SEQ ID NO:479

Het Lys Arg Leu Ile Val Phe Leu Ala Met Gly Gly Leu Leu Phe Thr
 1 5 10 15
 Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala Ser Asp Thr Pro Lys Lys
 20 25 30
 Asp Trp Thr Ile Lys Gly Val Thr Gly Leu Asn Ala Ser Gln Thr Ser
 35 40 45
 Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn Thr Val Ala Gly Asn Leu
 50 55 60
 Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys Asp Lys Trp Ser Trp Asp
 65 70 75 80
 Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr Tyr Thr Thr Ala Asn Lys
 85 90 95
 Trp Asn Lys Ser Val Asp Lys Ile Glu Leu Phe Thr Lys Ala Gly Tyr
 100 105 110
 Glu Ile Gly Lys His Trp Tyr Gly Ser Ala Leu Phe Thr Phe Leu Ser
 115 120 125
 Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser Asp His Leu Thr Gly Val
 130 135 140
 Lys His Ile Ser Asn Phe Phe Ala Pro Ala Tyr Leu Thr Leu Gly Ile
 145 150 155 160
 Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe Ser Leu Tyr Leu Ser Pro
 165 170 175
 Thr Thr Gly Lys Leu Thr Val Val Ala Asp Asp Tyr Leu Ser Ser Leu
 180 185 190
 Gly Ala Phe Gly Val Lys Val Gly Glu Lys Thr Met Phe Glu Leu Gly
 195 200 205
 Ala Leu Val Val Gly Ser Ala Asn Ile Asn Leu Met Glu Asn Val Asn
 210 215 220
 Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala Tyr Thr His Asp Phe Gly
 225 230 235 240
 Asn Ile Asp Ile Asn Trp Glu Ala Met Leu Ala Met Lys Ile Asn Lys
 245 250 255
 Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu Ile Tyr Asp Asp Asp Val
 260 265 270
 Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe Lys Glu Val Val Gly Val
 275 280 285
 Gly Val Ala Tyr Thr Phe
 290

(2) INFORMATION FOR SEQ ID NO:480

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...204

WO 99/29870

PCT/AU98/01023

429/ 490

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:480

5 Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile Gly
1 5 10 15
Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn Phe
20 25 30
Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn Asn
35 40 45
10 Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala Leu
50 55 60
Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met Arg
65 70 75 80
15 Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His Tyr
85 90 95
Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp Asn
100 105 110
Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val Ala
115 120 125
20 Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp Ala
130 135 140
Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu Ser
145 150 155 160
25 Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu His
165 170 175
Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu Arg
180 185 190
Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe
195 200

(2) INFORMATION FOR SEQ ID NO:481

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
40 (iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
45 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481

50 Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu Leu Ala Ser Val Thr
1 5 10 15
Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg Val Asp Ala Asn Phe
20 25 30
55 Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly Tyr Val Trp Asp Thr
35 40 45
Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Met Ile
50 55 60
60 Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu Asn Tyr Thr Met Lys
65 70 75 80
Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met Val Pro Gly Thr Tyr
85 90 95
Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu Gln Leu Pro Ile Asn
100 105 110
65 Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met Ala Val Ser Ile Glu
115 120 125
Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly Thr Tyr Arg Gln Lys
130 135 140
70 Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr Gly Phe Phe Gly Pro
145 150 155 160
Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp Ile Gly Ala Asn Ile
165 170 175
Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile Gln Ile Gly Tyr Glu
180 185 190
75 His Gly Phe Val Asp Ile Val Ser Gly Gly Gly Ser Asp Ile Pro Arg

WO 99/29870

PCT/AU98/01023

430/ 490

5 195 200 205
Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr Ala Leu Arg Glu Lys
710 215 220
Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe Phe Val Gly Ile Gly
225 230 235 240
Tyr Arg Phe

10 (2) INFORMATION FOR SEQ ID NO:482

15 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein

 (iii) HYPOTHETICAL: YES

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

 (ix) FEATURE:
25 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...207

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:482

30 Met Lys Arg Met Leu Leu Leu Val Val Leu Leu Tyr Gly Ile Ala
1 5 10 15
Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp Ser Leu Gln Val
20 25 30
Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly Gly Phe Thr Tyr
35 40 45
Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu Glu Val Gly Leu
50 55 60
Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn Ala Asp Ser Phe
65 70 75 80
Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn Met Ser Ser Pro
40 85 90 95
Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala Asn Cys Tyr Met
100 105 110
Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp Gln Asn Ser Arg
115 120 125
45 His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser Asn Lys His Asn
130 135 140
Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val Ser Ile Tyr Thr
145 150 155 160
Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val Ala Tyr Glu Tyr
50 165 170 175
Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val Met Tyr Asp His
180 185 190
Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser Thr His Phe
195 200 205

55 (2) INFORMATION FOR SEQ ID NO:483

60 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 951 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein

65 (iii) HYPOTHETICAL: YES

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

70 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...951

75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:483

432/ 490

595 600 605
 Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly Lys Leu
 610 615 620
 5 His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly Ala Pro
 625 630 635
 Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn Asn Leu
 645 650 655
 Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys Lys Ile
 660 665 670
 10 Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met Phe Ala
 675 680 685
 Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu Arg Leu
 690 695 700
 15 Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro Tyr Leu
 705 710 715
 Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr Lys Ser
 725 730 735
 Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu Ile Ser
 740 745 750
 20 Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu Ser Gly
 755 760 765
 Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu Lys Lys
 770 775 780
 25 Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp Ile Leu
 785 790 795
 Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Glu Ser Leu Leu Glu Arg
 805 810 815
 Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala Tyr Ser
 820 825 830
 30 Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala Thr Asp
 835 840 845
 Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg Val Thr
 850 855 860
 35 Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn Trp Ser
 865 870 875
 Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile Thr Ser
 885 890 895
 Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile Ser Ala
 900 905 910
 40 Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val Ile Ser
 915 920 925
 Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser Asn Arg
 930 935 940
 45 Pro Ile Thr Asn Thr Tyr
 945 950

(2) INFORMATION FOR SEQ ID NO:484

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1226 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 60 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...1226
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

Met Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys
 1 5 10 15
 70 Thr Val Phe Thr Phe Gln Ile Lys Ala Arg Pro Tyr-Glu Arg Phe Ala
 20 25 30
 Asp Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu
 35 40 45
 Val Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln
 50 55 60
 75 Ser Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile

WO 99/29870

PCT/AU98/01023

433/490

	65				70			75								80
	Arg	Pro	Ala	Asn	Arg	Phe	Pro	Ser	His	Arg	Lys	Ser	Phe	Phe	Ala	Glu
					85					90					95	
5	Asn	Leu	Arg	Ala	Ser	Pro	Pro	Val	Val	Pro	Val	Ala	Val	Asp	Lys	Tyr
				100					105					110		
	Ala	Val	Pro	Val	Ala	Asn	Pro	Met	Asp	Pro	Glu	Asn	Pro	Asn	Ala	Trp
				115					120					125		
	Asp	Val	Thr	Leu	Lys	Ile	Thr	Thr	Lys	Ala	Val	Thr	Val	Pro	Val	Asp
				130					135					140		
10	Val	Val	Met	Val	Ile	Asp	Gln	Ser	Ser	Ser	Met	Gly	Gly	Gln	Asn	Ile
					150						155				160	
	Ala	Arg	Leu	Lys	Ser	Ala	Ile	Ala	Ser	Gly	Gln	Arg	Phe	Val	Lys	Lys
					165					170					175	
15	Met	Leu	Pro	Lys	Gly	Thr	Ala	Thr	Glu	Gly	Val	Arg	Ile	Ala	Leu	Val
				180					185					190		
	Ser	Tyr	Asp	His	Glu	Pro	His	Arg	Leu	Ser	Asp	Phe	Thr	Lys	Asp	Thr
				195				200					205			
	Ala	Phe	Leu	Cys	Gln	Lys	Ile	Arg	Ala	Leu	Thr	Pro	Ile	Trp	Gly	Thr
				210				215					220			
20	His	Thr	Gln	Gly	Gly	Leu	Lys	Met	Ala	Arg	Asn	Ile	Met	Ala	Thr	Ser
					230						235				240	
	Thr	Ala	Val	Asp	Lys	His	Ile	Ile	Leu	Met	Ser	Asp	Gly	Leu	Ala	Thr
					245					250					255	
25	Glu	Gln	Tyr	Pro	Val	Lys	Asn	Val	Thr	Thr	Ala	Asp	Phe	Ile	Gly	Lys
				260					265						270	
	Thr	Gly	Asn	Ala	Asn	Asp	Pro	Ile	Asp	Leu	Val	Ile	Gln	Gly	Ala	Ile
				275				280					285			
30	Asn	Phe	Pro	Thr	Asn	Tyr	Val	Ser	Asn	Asn	Pro	Ser	Thr	Pro	Leu	Thr
				290				295					300			
	Pro	Asn	Tyr	Pro	Thr	His	Ser	Ser	Lys	Val	Gly	Arg	Arg	Asn	Leu	Pro
					310						315				320	
	Glu	Ser	Lys	Phe	Asp	Tyr	Ser	Asn	Leu	Ser	Ala	Arg	Ile	Thr	Phe	Asp
					325					330					335	
35	Gly	Val	Ala	Gly	Ala	Leu	Val	Tyr	Glu	Pro	Arg	Phe	Pro	His	Pro	Tyr
				340					345					350		
	Tyr	Tyr	Tyr	Phe	Pro	Cys	Asn	Ala	Ala	Ile	Asn	Glu	Ala	Gln	Phe	Ala
				355				360					365			
40	Lys	Asn	Ser	Gly	Tyr	Thr	Ile	His	Thr	Ile	Gly	Tyr	Asp	Leu	Gly	Asp
				370			375					380				
	Phe	Ala	Leu	Ala	Asn	Asn	Ser	Leu	Lys	Leu	Thr	Ala	Thr	Asp	Glu	Asn
					390						395				400	
	His	Phe	Phe	Thr	Ala	Thr	Pro	Ala	Asn	Leu	Ala	Ala	Ala	Phe	Asp	Asn
					405					410					415	
45	Ile	Ala	Gln	Thr	Ile	Asn	Ile	Gly	Ile	Gln	Arg	Gly	Glu	Val	Thr	Asp
				420					425					430		
	Phe	Val	Ala	Pro	Gly	Phe	Ile	Val	Lys	Asn	Leu	Thr	Gln	Ser	Gly	Asp
				435				440					445			
	Val	Thr	His	Leu	Leu	Asn	Val	Ser	Asn	Gly	Thr	Val	His	Tyr	Asp	Val
				450			455					460				
50	Ser	Thr	Lys	Lys	Leu	Thr	Trp	Thr	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Ser
					470					475					480	
	Glu	Ala	Thr	Ile	Thr	Tyr	Arg	Ile	Tyr	Ala	Asp	Leu	Asp	Tyr	Ile	Gln
					485					490				495		
55	Asn	Asn	Asp	Ile	Pro	Val	Asn	Thr	Thr	Ser	Ala	Ile	Gly	Pro	Asp	Leu
				500					505					510		
	Gly	Gly	Phe	Asp	Thr	Asn	Thr	Glu	Ala	Lys	Leu	Thr	Tyr	Thr	Asn	Ser
				515				520					525			
60	Asn	Gly	Glu	Pro	Asn	Gln	Gln	Leu	Ile	Phe	Pro	Arg	Pro	Thr	Val	Lys
				530				535					540			
	Leu	Gly	Tyr	Gly	Val	Ile	Lys	Arg	His	Tyr	Val	Leu	Val	Asn	Lys	Asp
				545			550				555				560	
	Gly	Gln	Pro	Ile	Gln	Ala	Asn	Gly	Thr	Val	Val	Ser	Ser	Leu	Ser	Glu
					565					570					575	
65	Ala	His	Val	Leu	Gln	Ser	Gln	Asp	Phe	Phe	Leu	Pro	Ser	Gly	Gly	Gly
				580					585					590		
	His	Ile	Val	Pro	Lys	Trp	Ile	Lys	Leu	Asp	Lys	Thr	Thr	Glu	Ala	Leu
				595				600					605			
	Gln	Tyr	Tyr	Ser	Val	Pro	Pro	Thr	Asn	Thr	Val	Ile	Thr	Thr	Ala	Asp
				610			615					620				
70	Gly	Lys	Arg	Tyr	Arg	Phe	Val	Glu	Val	Pro	Gly	Ser	Thr	Pro	Asn	Pro
					630						635				640	
	Gly	Gln	Ile	Gly	Ile	Ser	Trp	Lys	Lys	Pro	Ala	Gly	Asn	Ala	Tyr	Phe
					645					650					655	
75	Ala	Tyr	Lys	Leu	Leu	Asn	Tyr	Trp	Met	Gly	Gly	Thr	Thr	Asp	Gln	Gln
				660					665					670		

434/ 490

Ser Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu
 675 680 685
 Thr Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro
 690 695 700
 5 Ala Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly
 705 710 715 720
 Asn Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser
 725 730 735
 10 Gln Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly
 740 745 750
 Thr Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu
 755 760 765
 Phe Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe
 770 775 780
 15 Tyr Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser
 785 790 795 800
 Trp Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn
 805 810 815
 20 Asp Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn
 820 825 830
 Gly Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln
 835 840 845
 Lys Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr
 850 855 860
 25 Gly Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu
 865 870 875 880
 Asn Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile
 885 890 895
 30 Gly Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe
 900 905 910
 Pro Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg
 915 920 925
 Asp Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala
 930 935 940
 35 Gly Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu
 945 950 955 960
 Pro Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn
 965 970 975
 40 Gly Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn
 980 985 990
 Thr Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly
 995 1000 1005
 Asn Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly
 1010 1015 1020
 45 Asn Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser
 1025 1030 1035 1040
 Phe Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly
 1045 1050 1055
 50 Leu Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln
 1060 1065 1070
 Val Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala
 1075 1080 1085
 Asp Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe
 1090 1095 1100
 55 Ala Lys Gly Ala Val Tyr Leu His Asn Leu Gln Ser Gly Ala Lys His
 1105 1110 1115 1120
 Arg Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp
 1125 1130 1135
 60 Ser Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp
 1140 1145 1150
 Asp Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn
 1155 1160 1165
 Gln Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys
 1170 1175 1180
 65 Leu Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys
 1185 1190 1195 1200
 Val Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr
 1205 1210 1215
 70 Asn Asp Val His Lys Val Leu Val Glu Tyr
 1220 1225

(2) INFORMATION FOR SEQ ID NO:485

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1225 amino acids

WO 99/29870

PCT/AU98/01023

435 / 490

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys Thr
1 5 10 15
Val Phe Thr Phe Gln Ile Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp
20 20 25 30
Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu Val
35 40 45
Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser
50 55 60
Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile Arg
25 65 70 75 80
Pro Ala Asn Arg Phe Pro Ser His Arg Lys Ser Phe Phe Ala Glu Asn
85 90 95
Leu Arg Ala Ser Pro Pro Val Val Pro Val Ala Val Asp Lys Tyr Ala
30 100 105 110
Val Pro Val Ala Asn Pro Met Asp Pro Glu Asn Pro Asn Ala Trp Asp
115 120 125
Val Thr Leu Lys Ile Thr Thr Lys Ala Val Thr Val Pro Val Asp Val
130 135 140
Val Met Val Ile Asp Gln Ser Ser Ser Met Gly Gly Gln Asn Ile Ala
35 145 150 155 160
Arg Leu Lys Ser Ala Ile Ala Ser Gly Gln Arg Phe Val Lys Lys Met
165 170 175
Leu Pro Lys Gly Thr Ala Thr Glu Gly Val Arg Ile Ala Leu Val Ser
40 180 185 190
Tyr Asp His Glu Pro His Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala
195 200 205
Phe Leu Cys Gln Lys Ile Arg Ala Leu Thr Pro Ile Trp Gly Thr His
210 215 220
Thr Gln Gly Gly Leu Lys Met Ala Arg Asn Ile Met Ala Thr Ser Thr
45 225 230 235 240
Ala Val Asp Lys His Ile Ile Leu Met Ser Asp Gly Leu Ala Thr Glu
245 250 255
Gln Tyr Pro Val Lys Asn Val Thr Thr Ala Asp Phe Ile Gly Lys Thr
50 260 265 270
Gly Asn Ala Asn Asp Pro Ile Asp Leu Val Ile Gln Gly Ala Ile Asn
275 280 285
Phe Pro Thr Asn Tyr Val Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro
290 295 300
Asn Tyr Pro Thr His Ser Ser Lys Val Gly Arg Asn Leu Pro Glu
55 305 310 315 320
Ser Lys Phe Asp Tyr Ser Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly
325 330 335
Val Ala Gly Ala Leu Val Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr
60 340 345 350
Tyr Tyr Phe Pro Cys Asn Ala Ala Ile Asn Glu Ala Gln Phe Ala Lys
355 360 365
Asn Ser Gly Tyr Thr Ile His Thr Ile Gly Tyr Asp Leu Gly Asp Phe
370 375 380
Ala Leu Ala Asn Asn Ser Leu Lys Leu Thr Ala Thr Asp Glu Asn His
65 385 390 395 400
Phe Phe Thr Ala Thr Pro Ala Asn Leu Ala Ala Ala Phe Asp Asn Ile
405 410 415
Ala Gln Thr Ile Asn Ile Gly Ile Gln Arg Gly Glu Val Thr Asp Phe
70 420 425 430
Val Ala Pro Gly Phe Ile Val Lys Asn Leu Thr Gln Ser Gly Asp Val
435 440 445
Thr His Leu Leu Asn Val Ser Asn Gly Thr Val His Tyr Asp Val Ser
450 455 460
75 Thr Lys Lys Leu Thr Trp Thr Thr Gly Thr Ile Leu Ser Ser Ser Glu

436/ 490

465 470 475 480
Ala Thr Ile Thr Tyr Arg Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn
485 490 495
5 Asn Asp Ile Pro Val Asn Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly
500 505 510
Gly Phe Asp Thr Asn Thr Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn
515 520 525
10 Gly Glu Pro Asn Gln Gln Leu Ile Phe Pro Arg Pro Thr Val Lys Leu
530 535 540
Gly Tyr Gly Val Ile Lys Arg His Tyr Val Leu Val Asn Lys Asp Gly
545 550 555 560
Gln Pro Ile Gln Ala Asn Gly Thr Val Val Ser Ser Leu Ser Glu Ala
565 570 575
15 His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly Gly His
580 585 590
Ile Val Pro Lys Trp Ile Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln
595 600 605
Tyr Tyr Ser Val Pro Pro Thr Asn Thr Val Ile Thr Thr Ala Asp Gly
610 615 620
20 Lys Arg Tyr Arg Phe Val Glu Val Pro Gly Ser Thr Pro Asn Pro Gly
625 630 635 640
Gln Ile Gly Ile Ser Trp Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala
645 650 655
25 Tyr Lys Leu Leu Asn Tyr Trp Met Gly Gly Thr Thr Asp Gln Gln Ser
660 665 670
Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu Thr
675 680 685
Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala
690 695 700
30 Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn
705 710 715 720
Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Thr Thr Ser Ser Gln
725 730 735
35 Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly Thr
740 745 750
Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe
755 760 765
Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe Tyr
770 775 780
40 Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp
785 790 795 800
Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn Asp
805 810 815
45 Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn Gly
820 825 830
Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys
835 840 845
Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr Gly
850 855 860
50 Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu Asn
865 870 875 880
Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly
885 890 895
55 Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe Pro
900 905 910
Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp
915 920 925
Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly
930 935 940
60 Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro
945 950 955 960
Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn Gly
965 970 975
65 Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr
980 985 990
Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn
995 1000 1005
Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly Asn
1010 1015 1020
70 Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe
1025 1030 1035 1040
Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu
1045 1050 1055
75 Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln Val
1060 1065 1070

437/ 490

Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp
 1075 1080 1085
 Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe Ala
 1090 1095 1100
 5 Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His Arg
 1105 1110 1115 1120
 Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser
 1125 1130 1135
 10 Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp
 1140 1145 1150
 Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln
 1155 1160 1165
 Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys Leu
 1170 1175 1180
 15 Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys Val
 1185 1190 1195 1200
 Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr Asn
 1205 1210 1215
 20 Asp Val His Lys Val Leu Val Glu Tyr
 1220 1225

(2) INFORMATION FOR SEQ ID NO:486

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...425
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp Phe
 1 5 10 15
 45 Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu Gly
 20 25 30
 Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr His
 35 40 45
 Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr Arg
 50 55 60
 Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala Val
 65 70 75 80
 Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly Leu
 85 90 95
 55 Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly Leu
 100 105 110
 Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val Arg
 115 120 125
 Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala Gln
 130 135 140
 60 Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser Val
 145 150 155 160
 Phe Asn Glu Ser Met Lys Val Glu Val Val Val Leu Pro Val Phe Glu
 165 170 175
 65 Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe Ser
 180 185 190
 Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu Ala
 195 200 205
 Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg Trp
 210 215 220
 70 Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His Thr
 225 230 235 240
 Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr Glu
 245 250 255
 75 Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly Asp
 260 265 270

WO 99/29870

PCT/AU98/01023

438/ 490

Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala Phe
275 280 285
Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu Gly
290 295 300
5 Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro Gly
305 310 315 320
Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg Tyr
325 330 335
10 Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu Asn
340 345 350
Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe Thr
355 360 365
Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala Asp
370 375 380
15 Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp Phe
385 390 395 400
Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser Glu
405 410 415
20 Leu Trp Phe Lys Ala Arg Tyr Ser Phe
420 425

(2) INFORMATION FOR SEQ ID NO:487

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear
30 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
35 (A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...404
40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

Met Ser Ser Cys Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu
1 5 10 15
45 Gln Asn Ile Arg Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn
20 25 30
Leu Leu Asp Asn Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn
35 40 45
Asn Val Ile Asn Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu
50 55 60
Gln Thr Phe Val Phe Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr
65 70 75 80
Ile Leu Leu Thr Thr Val Leu Leu Leu Gly Glu Ile Leu Pro Lys
85 90 95
55 Val Tyr Ala Arg Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala
100 105 110
Ala Met Ser Val Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu
115 120 125
Val Lys Ser Thr Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Lys Tyr
130 135 140
60 Asp Met Ser Val Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr
145 150 155 160
Glu Gly Glu Pro Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe
165 170 175
65 Tyr Asn Lys Thr Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val
180 185 190
Asp Val Asp Leu Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val
195 200 205
Ser Ser Gly Tyr Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn
210 215 220
70 Ile Lys Gly Val Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys
225 230 235 240
Gly Asp Glu Phe Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val
245 250 255
75 Pro Glu Asn Lys Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn
260 265 270

WO 99/29870

PCT/AU98/01023

440/ 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

Met Lys Arg Ile Val Leu Ser Ser Phe Leu Phe Val Leu Ser Ile Leu
 1 5 10 15
 Ser Leu Met Ala Gln Asn Asn Thr Leu Asp Val His Ile Ser Gly Thr
 20 25 30
 Ile Lys Asp Ala Ser Ser Gly Glu Pro Val Pro Tyr Ala Thr Val Ser
 35 40 45
 Ile Arg Leu Thr Gly Ala Asp Thr Thr Gln Val Phe Arg Gln Val Thr
 50 55 60
 Asp Gly Asn Gly Tyr Phe Val Ile Gly Leu Pro Ala Ala Pro Ser Tyr
 65 70 75 80
 His Leu Thr Ala Ser Phe Val Gly Met Lys Thr His Thr Met Gln Ile
 85 90 95
 Ser Arg Gly Asn Gly Gln His Asp Ile Lys Ser Ile Asp Ile Ser Leu
 100 105 110
 Glu Ser Glu Asp Lys Gln Leu Ser Thr Val Thr Val Ser Ala Ala Arg
 115 120 125
 Pro Leu Val Lys Met Glu Ile Asp Arg Leu Ser Tyr Asn Met Lys Asp
 130 135 140
 Asp Pro Ala Ala Lys Thr Asn Asn Leu Leu Glu Met Leu Arg Asn Val
 145 150 155 160
 Pro Leu Val Thr Val Asp Gly Gln Gly Asn Ile Gln Val Lys Gly Ser
 165 170 175
 Ser Asn Phe Lys Ile His Leu Asn Gly Arg Pro Ser Thr Met Val Ser
 180 185 190
 Ser Asn Pro Lys Glu Val Phe Arg Ser Ile Pro Ala His Thr Ile Lys
 195 200 205
 Arg Val Glu Val Ile Thr Asp Pro Gly Val Lys Tyr Asp Ala Glu Gly
 210 215 220
 Thr Ser Ala Ile Leu Asp Ile Val Thr Glu Glu Gly Lys Lys Leu Glu
 225 230 235 240
 Gly Tyr Ser Gly Ser Ile Thr Ala Ser Val Ser Asn Asn Pro Thr Ala
 245 250 255
 Asn Gly Ser Ile Phe Leu Thr Ala Lys Ser Gly Lys Val Gly Leu Thr
 260 265 270
 Thr Asn Tyr Asn Tyr Tyr Gly Gly Lys Asn Lys Gly Ser Arg Tyr Phe
 275 280 285
 Thr Glu Arg Thr Thr Ser Met Leu Gln Thr Ile Glu Glu Gly Lys Gly
 290 295 300
 Gln Glu Thr Phe Gly Gly His Phe Gly Asn Ala Leu Leu Ser Phe Glu
 305 310 315 320
 Ile Asp Ser Leu Asn Leu Phe Thr Val Gly Gly Asn Val Arg Leu Trp
 325 330 335
 Glu Met Thr Thr Asp Arg Asn Ser Val Glu Lys Ser Phe Ala Gly Ser
 340 345 350
 Asn Leu Met Ser Tyr Ile Asp Arg Lys Leu Lys Thr Gln Met Asp Ala
 355 360 365
 Gly Ser Tyr Glu Leu Asn Ala Asp Tyr Gln His Ser Thr Arg Leu Pro
 370 375 380
 Gly Glu Leu Leu Thr Val Ser Tyr Arg Phe Thr His Asn Pro Asn Asn
 385 390 395 400
 Ser Glu Thr Phe Ile Asp Gln Trp Lys Arg Asp Pro Leu Asn Thr Ala
 405 410 415
 Asn Thr Ile Gln Tyr Ala Gly Gln His Ser Lys Ser Asp Ala Gly Met
 420 425 430
 Asp Glu His Thr Ala Gln Val Asp Tyr Thr Arg Pro Leu Gly Gln Ala
 435 440 445

WO 99/29870

PCT/AU98/01023

441/ 490

5 His Ser Leu Glu Ala Gly Leu Lys Tyr Ile Tyr Arg His Ala Thr Ser
450 455 460
Asp Pro Leu Tyr Glu Ile Arg Pro Ser Glu Asp Ala Pro Trp Gln Pro
465 470 475 480
Gly Ser Leu Tyr Ala Gln Asn Pro Ser Asn Gly Lys Phe Arg His Asp
485 490 495
Gln Tyr Ile Gly Ala Ala Tyr Ala Gly Tyr Asn Tyr Arg Lys Asp Gln
500 505 510
10 Tyr Ser Leu Gln Thr Gly Leu Arg Val Glu Ser Ser Arg Leu Lys Ala
515 520 525
Leu Phe Pro Glu Asn Ala Ala Ala Asp Phe Ser His Asn Ser Phe Asp
530 535 540
Trp Val Pro Gln Leu Thr Leu Gly Tyr Thr Pro Ser Pro Met Lys Gln
545 550 555 560
15 Leu Lys Leu Ala Tyr Asn Phe Arg Ile Gln Arg Pro Ala Ile Gly Gln
565 570 575
Leu Asn Pro Tyr Arg Leu Gln Thr Asn Asp Tyr Gln Val Gln Tyr Gly
580 585 590
20 Asn Pro Asp Leu Lys Ser Glu Lys Arg His His Val Gly Leu Ser Tyr
595 600 605
Asn Gln Tyr Gly Ala Lys Val Met Leu Thr Ala Ser Leu Asp Tyr Asp
610 615 620
Phe Cys Asn Asn Ala Ile Gln Asn Tyr Thr Phe Ser Asp Pro Ala Asn
625 630 635 640
25 Pro Asn Leu Phe His Gln Thr Tyr Gly Asn Ile Gly Arg Glu His Ser
645 650 655
Phe Ser Leu Asn Thr Tyr Ala Met Tyr Thr Pro Ala Val Trp Val Arg
660 665 670
30 Ile Met Leu Asn Gly Asn Ile Asp Arg Thr Phe Gln Lys Ser Glu Ala
675 680 685
Leu Gly Ile Asp Val Asn Ser Trp Ser Gly Met Val Tyr Ser Gly Leu
690 695 700
Met Phe Thr Leu Pro Lys Asp Trp Thr Val Asn Leu Phe Gly Gly Tyr
705 710 715 720
35 Tyr His Gly Gly Arg Ser Tyr Gln Thr Lys Tyr Asp Gly Asn Val Phe
725 730 735
Asn Asn Ile Gly Ile Ala Lys Gln Leu Phe Asp Lys Lys Leu Arg Val
740 745 750
40 Ser Leu Ser Ala Asn Asn Ile His Ala Lys Tyr Ser Thr Trp Lys Ser
755 760 765
Arg Thr Ile Gly Asn Gly Phe Thr Ile Tyr Ser Glu Asn Ala Gly Ile
770 775 780
Gln Arg Ser Val Ser Leu Ser Leu Thr Tyr Ser Phe Gly Lys Met Asn
785 790 795 800
45 Thr Gln Val Arg Lys Val Glu Arg Thr Ile Val Asn Asp Asp Leu Lys
805 810 815
Gln Thr Ser Ser Gln Gly Gln Gln Gly Gly Gly Gln Gly Asn Pro Thr
820 825 830
50 Gly Asn

(2) INFORMATION FOR SEQ ID NO:490

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
60 (iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
65 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...399
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met Leu Pro Ala
1 5 10 15
75 Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu Arg Leu Glu
20 25 30

443/490

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Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met Ser
65      70      75      80
Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln Arg
      85      90      95
5  Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser Asn
      100      105      110
Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val Ser
      115      120      125
10 Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr Asp
      130      135      140
Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr Met
145      150      155      160
Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro Glu
      165      170      175
15 Gln Gln Leu Gln Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe Ala
      180      185      190
Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr Pro
      195      200      205
20 Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala Leu
      210      215      220
His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg Asn
225      230      235      240
Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg Ile
      245      250      255
25 Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp Lys
      260      265      270
Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp Val
      275      280      285
30 Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp Gln
      290      295      300
Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro Ala
305      310      315      320
Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met Gly
      325      330      335
35 Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val Thr
      340      345      350
Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser Thr
      355      360      365
40 Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu
      370      375      380

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(2) INFORMATION FOR SEQ ID NO:492

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
- 55 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...222
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

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Met Lys His Leu Phe Lys Ser Thr Leu Val Leu Leu Cys Ala Leu Ser
1      5      10      15
Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn Asn Thr Glu Lys Ser
20      25      30
65 Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly Tyr Ile Ala Gly Ser
      35      40      45
Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala Asn Asp Arg Leu Leu
50      55      60
70 Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser Lys Lys Glu Asn Ala
      65      70      75      80
Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser Pro Gly Tyr Tyr Val
      85      90      95
75 Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr Ala Phe Tyr Val Val
      100      105      110

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WO 99/29870

PCT/AU98/01023

444/ 490

5 Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg Pro Ile Lys Asn Phe
115 120 125
Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala Trp Met Ser Arg His
130 135 140
10 Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp Asp Lys Gln Arg Lys
145 150 155 160
Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met His Leu Gln Unk His
165 170 175
10 Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Trp Asp Leu Thr Ser Cys
180 185 190
Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln Lys Asp Arg Thr Phe
195 200 205
15 Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly Leu Asn Leu
210 215 220

(2) INFORMATION FOR SEQ ID NO:493

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493

35 Met Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile
1 5 10 15
Leu Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Leu Asn
20 25 30
40 Val Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg
35 40 45
Ala Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr
50 55 60
45 Ser Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala
65 70 75 80
Gly Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp
85 90 95
Ile Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu
100 105 110
50 Asn Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu
115 120 125
Glu Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn
130 135 140
55 Glu Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe
145 150 155 160
Ser Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His
165 170 175
Asn Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala
180 185 190
60 Gly Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp
195 200 205
Ser Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp
210 215 220
65 Gly Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr
225 230 235 240
Gly Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu
245 250 255
Glu Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn
260 265 270
70 Asp Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser
275 280 285
Ser Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu
290 295 300
75 Lys Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser
305 310 315 320

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

446/ 490

Ile Met Leu Arg Ser Lys Glu Ser Phe Ile Thr Ser Phe Ile Ser Pro
 355 360 365
 Thr Val Val Gln Gly Val Asp Val Tyr Thr Leu Ala Gly Lys Ile Arg
 370 375 380
 5 Ile Glu Ser Glu Thr Pro Val Ser Glu Val Leu Leu Phe Asp Leu Ala
 385 390 395 400
 Gly Arg Met Val Leu Arg Gln Thr Ile Asp Asn Lys Ile Tyr Ser Asp
 405 410 415
 10 Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly Ile Tyr Val Val Ser Val
 420 425 430
 Arg Leu Ser Ser Gly Gln Val Phe Ser His Lys Val Gln Val
 435 440 445
 (2) INFORMATION FOR SEQ ID NO:495
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...308
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495
 Met Ile Ile Arg Cys Leu Ile Arg Arg Pro Arg Thr Val Leu Phe Gly
 1 5 10 15
 Leu Ile Phe Val Val Gly Leu Phe Ser Ala Met Ala Gln Glu Lys Lys
 20 25 30
 Asp Ser Leu Ser Thr Val Gln Pro Val Pro Asn Ser Ser Met Val Glu
 35 40 45
 40 Gln Thr Pro Leu Leu Ser Ile Asp His Pro Val Leu Pro Ala Ser Phe
 50 55 60
 Gln Asn Thr Arg Thr Leu Lys Arg Phe Arg Asp Lys His Leu Ser Asp
 65 70 75 80
 45 Ala Leu Leu Asn Gly Leu Lys Pro His Arg Ser Ser Leu Gln Leu Asn
 85 90 95
 Glu Glu Leu Asn Phe Ala Ala Glu Arg Arg Asp Phe Val Ser Pro Leu
 100 105 110
 Leu Gln Thr Arg His Ala Ala Gly Val Leu Ser Trp Arg Pro Thr Asp
 115 120 125
 50 Arg Met His Phe Tyr Thr Ser Gly Asn Ile Gly Leu Gly His Asp Leu
 130 135 140
 Leu Thr Gly Val Arg Lys Asp Phe Gly Trp Asn Ala Gly Ala Asp Phe
 145 150 155 160
 55 Leu Leu Ser Gln Asn Leu Thr Ala His Val Gln Gly Gly Trp Gln Gln
 165 170 175
 Asn Phe Gly Phe Ile Pro Met Thr Ala Val Asn Gly Gln Leu Arg Trp
 180 185 190
 Gln Ala Thr Glu Arg Leu Ser Phe Thr Thr Gly Ile Asp Tyr Arg Gln
 195 200 205
 60 Val Gln Trp Asn Ala Phe Asp Asn Arg Thr Phe Ser Leu Lys Gly Ser
 210 215 220
 Ala Arg Tyr Glu Val Met Asp Asn Val Phe Val Asn Gly Phe Gly Ser
 225 230 235 240
 Tyr Pro Leu Tyr Ser Ser Thr Arg Ser Gly Leu Asn Met Ala Val Pro
 245 250 255
 65 Met His Gly Phe Gly Pro Gln Tyr Gly Gly Ser Leu Glu Leu Lys Val
 260 265 270
 Ser Glu Arg Phe Gly Phe Ala Val Gly Met Glu Arg Glu Tyr Asn Ile
 275 280 285
 70 Trp Thr Arg Arg Trp Glu Thr His Tyr Phe Ala Tyr Pro Val Phe Tyr
 290 295 300
 Gly Asp Lys Lys
 305
 (2) INFORMATION FOR SEQ ID NO:496

447/ 490

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

Met	Lys	Thr	Asn	Arg	Arg	Tyr	Ala	Phe	Val	Leu	Pro	Leu	Leu	Leu	Leu
1			5						10					15	
Thr	Gly	Leu	Leu	Ala	Trp	Gly	Gln	Asp	Ser	Ser	His	Gly	Ser	Asn	Thr
			20				25						30		
Ala	Phe	Ala	Thr	Asp	Ser	Ser	Ser	Arg	Glu	Leu	Pro	Thr	Glu	Gln	Ser
		35					40					45			
Ala	Tyr	Arg	Ile	His	Ser	Ala	Tyr	Met	Val	Gly	Gly	Gly	Gly	Ser	Ile
	50				55					60					
Thr	Arg	Asp	Thr	Tyr	Leu	Ser	Pro	Leu	Arg	Tyr	Gly	Gly	Trp	Thr	Leu
	65				70				75					80	
Asn	Leu	Leu	Gly	Glu	Lys	Thr	Phe	Pro	Leu	Lys	Ala	Ser	Asp	Ser	Arg
			85					90					95		
Trp	Met	Ile	Arg	Thr	Gly	His	Glu	Leu	Asp	Phe	Ala	Leu	Met	Asp	Asn
			100				105						110		
Pro	Ala	Asn	Asn	Ala	His	Phe	Tyr	Ser	Leu	Leu	Tyr	Asn	Gly	Ser	Ala
		115					120					125			
Ala	Ala	Leu	Tyr	Arg	Leu	Gly	Ala	Lys	His	Leu	Arg	Ala	Ala	Trp	Met
	130					135						140			
Asp	Asn	Leu	Arg	Leu	Ala	Phe	Gly	Pro	Gly	Leu	Glu	Ile	Gly	Leu	Gly
	145				150					155				160	
Gly	Ile	Tyr	Ser	Thr	Arg	Asn	Gly	Asn	Asn	Pro	Ala	Thr	Leu	Lys	Leu
			165				170						175		
Tyr	Thr	Asn	Ala	Ile	Ala	Gln	Ala	Ser	Ile	Gly	Tyr	Tyr	Val	Pro	Ser
		180					185						190		
Glu	Thr	Phe	Pro	Leu	Tyr	Phe	Arg	Leu	Leu	Ser	Gln	Ile	Asn	Leu	Phe
	195						200					205			
Gly	Ile	Ala	Tyr	Gly	Asn	Gly	Phe	Gly	Glu	Ser	Tyr	Tyr	Glu	Asn	Phe
	210				215						220				
Leu	Leu	Asn	Asn	Gly	Ile	Ala	Gly	Ser	Leu	His	Phe	Thr	Tyr	Pro	Gly
	225				230					235				240	
Lys	Phe	Thr	Arg	Phe	Thr	Thr	Leu	Ile	Thr	Ala	Asp	Ile	Pro	Ile	Arg
			245						250				255		
Asn	Phe	Cys	Thr	Leu	Arg	Val	Gly	Tyr	Arg	Tyr	Ser	His	Leu	Gly	Ser
		260					265						270		
Ser	Leu	Asn	Ala	Leu	Asp	Thr	Arg	Ile	His	Ser	His	Thr	Ala	Phe	Ile
	275					280						285			
Gly	Phe	Val	Thr	Glu	Phe	Tyr	Arg	Phe	Arg	Gly	Arg	Lys	Ala	Met	Asn
	290					295					300				
Thr	Gly	Arg	Arg	Thr	Ser	Leu	Tyr	Tyr	His	Asp					
	305				310					315					

(2) INFORMATION FOR SEQ ID NO:497

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

WO 99/29870

PCT/AU98/01023

449/ 490

100 105 110
Ala Ala Arg Ser Tip Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu
115 120 125
5 Ile Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val
130 135 140
Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val
145 150 155 160
Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe
165 170 175
10 Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His
180 185 190
Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile
195 200 205
15 Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile
210 215 220
Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile
225 230 235 240
His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile
245 250 255
20 Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu
260 265 270
Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro
275 280 285
25 Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly
290 295 300
Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln
305 310 315 320
Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His
325 330 335
30 Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala
340 345 350
Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu
355 360 365
35 Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro
370 375 380
Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly
385 390 395 400
Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser
405 410 415
40 Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu
420 425 430
Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn
435 440 445
45 Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp
450 455 460
Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val
465 470 475 480
Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val
485 490 495
50 Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln
500 505 510
Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys
515 520 525
55 Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu
530 535 540
Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala
545 550 555 560
Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Asn Pro Ala Gln
565 570 575
60 Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu
580 585 590
Lys Glu Lys Leu Ser Glu Asn
595

65 (2) INFORMATION FOR SEQ ID NO:499

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

70 (ii) MOLECULE TYPE: protein

75 (iii) HYPOTHETICAL: YES

450/ 490

(v1) ORIGINAL SOURCE:
(A) ORGANISM: *Porphyromonas gingivalis*

5 (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

```

10 Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val
    1      5      10      15
    Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn
    20      25      30
15 Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln
    35      40      45
    Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala
    50      55      60
    Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile
    65      70      75      80
20 Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp
    85      90      95
    Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg
    100      105      110
25 Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys
    115      120      125
    Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys
    130      135      140
    Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly
    145      150      155      160
30 Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr
    165      170      175
    Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His
    180      185      190
35 Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile Val
    195      200      205
    Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp
    210      215      220
    Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp
    225      230      235      240
40 Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys
    245      250      255
    Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly
    260      265      270
45 Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu
    275      280      285
    Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val
    290      295      300
    Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu Lys
    305      310      315      320
50 Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val
    325      330      335
    Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val
    340      345      350
55 Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp
    355      360      365
    Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val
    370      375      380
    Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg
    385      390      395      400
60 Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val
    405      410      415
    Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile
    420      425      430
65 Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu
    435      440      445
    Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala
    450      455      460
    Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp
    465      470      475      480
70 Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln
    485      490      495
    Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys
    500      505      510
75 Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala
    515      520      525

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WO 99/29870

PCT/AU98/01023

451/ 490

Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys
530 535 540
Glu Lys Leu Ser Glu Asn
545 550

5

(2) INFORMATION FOR SEQ ID NO:500

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 458 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

20

(ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

25

Met Ile Val Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln
1 5 10 15
Ile Asp Val Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr
20 25 30
Met Glu Phe Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val
35 40 45
Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Lys Lys
50 55 60
Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val
65 70 75 80
Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp
85 90 95
Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro
100 105 110
Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp
115 120 125
Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met
130 135 140
Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys
145 150 155 160
Val Lys Gly Lys Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu
165 170 175
Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp
180 185 190
Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu
195 200 205
Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser
210 215 220
Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr
225 230 235 240
Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr
245 250 255
Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile
260 265 270
His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu
275 280 285
Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp
290 295 300
Lys Glu Asn Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn
305 310 315 320
Pro Trp Asp Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu
325 330 335
Gly Thr Val Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro
340 345 350
Tyr Gly Val Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp
355 360 365
Gly Ser Gln Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu
370 375 380
Phe Asn Lys Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe
385 390 395 400

WO 99/29870

PCT/AU98/01023

454/ 490

(A) NAME/KEY: misc_feature
(B) LOCATION 1...434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503

5 Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp Tyr Ala
1 5 10 15
Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala Gln Asn
20 25 30
10 Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly Arg Leu
35 40 45
Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu Gly Val
50 55 60
15 Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala Ser Tyr
65 70 75 80
Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala Ser Thr
85 90 95
Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg Lys Met
100 105 110
20 Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys Ser Ile
115 120 125
Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr Gln Phe
130 135 140
25 Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr Arg Lys
145 150 155
Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile Gly Ala
160 165 170 175
Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser Leu Phe
180 185 190
30 Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu Ala Pro
195 200 205
Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala Lys Phe
210 215 220
35 Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg Ser Leu
225 230 235
Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser Glu Leu
240 245 250 255
Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu Ser Glu
260 265 270
40 Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro His Thr
275 280 285
Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu Gly
290 295 300
45 Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr Lys Ser
305 310 315 320
Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly Glu Ile
325 330 335
Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg Tyr Arg
340 345 350
50 Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr Lys Gly
355 360 365
Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly Ile Gly
370 375 380
55 Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu Glu Tyr
385 390 395 400
Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala Leu Lys
405 410 415
Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys Leu Lys
420 425 430
60 Leu Asn

(2) INFORMATION FOR SEQ ID NO:504

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 926 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
70 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
75 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

456/ 490

Tyr Ser Asn Glu Phe Thr Gln Tyr Arg Ile Gly Leu Asn Leu Lys Lys
 545 550 555 560
 Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val Asp Pro Asn
 565 570 575
 5 Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln Asp Lys Leu
 580 585 590
 Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile Asn Tyr Lys
 595 600 605
 10 Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly Arg Thr Thr
 610 615 620
 Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile Thr Asn Pro
 625 630 635 640
 Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser Tyr Ser Asn
 645 650 655
 15 Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser Gln Arg Ala
 660 665 670
 Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp Ile Val Pro
 675 680 685
 20 Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr Arg Tyr Glu
 690 695 700
 Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr Leu Ser Leu
 705 710 715 720
 Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu Phe Asn Arg
 725 730 735
 25 Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn Lys Ala Leu
 740 745 750
 Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg Asn Asn Trp
 755 760 765
 30 Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met Ala Asn Asn
 770 775 780
 Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe Gly Gly Asn
 785 790 795 800
 Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile Asp Ser Asp
 805 810 815
 35 Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe Ser Leu Asp
 820 825 830
 Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu Arg Asp Lys
 835 840 845
 40 Ala Gly Thr Leu Arg Val Asn Asn Gly Tyr Asp Ile Leu Gly Gln Arg Ser
 850 855 860
 Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu Ser Met Ser
 865 870 875 880
 Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr Arg Phe Asn
 885 890 895
 45 Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg Gly Asn Met
 900 905 910
 Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro Ser
 915 920 925
 50 (2) INFORMATION FOR SEQ ID NO:505
 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (11) MOLECULE TYPE: protein
 (111) HYPOTHETICAL: YES
 (11) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 60 (12) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...400
 (121) SEQUENCE DESCRIPTION: SEQ ID NO:505
 70 Met Val Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val
 1 5 10 15
 Leu Leu Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu
 20 25 30
 75 Asp Asp Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val
 35 40 45

WO 99/29870

PCT/AU98/01023

457 / 490

5 Lys Asp Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr
50 55 60
Thr Val Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly
65 70 75
Gln Ser Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser
85 90 95
Thr Arg Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe
100 105 110
Tyr Lys Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val
115 120 125
10 Thr Asp Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp
130 135 140
Ala Ser Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe
145 150 155
15 Pro Tyr Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr
160 165 170 175
Trp Asn Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly
180 185 190
Tyr Tyr Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe
195 200 205
20 Tyr Asn Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp
210 215 220
Gly Ser Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr
225 230 235 240
25 His His Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala
245 250 255
Tyr Tyr Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly
260 265 270
30 Ala Lys Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser
275 280 285
Gln Lys Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu
290 295 300
Gln Asn Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn
305 310 315 320
35 Ile Glu Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val
325 330 335
Phe Gln Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile
340 345 350
40 Arg Ser Glu Arg Gln Gly Glu Asn Asp Arg Thr Phe Ser Thr Pro
355 360 365
Ser Arg Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser
370 375 380
Ser Gly Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
385 390 395 400

(2) INFORMATION FOR SEQ ID NO:506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

65 Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu
1 5 10 15
Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp
20 25 30
70 Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp
35 40 45
Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val
50 55 60
75 Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser
65 70 75 80

458/490

Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg
 85 90 95
 Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys
 100 105 110
 5 Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp
 115 120 125
 Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser
 130 135 140
 10 Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr
 145 150 155 160
 Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn
 165 170 175
 Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr
 180 185 190
 15 Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn
 195 200 205
 Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser
 210 215 220
 20 Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His
 225 230 235 240
 Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr
 245 250 255
 Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys
 260 265 270
 25 Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys
 275 280 285
 Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn
 290 295 300
 30 Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu
 305 310 315 320
 Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln
 325 330 335
 Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser
 340 345 350
 35 Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg
 355 360 365
 Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly
 370 375 380 385
 40 Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
 385 390 395

(2) INFORMATION FOR SEQ ID NO:507

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 581 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 55 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...581
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met Pro Val Ala Ser
 1 5 10 15
 Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser Lys Asp Asn Arg
 20 25 30
 65 Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg Asp Asp Ala Pro
 35 40 45
 Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile Gln Ser Asp Met
 50 55 60
 70 Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp Phe Gly Asn Ser
 65 70 75 80
 Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu Phe Gly Ala Arg
 85 90 95
 75 Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu Pro Glu Met Gly
 100 105 110

WO 99/29870

PCT/AU98/01023

459/ 490

Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr His Trp Ala Glu
 115 120 125
 Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser Gly Met Val Phe
 130 135 140
 5 Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn Ala Val Arg Gly
 145 150 155 160
 Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg Val Lys Gly Ile
 165 170 175
 10 Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly Lys Val Phe Asn
 180 185 190
 Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu Leu Asn Val Glu
 195 200 205
 Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His Leu Ala Ile Gly
 210 215 220
 15 Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp Ile Phe Val Gly
 225 230 235 240
 Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu Asn Val Pro Ile
 245 250 255
 20 Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu Ala Leu Tyr Ala
 260 265 270
 Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp Asn Asp Tyr Ile
 275 280 285
 Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser Tyr Ser Lys Lys
 290 295 300
 25 Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu Asn Phe Ala Phe
 305 310 315 320
 Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met Ile Asn Tyr Met
 325 330 335
 30 Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala Ala Ile Tyr Pro
 340 345 350
 Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln Gly Glu Leu Arg
 355 360 365
 Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg Tyr Gly Thr Gly
 370 375 380
 35 Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp Lys Lys Met Leu
 385 390 395 400
 Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly Tyr Thr Val Ser
 405 410 415
 40 Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile Asp Val Glu Ile
 420 425 430
 Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu Thr Tyr Leu Asn
 435 440 445
 Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala Gly Glu Lys Pro
 450 455 460
 45 Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly Lys Tyr Lys Leu
 465 470 475 480
 Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr Leu His Thr Lys
 485 490 495
 50 Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu Leu Ser Ile Leu
 500 505 510
 Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn Ile Gly Glu Thr
 515 520 525
 Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr His Gly Ala His
 530 535 540
 55 Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly Met Asn Cys Ser
 545 550 555 560
 Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly Phe Tyr Leu Ser
 565 570 575
 60 Tyr Ser Thr Asn Leu
 580

(2) INFORMATION FOR SEQ ID NO:500

- 65 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 70 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 75 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

WO 99/29870

PCT/AU98/01023

462/ 490

Leu Pro Gly Tyr Leu Tyr Thr Asp Thr Gly Phe Trp Asp Thr Phe Arg
355 360 365
Ala Leu Phe Pro Leu Leu Asn Leu Leu Tyr Pro Asp Glu Asn Ile Lys
370 375 380
5 Ile Gln Glu Gly Leu Leu Asn Val Tyr Arg Glu Ser Gly Phe Phe Pro
385 390 395 400
Glu Trp Ala Ser Pro Gly His Arg Asp Cys Met Ile Gly Asn Asn Ser
405 410 415
10 Ala Ser Val Leu Ala Asp Ala Tyr Leu Lys Gly Val Arg Val Glu Asp
420 425 430
Thr Arg Thr Leu Met Asn Gly Leu Leu His Ala Thr Lys Ala Val His
435 440 445
Pro Lys Ile Ser Ser Thr Gly Arg Lys Gly Trp Glu Trp Tyr Asn Ser
450 455 460
15 Leu Gly Tyr Val Pro Ala Asp Ala Gly Ile Asp Glu Ser Ala Ala Arg
465 470 475 480
Thr Leu Glu Tyr Ala Tyr Asn Asp Trp Cys Ile Leu Arg Leu Gly Arg
485 490 495
20 Thr Leu Gly Trp Asp Arg Ala Ala Leu Asp Thr Leu Ala His Arg Ser
500 505 510
Met Asn Tyr Arg His Leu Phe Asp Pro Glu Thr Lys Leu Met Arg Gly
515 520 525
Arg Asn Gln Asp Gly Ser Phe Arg Thr Pro Phe Ser Pro Phe Lys Trp
530 535 540
25 Gly Asp Val Phe Thr Glu Gly Asn Ala Trp His Tyr Thr Trp Ser Val
545 550 555 560
Phe His Asp Val Gln Gly Leu Ile Asp Leu Met Gly Gly Asp Arg Pro
565 570 575
30 Phe Val Ser Met Leu Asp Ser Val Phe Asn Thr Pro Pro Met Phe Asp
580 585 590
Glu Ser Tyr Tyr Gly Phe Val Ile His Glu Ile Arg Glu Met Gln Ile
595 600 605
Ala Asp Met Gly Asn Tyr Ala His Gly Asn Gln Pro Ile Gln His Met
610 615 620
35 Ile Tyr Leu Tyr Asn His Ala Gly His Pro Trp Lys Ala Gln Glu Arg
625 630 635 640
Leu Arg Glu Val Met Gly Arg Leu Tyr Arg Pro Thr Pro Asp Gly Tyr
645 650 655
40 Cys Gly Asp Glu Asp Asn Gly Gln Thr Ser Ala Trp Tyr Val Phe Ser
660 665 670
Ala Leu Gly Phe Tyr Pro Val Thr Pro Ala Thr Asp Gln Tyr Val Leu
675 680 685
Gly Ser Pro Ile Phe Ser Lys Val Ile Leu Ser Phe Pro Asp Gly His
690 695 700
45 Lys Thr Val Leu His Ala Pro Ala Asn Ser Ala Asp Thr Pro Tyr Ile
705 710 715 720
Arg Ser Ile Ser Val Glu Gly Lys Glu Trp Ser Cys Asn Tyr Leu Thr
725 730 735
50 His Glu Gln Leu Arg Ser Ser Ala Ser Ile Gln Trp Met Met Asp Thr
740 745 750
Lys Pro Asn Tyr Asn Arg Gly Met Lys Glu Ser Asp Arg Pro Tyr Ser
755 760 765
Phe Ser Thr Glu Gln Gln Arg Arg Ala Asn His Ser Asn
770 775 780

(2) INFORMATION FOR SEQ ID NO:511

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

463/ 490

```

Met Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser
1      5      10      15
Leu Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys
20      25      30
5 Ser Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg
35      40      45
Ala Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr
50      55      60
10 Pro Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe
65      70      75      80
Gly Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly
85      90      95
Tyr Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala
100      105      110
15 Asn Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln
115      120      125
Glu Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile
130      135      140
20 Asn Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg
145      150      155      160
Phe Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp
165      170      175
Ile Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly
180      185      190
25 Glu Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala
195      200      205
Ile Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met
210      215      220
30 Ile Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala
225      230      235      240
Ala Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu
245      250      255
Ala Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
260      265      270

```

(2) INFORMATION FOR SEQ ID NO:512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

```

Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
1      5      10      15
Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
20      25      30
60 Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
35      40      45
Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
50      55      60
65 Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
65      70      75      80
Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr
85      90      95
Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
100      105      110
70 Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
115      120      125
Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
130      135      140
75 Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
145      150      155      160

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WO 99/29870

PCT/AU98/01023

464/490

Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
 165 170 175
 Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
 180 185 190
 5 Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
 195 200 205
 Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
 210 215 220
 10 Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
 225 230 235 240
 Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala
 245 250 255
 Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
 260 265 270

(2) INFORMATION FOR SEQ ID NO:513

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513

35 Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu Ile Thr Ala
 1 5 10 15
 Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser Val Ser Phe
 20 25 30
 40 Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala Asp Ile Asp
 35 40 45
 Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro Ser Gly Asp
 50 55 60
 45 Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly Asp Ser Leu
 65 70 75 80
 Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr Ala Gln Met
 85 90 95
 Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn Leu Gln Gly
 100 105 110
 50 Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu Asn Thr Ile
 115 120 125
 Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn Thr Tyr Thr
 130 135 140
 55 Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe Ala Asn Ile
 145 150 155 160
 Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile Phe Lys Ile
 165 170 175
 Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln Leu Val His
 180 185 190
 60 Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile Gly Phe Phe
 195 200 205
 Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile Asp Asp Lys
 210 215 220
 65 Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala Tyr Ala Arg
 225 230 235 240
 Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala Pro Leu Leu
 245 250 255
 Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
 260 265

(2) INFORMATION FOR SEQ ID NO:514

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid

SUBSTITUTE SHEET (Rule 26) (RO/AU)

465 / 490

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

10 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

15

Met	Lys	Lys	Thr	Thr	Leu	Thr	Gly	Ser	Ile	Cys	Ala	Leu	Leu	Leu	Phe
1				5				10					15		
Leu	Gly	Leu	Ser	Ala	Asn	Ala	Gln	Ser	Lys	Leu	Lys	Ile	Lys	Ser	Ile
			20				25					30			
20	Glu	Ala	Ala	Thr	Thr	Phe	Ser	Ser	Ala	Thr	Ala	Gly	Asn	Gly	Phe
			35				40					45			
Gly	Asn	Ile	Phe	Gly	Met	Asp	Met	Ser	Ile	Arg	Met	Arg	Val	His	His
	50				55				60						
Ser	Ile	Leu	Pro	Glu	Gly	Leu	Asp	Phe	Ser	Val	Gly	Ile	His	Glu	Arg
	65			70					75				80		
Arg	Ala	His	Trp	Glu	Ala	Gly	Ser	Pro	Lys	Leu	Met	Tyr	Thr	Asn	
			85				90					95			
Val	Pro	Ser	Ile	Ile	Gly	Ile	Val	Glu	Lys	Val	Ile	Val	Phe	Glu	Asp
	100				105							110			
30	Ala	Glu	Asp	Phe	Phe	Asp	Lys	Lys	Ala	Leu	Gly	Arg	Phe	Leu	Ile
			115				120					125			
Leu	Gly	Ile	Ser	Tyr	Thr	Lys	His	Leu	Gly	Ala	Tyr	Trp	Gly	Trp	Thr
	130					135					140				
Asn	Asp	Ala	His	Ile	Leu	Phe	Ser	Pro	Ile	Pro	Lys	Ser	Lys	Val	His
	145					150				155				160	
Tyr	Asp	Thr	Tyr	Thr	Arg	Ala	Gly	Ser	Asp	Leu	Val	Leu	Gln	Ser	Glu
			165				170					175			
Asp	Val	Ala	Thr	Val	Ser	Asn	Gly	Phe	Ser	Pro	Gly	Ile	Gly	Leu	Lys
	180						185					190			
40	Ser	Ser	Ile	Trp	Trp	Lys	Met	Pro	Ile	Lys	Ser	Lys	Tyr	Asp	Phe
			195				200					205			
Leu	Gly	Phe	Ser	Leu	Gly	Tyr	Glu	Tyr	Leu	Asn	Leu	Leu	Tyr	Pro	Tyr
	210				215						220				
Arg	Asn	Phe	Lys	Leu	Asp	Gly	Asn	Lys	Pro	Leu	Ser	Ala	Leu	Ser	Pro
	225				230				235					240	
Arg	Met	Asn	His	Ile	Gly	His	Val	Gly	Phe	Asn	Phe	Thr	Val	Gly	Leu
			245					250						255	
Trp	Thr	Asn													

50 (2) INFORMATION FOR SEQ ID NO:515

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1266 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

60 (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

65 (ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

70

Met	Gly	Lys	Tyr	Lys	Arg	Ala	Lys	Tyr	Arg	Tyr	Trp	Leu	Phe	Pro	Phe
1				5				10				15			
Cys	Ser	Asp	Tyr	Tyr	Thr	Phe	Glu	Gly	Val	Thr	Phe	Leu	Cys	Ala	Ser
			20				25					30			
75	Asp	Asp	Met	Thr	Thr	Lys	Lys	Pro	Gln	Ala	Ile	Leu	Asp	Leu	Glu

WO 99/29870

PCT/AU98/01023

467/ 490

	Val	Gly	Gly	Asn	Pro	Asp	Gly	Lys	Asp	Thr	Pro	Gln	Thr	Thr	Asp	Asp	
				645						650					655		
	Thr	Ile	Ile	Ile	Gln	Thr	His	Ala	Asp	Glu	Thr	Gly	Ala	Lys	Gln	Gln	
				660						665					670		
5	Thr	Leu	Gly	Cys	Ala	Ala	Glu	Asn	Gly	Val	Leu	Glu	Glu	Ile	Tyr	Val	
				675				680						685			
	Ser	Leu	Glu	Pro	Lys	Ala	Asn	Ser	Ala	Val	His	Ala	Leu	Asn	Tyr	Leu	
				690			695					700					
10	Asn	Glu	Arg	Val	Arg	Glu	Val	Val	Ala	Ser	Arg	Ser	Lys	Ser	Ile	Gln	
				705		710				715					720		
	Ile	Thr	Glu	Lys	Asp	Lys	Gly	Leu	Tyr	Glu	Ala	Leu	Pro	Thr	Ile	Ala	
				725						730					735		
	Gly	Asp	Asn	Lys	His	Ile	Pro	Ile	Ser	Leu	Glu	Ala	Leu	Ala	Ala	Gln	
				740					745					750			
15	Leu	Asn	Lys	Gly	Arg	Ala	Glu	Asn	Asp	Leu	Tyr	Thr	Ile	Glu	Tyr	Leu	
				755					760					765			
	Gln	Thr	Glu	Leu	Asn	Gln	Leu	Ser	Leu	Arg	Gly	Glu	Val	Leu	Tyr	Tyr	
				770			775					780					
20	Arg	Glu	Asn	Glu	Lys	Leu	Asn	Asn	Tyr	Val	Trp	Leu	Asp	Pro	Ala	Ala	
				785		790				795					800		
	Phe	Val	Gln	Met	Ile	His	Gly	Glu	Ile	Leu	Gln	Lys	Asp	Asn	Ile	Asn	
				805					810					815			
	Arg	Gly	Thr	Val	Pro	Lys	Asp	Ile	Phe	Glu	Cys	Lys	Leu	His	Asn	Leu	
				820					825					830			
25	Ser	Ser	Gly	Ser	Ile	Phe	Glu	Glu	Asp	Gly	Gln	Asn	Gly	Asn	Met	Ile	
				835				840					845				
	Leu	Gln	Leu	Leu	Leu	Glu	Glu	Leu	Ile	Val	Tyr	Glu	Asp	Lys	Asp	Cys	
				850			855					860					
30	Tyr	Val	Ile	Pro	Gly	Tyr	Leu	Pro	Leu	His	Ser	Asp	Asp	Glu	Ala	Tyr	
				865		870				875				880			
	Lys	Trp	Leu	Thr	Leu	Gly	Phe	Glu	Arg	Pro	Asn	Phe	Val	Leu	Lys	Phe	
				885					890					895			
	Glu	Arg	Phe	Ile	Pro	Phe	Gly	Leu	Ile	Asn	Gln	Ile	Ile	Ala	Tyr	Tyr	
				900					905					910			
35	Gly	Arg	Glu	Gly	Ala	Leu	Lys	Arg	Tyr	Trp	Arg	Asp	Gln	Val	Ile		
				915				920				925					
	Phe	Thr	Ala	Gly	Arg	Glu	Met	Asp	Arg	Gln	Thr	Leu	Glu	Gln	Glu	Glu	
				930			935					940					
40	Glu	Lys	Glu	Gly	Leu	Pro	Lys	Thr	Asn	Ala	Glu	Asp	Tyr	Gln	Ile	Trp	
				945		950				955					960		
	Ile	Lys	Leu	Asp	Phe	Thr	Asp	Leu	Ala	Ile	Ser	Val	Phe	Ile	Lys	Glu	
				965				970						975			
	Gln	Arg	Lys	Thr	Ser	Ala	Lys	Asp	Met	Gln	Arg	Lys	Glu	Ala	Thr	Ile	
				980				985					990				
45	Leu	Ser	Asp	Met	Leu	Asp	Met	Tyr	Trp	Asn	Asn	Ile	Pro	Pro	Arg	Glu	
				995				1000					1005				
	Gln	Ile	Gly	Asp	Lys	Asp	Thr	Glu	Gln	Thr	Arg	Ser	Thr	Ile	Arg	Glu	
				1010			1015					1020					
50	Thr	Asn	Arg	Lys	Lys	Arg	Pro	Ile	Gln	Asp	Leu	Tyr	Leu	Ser	Cys	Ala	
				1025			1030				1035				1040		
	Gln	Ala	Asp	Lys	Asp	Leu	Thr	Glu	Ser	His	Tyr	Ile	His	Leu	Gly	Thr	
				1045					1050					1055			
	Leu	Asp	Asp	Glu	Ser	Lys	Thr	Thr	Ala	Arg	Ile	Ala	Ala	Tyr	Pro	Leu	
				1060				1065						1070			
55	Lys	Asn	Gly	Val	Ile	Asp	Lys	Glu	Arg	Val	Arg	Glu	Val	Ser	Thr	Arg	
				1075					1080					1085			
	Pro	Tyr	Lys	His	Leu	Ser	Val	Asn	Lys	Asn	Leu	Ala	Thr	Ala	Lys	Gln	
				1090			1095					1100					
60	Ile	Phe	Ile	Ser	Tyr	Ser	Lys	Glu	Asp	Gln	Thr	Glu	Leu	Glu	Thr	Cys	
				1105			1110				1115				1120		
	Leu	Gln	Phe	Phe	Lys	Pro	Leu	Glu	Lys	Asn	Gly	Gln	Ile	Glu	Ile	Tyr	
				1125					1130					1135			
	Tyr	Asp	Lys	Leu	Thr	Lys	Phe	Glu	Thr	Pro	Ile	His	Pro	Glu	Ile	Arg	
				1140					1145					1150			
65	Lys	Arg	Ile	Val	Glu	Ala	Asp	Cys	Ile	Ile	Ala	Leu	Ile	Ser	Gln	Arg	
				1155				1160						1165			
	Tyr	Leu	Ala	Thr	Asp	Tyr	Ile	Leu	Asp	His	Glu	Leu	Pro	Val	Phe	Arg	
				1170			1175					1180					
70	Glu	Tyr	Asn	Lys	Thr	Ile	Val	Pro	Ile	Leu	Ile	Lys	Pro	Cys	Thr	Phe	
				1185			1190				1195				1200		
	Glu	Asp	Asp	Glu	Phe	Leu	Arg	Glu	Lys	Tyr	Phe	Ala	Gln	Lys	Ala	Gln	
				1205					1210					1215			
	Ile	Ile	Asn	Leu	Gly	Lys	Glu	Gly	Lys	Thr	Ile	Lys	Ala	Tyr	Asp	Ser	
				1220					1225					1230			
75	Ile	Thr	Ala	Ser	Ala	His	Arg	Asp	Glu	Asn	Trp	Val	Ala	Val	Val	Arg	

WO 99/29870

PCT/AU98/01023

468/490

1235 1240 1245
Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr
1250 1255 1260
Asp Glu
1265

5

(2) INFORMATION FOR SEQ ID NO:516

10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1232 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

20

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1232

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys Ala Tyr
1 5 10 15
Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu Gly Ile Ser Trp Ser
20 25 30
Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val Glu Leu
35 40 45
Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile Asp Phe
50 55 60
Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser Lys Leu
65 70 75 80
Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser
85 90 95
Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser Leu Thr
100 105 110
Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu
115 120 125
Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Ser
130 135 140
Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu
145 150 155 160
Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser
165 170 175
Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly
180 185 190
Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln
195 200 205
Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu
210 215 220
Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu
225 230 235 240
Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser Lys Leu
245 250 255
Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu Arg Ser
260 265 270
Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr
275 280 285
Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu
290 295 300
Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Arg
305 310 315 320
Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu
325 330 335
Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser
340 345 350
Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly
355 360 365
Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln
370 375 380
Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr Arg Leu

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

469/490

		385				390				395						400	
		Ser	Leu	Arg	Arg	Asn	Gln	Ile	Ser	Lys	Leu	Glu	Gly	Leu	Asp	Arg	Leu
						405					410				415		
5		Lys	Val	Leu	Arg	Lys	Leu	Asp	Val	Ser	Gly	Asn	Asp	Ile	Gln	Ser	Ile
					420					425					430		
		Asp	Asp	Ile	Lys	Leu	Leu	Ala	Pro	Ile	Leu	Glu	Gln	Thr	Leu	Glu	Lys
				435					440					445			
		Leu	Arg	Ile	His	Asp	Asn	Pro	Phe	Val	Ala	Ser	Ser	Gly	Leu	Ile	Leu
10				450				455					460				
		Ser	Pro	Tyr	Asp	Asn	His	Leu	Pro	Glu	Ile	Lys	Ala	Leu	Leu	Glu	Lys
				465			470					475				480	
		Glu	Lys	Glu	Lys	Gln	Lys	Lys	Thr	Ser	Val	Glu	Tyr	His	Pro	Phe	Cys
					485						490				495		
15		Lys	Val	Met	Leu	Leu	Gly	Asn	His	Ser	Ser	Gly	Lys	Thr	Thr	Phe	Leu
					500					505					510		
		Ser	Gln	Tyr	Asp	Thr	Asn	Tyr	Thr	Tyr	Gln	Lys	Asn	Thr	His	Val	Leu
				515					520					525			
		Ser	Ile	His	Arg	Ser	Asn	Asn	Pro	Asn	Ala	Ile	Phe	Tyr	Asp	Phe	Gly
20				530				535					540				
		Gly	Gln	Asp	Tyr	Tyr	His	Gly	Ile	Tyr	Gln	Ala	Phe	Phe	Thr	Thr	Gln
				545			550					555				560	
		Ser	Leu	Tyr	Leu	Leu	Phe	Trp	Asp	Ala	Lys	Lys	Asp	Arg	Asn	Phe	Val
					565						570				575		
25		Ser	Val	Asp	Asp	Lys	Glu	Tyr	Gln	Thr	Leu	Asn	Phe	Asn	Arg	Pro	Tyr
				580						585					590		
		Trp	Leu	Gly	Gln	Ile	Ala	Tyr	Ala	Cys	Asn	Arg	Cys	Met	Ser	Val	Gly
				595					600					605			
		Gly	Asn	Pro	Asp	Gly	Lys	Asp	Thr	Pro	Gln	Thr	Thr	Asp	Asp	Thr	Ile
30				610				615					620				
		Ile	Ile	Gln	Thr	His	Ala	Asp	Glu	Thr	Gly	Ala	Lys	Gln	Gln	Thr	Leu
				625			630					635				640	
		Gly	Cys	Ala	Ala	Glu	Asn	Gly	Val	Leu	Glu	Glu	Ile	Tyr	Val	Ser	Leu
					645						650				655		
35		Glu	Pro	Lys	Ala	Asn	Ser	Ala	Val	His	Ala	Leu	Asn	Tyr	Leu	Asn	Glu
					660					665					670		
		Arg	Val	Arg	Glu	Val	Val	Ala	Ser	Arg	Ser	Lys	Ser	Ile	Gln	Ile	Thr
				675					680					685			
		Glu	Lys	Asp	Lys	Gly	Leu	Tyr	Glu	Ala	Leu	Pro	Thr	Ile	Ala	Gly	Asp
40				690				695					700				
		Asn	Lys	His	Ile	Pro	Ile	Ser	Leu	Glu	Ala	Leu	Ala	Ala	Gln	Leu	Asn
					710						715				720		
		Lys	Gly	Arg	Ala	Glu	Asn	Asp	Leu	Tyr	Thr	Ile	Glu	Tyr	Leu	Gln	Thr
					725						730				735		
45		Glu	Leu	Asn	Gln	Leu	Ser	Leu	Arg	Gly	Glu	Val	Leu	Tyr	Tyr	Arg	Glu
					740					745					750		
		Asn	Glu	Lys	Leu	Asn	Asn	Tyr	Val	Trp	Leu	Asp	Pro	Ala	Ala	Phe	Val
				755					760					765			
		Gln	Met	Ile	His	Gly	Glu	Ile	Leu	Gln	Lys	Asp	Asn	Ile	Asn	Arg	Gly
50				770				775					780				
		Thr	Val	Pro	Lys	Asp	Ile	Phe	Glu	Cys	Lys	Leu	His	Asn	Leu	Ser	Ser
						790					795				800		
		Gly	Ser	Ile	Phe	Glu	Glu	Asp	Gly	Gln	Asn	Gly	Asn	Met	Ile	Leu	Gln
					805						810				815		
55		Leu	Leu	Leu	Glu	Glu	Leu	Ile	Val	Tyr	Glu	Asp	Lys	Asp	Cys	Tyr	Val
					820					825					830		
		Ile	Pro	Gly	Tyr	Leu	Pro	Leu	His	Ser	Asp	Asp	Glu	Ala	Tyr	Lys	Trp
				835					840					845			
		Leu	Thr	Leu	Gly	Phe	Glu	Arg	Pro	Asn	Phe	Val	Leu	Lys	Phe	Glu	Arg
60				850				855					860				
		Phe	Ile	Pro	Phe	Gly	Leu	Ile	Asn	Gln	Ile	Ile	Ala	Tyr	Tyr	Gly	Arg
				865			870					875				880	
		Glu	Glu	Gly	Ala	Leu	Lys	Arg	Tyr	Trp	Arg	Asp	Gln	Val	Ile	Phe	Thr
					885						890				895		
65		Ala	Gly	Arg	Glu	Met	Asp	Arg	Gln	Thr	Leu	Glu	Gln	Glu	Glu	Glu	Lys
					900					905					910		
		Glu	Gly	Leu	Pro	Lys	Thr	Asn	Ala	Glu	Asp	Tyr	Gln	Ile	Trp	Ile	Lys
				915					920					925			
		Leu	Asp	Phe	Thr	Asp	Leu	Ala	Ile	Ser	Val	Phe	Ile	Lys	Glu	Gln	Arg
70				930				935					940				
		Lys	Thr	Ser	Ala	Lys	Asp	Met	Gln	Arg	Lys	Glu	Ala	Thr	Ile	Leu	Ser
						950						955				960	
		Asp	Met	Leu	Asp	Met	Tyr	Trp	Asn	Asn	Ile	Pro	Pro	Arg	Glu	Gln	Ile
					965						970				975		
75		Gly	Asp	Lys	Asp	Thr	Glu	Gln	Thr	Arg	Ser	Thr	Ile	Arg	Glu	Thr	Asn
					980					985					990		

WO 99/29870

PCT/AU98/01023

470/ 490

Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala Gln Ala
995 1000 1005
Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr Leu Asp
1010 1015 1020
5 Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu Lys Asn
1025 1030 1035 1040
Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg Pro Tyr
1045 1050 1055
Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln Ile Phe
1060 1065 1070
10 Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys Leu Gln
1075 1080 1085
Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr Tyr Asp
1090 1095 1100
15 Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg Lys Arg
1105 1110 1115 1120
Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg Tyr Leu
1125 1130 1135
20 Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg Glu Tyr
1140 1145 1150
Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe Glu Asp
1155 1160 1165
Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln Ile Ile
1170 1175 1180
25 Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser Ile Thr
1185 1190 1195 1200
Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg Glu Phe
1205 1210 1215
30 Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr Asp Glu
1220 1225 1230

(2) INFORMATION FOR SEQ ID NO:517

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 45 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1175
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

Met Thr Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser
1 5 10 15
55 Tyr Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu
20 25 30
Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu
35 40 45
Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile
50 55 60
60 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr
65 70 75 80
Leu Leu Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr
85 90 95
65 Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu
100 105 110
Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn
115 120 125
Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys
130 135 140
70 Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg
145 150 155 160
Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys
165 170 175
75 Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser
180 185 190

471/ 490

Gly Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu
 195 200 205
 Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu
 210 215 220
 5 Glu Arg Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile
 225 230 235 240
 Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr
 245 250 255
 10 Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr
 260 265 270
 Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu
 275 280 285
 Gly Leu Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn
 290 295 300
 15 Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu
 305 310 315 320
 Leu Tyr Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly
 325 330 335
 20 Leu Ala Ser Leu Thr Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys
 340 345 350
 Leu Glu Gly Leu Asp Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser
 355 360 365
 Gly Asn Asp Ile Gln Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile
 370 375 380
 25 Leu Glu Gln Thr Leu Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val
 385 390 395 400
 Ala Ser Ser Gly Leu Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu
 405 410 415
 30 Ile Lys Ala Leu Leu Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser
 420 425 430
 Val Glu Tyr His Pro Phe Cys Lys Val Met Leu Leu Gly Asn His Ser
 435 440 445
 Ser Gly Lys Thr Thr Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr
 450 455 460
 35 Gln Lys Asn Thr His Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn
 465 470 475 480
 Ala Ile Phe Tyr Asp Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr
 485 490 495
 40 Gln Ala Phe Phe Thr Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala
 500 505 510
 Lys Lys Asp Arg Asn Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr
 515 520 525
 Leu Asn Phe Asn Arg Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys
 530 535 540
 45 Asn Arg Cys Met Ser Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro
 545 550 555 560
 Gln Thr Thr Asp Asp Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr
 565 570 575
 50 Gly Ala Lys Gln Gln Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu
 580 585 590
 Glu Glu Ile Tyr Val Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His
 595 600 605
 Ala Leu Asn Tyr Leu Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg
 610 615 620
 55 Ser Lys Ser Ile Gln Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala
 625 630 635 640
 Leu Pro Thr Ile Ala Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu
 645 650 655
 60 Ala Leu Ala Ala Gln Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr
 660 665 670
 Thr Ile Glu Tyr Leu Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly
 675 680 685
 Glu Val Leu Tyr Tyr Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp
 690 695 700
 65 Leu Asp Pro Ala Ala Phe Val Gln Met Ile His Gly Glu Ile Leu Gln
 705 710 715 720
 Lys Asp Asn Ile Asn Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys
 725 730 735
 70 Lys Leu His Asn Leu Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln
 740 745 750
 Asn Gly Asn Met Ile Leu Gln Leu Leu Leu Glu Glu Leu Ile Val Tyr
 755 760 765
 Glu Asp Lys Asp Cys Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser
 770 775 780
 75 Asp Asp Glu Ala Tyr Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn

WO 99/29870

PCT/AU98/01023

473/ 490

5 Val Ser 35 Thr Glu Val Trp Gly 40 Met Thr His Asp Ala 45 Asn Gly Leu Pro
50 Phe Glu Ile Pro Ile Ser 55 Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile
65 Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp
85 Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe
100 Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg
115 Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro
130 Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile
145 Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr
165 Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe
180 Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr
195 Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr
210 Val Ser Gln Gln Lys 215 220 225

(2) INFORMATION FOR SEQ ID NO:519

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(R) TYPE: amino acid
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
40 (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(D) LOCATION 1...228
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser Ser
1 5 10 15
50 Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr Phe
20 25 30
Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro Val
35 40 45
Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro Phe
50 55 60
55 Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile Ala
65 70 75 80
Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp Cys
85 90 95
60 Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe Trp
100 105 110
Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg Ile
115 120 125
Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro Lys
130 135 140
65 Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile Arg
145 150 155 160
Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr Phe
165 170 175
70 Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe Leu
180 185 190
Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr Ala
195 200 205
Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr Val
210 215 220
75 Ser Gln Gln Lys

WO 99/29870

PCT/AU98/01023

474/ 490

225

(2) INFORMATION FOR SEQ ID NO:520

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...540

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

Met Lys Thr Lys Val Leu Arg Lys Phe Val Val Ala Ala Phe Ala Val
 1 5 10 15
 25 Ala Thr Leu Cys Pro Leu Ala Gln Ala Gln Thr Met Gly Gly Asp Asp
 20 25 30
 Val Lys Val Val Gln Tyr Asn Gln Glu Lys Leu Val Gln Thr Arg Met
 35 40 45
 30 Ser Val Ala Asp Asn Gly Trp Ile Tyr Val Met Thr His Ser Gly Tyr
 50 55 60
 Asp Thr Gly Asn Ser Asn Val Lys Ile Phe Arg Ser Lys Asp Gln Gly
 65 70 75 80
 Ala Thr Tyr Gln Lys Leu Arg Asp Trp Asp Pro Ser Asp Asp Tyr Gln
 85 90 95
 35 Phe Gln Asp Phe Asp Ile Val Val Thr Gly Lys Asn Glu Ser Asp Ile
 100 105 110
 Lys Ile Trp Ser Val Glu Leu Met Asn Lys Pro Gly Gly Tyr Lys Ser
 115 120 125
 40 Arg Val Ala Val Phe Ser Arg Asp Ala Asn Ala Gln Asn Ala Lys Leu
 130 135 140
 Val Tyr Lys Glu Asp Phe Ser Asn Val Gln Leu Tyr Asp Val Asp Ile
 145 150 155 160
 Ala Ser Asn Tyr Arg Ser Pro Ser Ser Leu Asn Asn Gly Gly Asn Pro
 165 170 175
 45 Phe Ala Leu Ala Phe Ala Tyr Thr Gly Phe Asn Asn Thr His Lys Ile
 180 185 190
 Ser Phe Val Asp Tyr Val Phe Ser Leu Asn Gly Gly Gln Asn Phe Asn
 195 200 205
 50 Lys Asn Leu Leu Phe Ser Gln Asp Gly Glu Lys Lys Ile Asp Lys Val
 210 215 220
 Asp Leu Ser Leu Gly Ser Thr Ser Glu Ser Met Gly His Asn Ala Trp
 225 230 235 240
 Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Gln Gly Gly Lys Ser
 245 250 255
 55 Asp Ile Gly Phe Leu Ser Asn Phe Val Asp Asn Asp Pro Glu Phe Gln
 260 265 270
 Trp Ser Gly Pro Ile Lys Val Ser Glu Ser Asp Met Ser Phe Ser Pro
 275 280 285
 60 Lys Ile Gln Met Leu Leu Asp Glu Asp Asn Asn Thr Ile Asn Gly Glu
 290 295 300
 Ser Cys His Asn Phe Met Ile Thr Tyr Ser Asp Tyr Asp Ser Glu Tyr
 305 310 315 320
 Ser Asp Trp Asp Ile Arg Tyr Val Tyr Pro Lys Lys Ser Phe Lys Tyr
 325 330 335
 65 Glu Lys Gly Lys Thr Pro Thr Met Asp Asp Leu Val Glu Ala Phe Leu
 340 345 350
 Thr Ala Ser Tyr Gln Ser Glu Thr Asn Ser Gly Leu Gly Tyr Asp Lys
 355 360 365
 70 Asn Ala Asn His Tyr Leu Ile Thr Tyr Ala Lys Lys Glu Glu Asn Gly
 370 375 380
 Thr Asn Thr Leu Lys Tyr Arg Trp Ala Asn Tyr Asp Lys Ile His Asn
 385 390 395 400
 Lys Asp Leu Trp Ser Asp Thr Phe Thr Tyr Thr Ser Ser Ala Asn Ala
 405 410 415
 75 Leu Tyr Thr Pro Gln Val Asp Ile Asn Pro Thr Lys Gly Leu Val Cys

WO 99/29870

PCT/AU98/01023

476/ 490

305 310 315 320
Ile Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val
325 330 335
5 Glu Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala
340 345 350
Leu Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly
355 360 365
Glu Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp
370 375 380
10 Arg Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro
385 390 395 400
Leu Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr
405 410 415
15 Leu Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu
420 425 430
Tyr Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val
435 440 445
Ile Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr
450 455 460
20 Ala Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His
465 470 475 480
Pro Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro
485 490 495
25 Leu Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr
500 505 510
Leu Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys
515 520 525
Glu Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr
530 535 540
30 Tyr Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser
545 550 555
Phe Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn
565 570 575
35 Pro Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro
580 585 590
His Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe
595 600 605
Ser Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr
610 615 620
40 Asn Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys
625 630 635
Glu Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His
645 650 655
45 Phe Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr
660 665 670
Met Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys
675 680 685
Pro Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val
690 695 700
50 Arg Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile
705 710 715 720
Thr Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr
725 730 735
Val Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser
740 745 750
55 His Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn
755 760 765
Arg Pro Arg
770

(2) INFORMATION FOR SEQ ID NO:522

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 776 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

SUBSTITUTE SHEET (Rule 26) (RO/AU)

WO 99/29870

PCT/AU98/01023

477/ 490

(A) NAME/KEY: misc feature
(B) LOCATION 1...776

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:522

5 Met Cys Lys Ile Arg Phe Ser Leu Leu Gln Ala Leu Val Val Cys Leu
1 5 10 15
Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln Glu Glu Gly Ile Trp Asn
20 25 30
10 Thr Leu Leu Ala Ile His Lys Thr Glu Lys Ala Val Glu Thr Pro Lys
35 40 45
Lys Val Phe Ala Val Ala Asn Gly Val Leu Tyr Ser Val Gly Lys Glu
50 55 60
15 Ala Pro His Glu Ala Lys Ile Phe Asp Arg Ile Ser Gly Leu Ser Asp
65 70 75 80
Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu Gln Leu Lys Ser Leu Val
85 90 95
Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile Leu Asp Glu Ala Gly Arg
100 105 110
20 Val Thr Asn Val Pro Ala Leu Lys Asp Asn Ile Asp Leu Ile Asp Lys
115 120 125
Thr Leu Asn Arg Leu Leu Ile Val Gly Asn Arg Ala Tyr Leu Ala Gly
130 135 140
25 Gly Phe Gly Leu Ser Val Leu Asp Val Ala Glu Ala Arg Ile Pro Ala
145 150 155 160
Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp Val Ala Lys Leu Asp Asn
165 170 175
Asp Arg Leu Leu Met Leu Lys Glu Gly Gln Leu Phe Ile Gly Lys Glu
180 185 190
30 Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp Thr Ala Leu Ser Leu Asn
195 200 205
Leu Pro Met Gly Ser Val Thr Gly Leu Gly Ile Val Gly Glu Asp Ile
210 215 220
35 Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr Val Ala Ala Asn Gln Ser
225 230 235 240
Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser Ala Asp Ser Arg Leu Tyr
245 250 255
Val Thr Asp Arg Gly Leu Phe Ile Cys Ala Glu Asn Arg Ile Tyr Phe
260 265 270
40 Ile Glu Lys Gly Arg Lys Thr Thr Thr Phe Pro Ile Ala Asp Val Leu
275 280 285
Gly Val Gly Ala Met Asn Glu Ser Asn Thr Ala Tyr Ile Ala Leu Gly
290 295 300
45 Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala Glu Gly Ser Thr Ala Glu
305 310 315 320
Ala Met Pro Val Ala Phe Asp Gly Pro Gly Asp Asn Asp Phe Tyr Glu
325 330 335
Met Arg Phe Ser His Gly Arg Leu Tyr Ala Ala Ser Gly Leu Trp Gly
340 345 350
50 Thr Asn Leu Met Gly His Ala Gly Met Val Lys Leu Tyr Asp Gly Asn
355 360 365
Arg Trp Thr Asn Phe Asp Lys Lys Thr Val Gln Glu Gln Leu Gly Gly
370 375 380
Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile Ala Val Ser Asn Gly Asp
385 390 395 400
55 Pro Asp His Phe Phe Val Gly Thr Trp Gly Asn Gly Leu Phe Glu Phe
405 410 415
Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser Gly Asn Glu Thr Ala Ile
420 425 430
60 Ala Glu Cys Asn Pro Gly Asp Ala Arg Val Lys Ala Ile Ala Phe Asp
435 440 445
Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly Ala Val Gly Lys Asn Ile
450 455 460
65 Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp His Ser Phe Ser Tyr Pro
465 470 475 480
Asp Val Ala Asn Leu Ala Ser Phe Gly Asn Met Ile Ile Leu Pro Asn
485 490 495
Gly Asp Lys Trp Val Asn Ile Leu His Arg Ser Gly Gly Ser Thr Arg
500 505 510
70 Lys Gly Val Leu Ile Phe Asn Asp Arg Gly Thr Pro Glu Thr Thr Ser
515 520 525
Asp Asp Ser His Leu Tyr Val Glu Gln Phe Val Asn Arg Leu Gly Ala
530 535 540
75 Ala Ile Gly His Lys Thr Ile Tyr Ala Met Ala Val Asp His Asn Gly
545 550 555 560

478/ 490

Ser Val Trp Met Gly Ser Asp Ile Gly Ile Phe Gly Val Tyr Asn Ala
 565 570 575
 Ala Gly Val Leu Ser Ser Thr Ser Thr Pro Ile Ala Val Arg Pro Val
 580 585 590
 5 Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val Leu Asp Lys Val Thr Val
 595 600 605
 Thr Asp Ile Val Val Asp Lys Leu Asn His Lys Trp Val Ala Thr Gln
 610 615 620
 10 Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp Cys Ser Lys Ile Leu Ala
 625 630 635 640
 Gln Phe Thr Val Glu Asn Ser Pro Leu Leu Ser Asn Asn Ile Leu Ser
 645 650 655
 Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu Tyr Ile Gly Thr Ala Asp
 660 665 670
 15 Gly Leu Met Thr Phe Gln Thr Gly Thr Gly Ser Gly Ser Ala Ser Glu
 675 680 685
 Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro Leu Arg Pro Glu Tyr Pro
 690 695 700
 20 Asp Gly Val Thr Ile Ala Gly Leu Gln Ala Gly Cys Ser Val Lys Ile
 705 710 715 720
 Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln Thr Glu Ser Val Thr Thr
 725 730 735
 Glu Val Lys Trp Asn Ala Arg Gly Ala Asp Gly Asn Arg Val Ala Ser
 740 745 750
 25 Gly Val Tyr Ala Val Ala Val Tyr Asp Pro Val Ser Lys Lys Ser Lys
 755 760 765
 Leu Ile Arg Phe Ala Val Ile Arg
 770 775
 30 (2) INFORMATION FOR SEQ ID NO:523
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1158 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35
 (ii) MOLECULE TYPE: protein
 40 (iii) HYPOTHETICAL: YES
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 45 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...1158
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:523
 50 Met Lys Arg Ile Leu Pro Ile Val Ala Phe Leu Ser Leu Phe Leu Ala
 1 5 10 15
 Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly Lys Thr Ala Asp
 20 25 30
 55 Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile Arg Val Asp Ala
 35 40 45
 Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg Ala Asn Gly Phe
 50 55 60
 Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly Gly Gly Val Leu
 65 70 75 80
 60 Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu Pro Pro Val Pro
 85 90 95
 Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala Val Gly Pro Val
 100 105 110
 65 Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu His Thr Val Asn
 115 120 125
 Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp Ala Ala Gly Ala
 130 135 140
 Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala Ser Ala Glu Ala
 145 150 155 160
 70 Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu Gln Glu Leu Tyr
 165 170 175
 Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu Ser Phe Ser Ala
 180 185 190
 75 Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly Asn Thr Arg Ser
 195 200 205

WO 99/29870

PCT/AU98/01023

479/ 490

	Ser	Gly	Glu	Leu	Gly	Thr	Val	Phe	Ser	Tyr	Ile	Ala	Lys	Ala	Arg	Ser	
	210						215					220					
	Ala	Gly	Gly	Gly	Arg	Glu	Met	Ser	Leu	Ser	Ala	Asn	Gly	Ile	Leu	Ile	
	225					230					235					240	
5	Phe	Ser	Asp	Pro	Phe	Ser	Met	Thr	Ser	Asn	Glu	Val	Ser	Asn	Ser	Tyr	
					245					250					255		
	Leu	Ala	Gly	Lys	Lys	Arg	Arg	Leu	Tyr	His	Ser	Thr	Pro	Met	Asn	Ser	
				260					265						270		
10	Leu	Val	Asn	Glu	Leu	Arg	Leu	Asp	Ala	Asn	Tyr	Ser	Met	Thr	Gly	Asp	
		275						280						285			
	Ala	Val	Asn	Leu	Asp	Phe	Ile	Glu	Val	Ala	Thr	Gln	Asn	Asp	Leu	Arg	
		290					295					300					
	Tyr	Asp	Gly	Ala	Pro	Met	His	Ile	Arg	Arg	Phe	Ser	Asn	Leu	Pro	Val	
		305				310					315					320	
15	Leu	Gly	Gly	Glu	Ser	Cys	Arg	Phe	Val	Ile	Ser	Glu	Val	Pro	Glu	Ser	
				325						330					335		
	Leu	Val	Val	Leu	Gln	Ala	Asn	Ser	Ser	Leu	Thr	Ala	Ser	Leu	Val	Pro	
				340					345					350			
20	Val	Lys	Thr	Val	Gly	Asp	Lys	Thr	Ile	Glu	Phe	Val	Ala	Pro	Pro	Lys	
		355						360					365				
	Gly	Gln	Asp	Arg	Arg	Thr	Ile	Asn	Thr	Phe	Tyr	Ala	Val	Asp	Leu	Ser	
		370					375					380					
	Gln	Ala	Ser	Ala	Pro	Glu	Ile	Leu	Gly	Ala	Val	Pro	Asn	Gln	Asn	Leu	
		385				390					395					400	
25	His	Gly	Glu	Glu	Ile	Pro	Asp	Leu	Ile	Ile	Val	Ser	Thr	Gln	Ala	Leu	
				405					410						415		
	Leu	Leu	Glu	Ala	Asp	Arg	Leu	Ala	Thr	Tyr	Arg	Arg	Glu	Lys	Asn	Gly	
			420					425						430			
30	Leu	Lys	Val	Leu	Val	Val	Leu	Gln	Glu	Gln	Val	Phe	Asn	Glu	Phe	Ser	
		435					440					445					
	Gly	Gly	Thr	Pro	Asp	Ala	Thr	Ala	Tyr	Arg	Leu	Phe	Ala	Lys	Met	Phe	
		450					455				460						
	Tyr	Asp	Arg	Trp	Lys	Ala	Asn	Ala	Pro	Val	Gly	Glu	Thr	Phe	Pro	Met	
		465				470				475						480	
35	Gln	Met	Leu	Leu	Phe	Gly	Asp	Gly	Ala	His	Asp	Asn	Arg	Lys	Val	Ser	
				485					490						495		
	Val	Ala	Trp	Gln	Lys	Pro	Tyr	Leu	Gln	Gln	Thr	Glu	Phe	Leu	Leu	Thr	
				500					505					510			
40	Phe	Gln	Ala	Val	Asn	Ser	Thr	Asn	Val	Asn	Ser	Tyr	Val	Thr	Asp	Asp	
		515					520					525					
	Tyr	Phe	Gly	Leu	Leu	Asp	Asp	Gln	Pro	Ala	Ser	Val	Asn	Ile	Gly	Trp	
		530				535					540						
	Arg	Asn	Tyr	Asn	Met	Ala	Val	Gly	Arg	Phe	Pro	Val	Arg	Thr	Pro	Ala	
		545			550					555						560	
45	Glu	Ala	Arg	Ile	Ala	Val	Asp	Lys	Thr	Ile	Arg	Tyr	Glu	Glu	Asp	Arg	
				565						570					575		
	Glu	Ser	Gly	Ala	Trp	Arg	Ile	Arg	Ala	Cys	Phe	Ala	Ala	Asp	Asn	Gly	
		580						585					590				
50	Asp	Lys	His	Ala	Thr	Glu	Thr	Ser	Arg	Leu	Ile	Asp	Thr	Val	Lys	Arg	
		595						600					605				
	Tyr	Ala	Pro	Ala	Ile	Met	Pro	Val	Arg	Ala	Phe	Gln	Asp	Val	Tyr	Pro	
		610				615						620					
	His	Val	Ile	Glu	Asn	Gly	Leu	His	Ser	Ile	Pro	Gly	Ala	Lys	Lys	Lys	
		625			630					635						640	
55	Met	Leu	Glu	Thr	Leu	Gln	Ser	Gly	Ile	Ile	Leu	Leu	Asn	Tyr	Ala	Gly	
				645					650						655		
	His	Gly	Gly	Pro	Ala	Gly	Trp	Ser	Asp	Glu	His	Leu	Leu	Thr	Leu	Asn	
		660						665					670				
60	Asp	Ile	His	Lys	Phe	Asn	Tyr	Lys	His	Met	Pro	Ile	Trp	Ile	Thr	Ala	
		675					680					685					
	Thr	Cys	Asp	Phe	Ala	Asn	Tyr	Asp	Ser	Gln	Thr	Thr	Ser	Ala	Gly	Glu	
		690				695					700						
	Glu	Val	Phe	Leu	His	Glu	Lys	Ser	Gly	Thr	Pro	Ile	Met	Phe	Ser	Thr	
		705				710				715						720	
65	Thr	Arg	Val	Val	Tyr	Asn	Thr	Gln	Asn	Glu	Lys	Ile	Asn	Gly	Phe	Met	
				725					730						735		
	Leu	Arg	Arg	Met	Phe	Glu	Lys	Ala	Lys	Asp	Gly	Arg	Tyr	Arg	Thr	Met	
			740					745					750				
70	Gly	Glu	Ile	Ile	Arg	Ser	Ala	Lys	Gln	Gly	Met	Leu	Ser	Thr	Val	Phe	
		755					760					765					
	Pro	Asp	Ser	Ile	Asn	Gln	Leu	Ser	Phe	Phe	Leu	Met	Gly	Asp	Pro	Ser	
		770				775					780						
	Val	Arg	Met	Asn	Leu	Pro	Thr	His	Lys	Val	Gln	Leu	Thr	Ala	Ile	Asn	
		785				790				795						800	
75	Gly	Gln	Asp	Pro	Glu	Gly	Gln	Tyr	Gly	Thr	Ile	Met	Leu	Lys	Ser	Leu	

WO 99/29870

PCT/AU98/01023

481/490

	65					70					75					80
	Ser	Gln	Tyr	Thr	Asp	Ala	Met	Leu	Tyr	His	Gln	Lys	Gly	Leu	Asn	Ala
					85					90					95	
5	Ala	Leu	Asn	Leu	Arg	Asp	Thr	Ile	Val	Ala	Ala	Gln	Ala	Trp	Asn	His
				100					105						110	
	Leu	Gly	Thr	Asp	Ser	Arg	Arg	Ile	Gly	Ala	Leu	Ala	Glu	Ala	Ser	Asp
			115					120					125			
	Tyr	His	Tyr	Lys	Ala	Leu	Ser	Leu	Ile	Glu	Ser	Phe	Ser	Gly	Asn	Gln
			130				135					140				
10	Asn	Arg	Pro	Ala	Ile	Lys	Ala	Arg	Ser	Ala	Ala	Leu	Asn	Gly	Ile	Gly
					145		150				155				160	
	Asn	Ile	Asn	Leu	Glu	Leu	Gly	Tyr	His	Asp	Glu	Ala	Glu	Lys	Asn	Phe
					165					170				175		
15	Leu	Lys	Ala	Leu	Gln	Gly	Glu	Lys	Glu	Leu	Asp	Ser	Pro	Leu	Gly	Gln
				180					185					190		
	Ala	Ile	Asn	Tyr	Ala	Asn	Leu	Gly	Arg	Ile	Tyr	Arg	Gln	Arg	Lys	Glu
			195					200					205			
	Tyr	Asp	Lys	Ala	Arg	Thr	Tyr	Phe	Leu	Leu	Ser	Leu	Glu	Gln	Asn	Asn
			210				215					220				
20	Met	Ala	Glu	Asn	Leu	Met	Gly	Ile	Gly	Leu	Cys	Ser	Ile	Asn	Leu	Gly
					225		230				235					240
	Glu	Val	Asp	Glu	Glu	Lys	Gly	Asp	Tyr	Gln	Lys	Ala	Leu	Gln	Glu	Tyr
					245				250					255		
25	Ala	Thr	Ala	Tyr	Lys	Leu	Met	Glu	Gln	Leu	Ser	Asp	Arg	Trp	His	Trp
				260					265					270		
	Leu	Asn	Ser	Cys	Ile	Pro	Met	Ala	Arg	Ile	Asn	Leu	Lys	Gln	Gly	Asn
				275				280					285			
	Glu	Arg	Leu	Tyr	Gln	His	Phe	Ile	Ser	Leu	Ala	Glu	Gly	Thr	Ala	Lys
			290				295					300				
30	Glu	Ile	Asn	Ser	Thr	Ser	His	Leu	Ile	Glu	Ile	Tyr	Asn	Leu	Gln	Tyr
					305		310				315				320	
	Glu	Asn	Leu	Glu	Arg	Lys	Lys	Glu	Tyr	Lys	Gln	Ala	Leu	Glu	Ala	Phe
					325				330					335		
35	Cys	Leu	Ser	Lys	Thr	Leu	Ser	Asp	Ser	Met	Ser	Ile	Ala	His	Lys	Val
				340					345					350		
	Ser	Ser	Ile	Gln	Glu	Thr	Arg	Phe	Asn	Tyr	Glu	Arg	Asn	Lys	Ser	Gln
			355					360					365			
	Lys	Glu	Leu	Glu	Glu	Ile	Gln	Gln	Val	Ser	Lys	Ala	Lys	Gln	Glu	Lys
			370				375					380				
40	Ser	Lys	Phe	Ile	Leu	Leu	Ser	Thr	Leu	Phe	Ala	Leu	Phe	Ile	Ser	Ile
					385		390				395				400	
	Leu	Leu	Ile	Ser	Val	Leu	Thr	Tyr	Ala	Tyr	Arg	Gln	Gly	Lys	Lys	His
					405				410					415		
45	Asn	Lys	Leu	Ile	Lys	Glu	Thr	Asp	Lys	Leu	Arg	Ser	Gly	Phe	Phe	Thr
				420					425					430		
	Gly	Ile	Thr	His	Glu	Phe	Arg	Thr	Pro	Ile	Thr	Val	Ile	Gln	Gly	Leu
				435				440					445			
	Asn	Glu	Lys	Met	Ser	Ser	Ser	Pro	Asp	Leu	Gln	Ala	Ser	Asp	Arg	Thr
				450			455					460				
50	Glu	Leu	His	Lys	Ile	Ile	Asp	Arg	Gln	Ser	Ser	His	Met	Leu	Asn	Leu
					465		470				475				480	
	Val	Asn	Gln	Leu	Leu	Asp	Ile	Cys	Lys	Ile	Arg	Ser	Gly	Val	Ser	Thr
					485				490					495		
55	Pro	Glu	Trp	Arg	Asn	Gly	Asp	Ile	Val	Ser	Phe	Val	Gln	Ile	Leu	Ile
				500					505					510		
	Asp	Ser	Phe	Ala	Pro	Tyr	Ala	Gln	Ala	Gln	Asp	Ile	Thr	Leu	Glu	Leu
				515				520					525			
	Gln	Pro	Glu	Ser	Lys	Pro	Ile	Val	Val	Asp	Phe	Val	Pro	Ser	Tyr	Leu
				530			535					540				
60	Gln	Lys	Ile	Ile	Ser	Asn	Leu	Leu	Ser	Asn	Ala	Ile	Lys	Tyr	Ser	Leu
					545		550				555				560	
	Ala	Gly	Gly	Arg	Val	Val	Ile	Ser	Leu	Ala	Lys	Thr	Lys	Asn	Glu	Lys
					565				570					575		
65	Asn	Leu	Ile	Ile	Arg	Val	Ala	Asp	Asn	Gly	Ile	Gly	Ile	Asp	Lys	Thr
				580					585					590		
	Asp	Gln	Ala	His	Ile	Phe	Asp	Ile	Phe	Tyr	Arg	Gly	Gln	Ser	Ala	Thr
				595				600					605			
	Glu	Lys	His	Gly	Ser	Gly	Val	Gly	Leu	Ser	Phe	Thr	Asn	Ile	Leu	Val
				610			615					620				
70	Glu	Asn	Leu	Arg	Gly	Thr	Ile	Lys	Val	Glu	Ser	Gln	Pro	Gly	Lys	Gly
					625		630				635				640	
	Ser	Ala	Phe	Thr	Ile	Ser	Ile	Pro	Thr	Gln	Asn	Gln	Ser	Ser	Ser	Ala
					645				650					655		
75	Glu	Ile	Leu	Pro	Trp	Leu	Pro	Ser	Ser	Asp	Asp	Ile	Val	Met	Pro	Val
				660					665					670		

WO 99/29870

PCT/AU98/01023

483/490

Arg Asp Tyr Thr Gly Trp Phe Ala Met Tyr Asp Thr Asn Lys Val Gly
130 135 140
Leu Val Asp Phe Ile Tyr Asn Arg Pro Arg Pro Asn Asp Asp Glu Phe
145 150 155 160
5 Pro Lys Tyr Glu Ala Gln Tyr Leu Gly Ile Glu Met Phe Gly Met Lys
165 170 175
Leu Lys Gln Thr Gly Gly Asn Tyr Met Thr Asp Gly Tyr Gly Ser Ala
180 185 190
10 Val Gln Ser His Ile Ala Tyr Thr Glu Asn Ser Ser Leu Ser Gln Ala
195 200 205
Gln Val Asn Gln Lys Met Lys Asp Tyr Leu Gly Ile Thr His His Asp
210 215 220
Val Val Gln Asp Pro Asn Gly Glu Tyr Ile Asn His Val Asp Cys Trp
225 230 235 240
15 Gly Lys Tyr Leu Ala Pro Asn Lys Ile Leu Ile Arg Lys Val Pro Asp
245 250 255
Asn His Pro Gln His Gln Ala Leu Glu Asp Met Ala Ala Tyr Phe Ala
260 265 270
20 Ala Gln Thr Cys Ala Trp Gly Thr Lys Tyr Glu Val Tyr Arg Ala Leu
275 280 285
Ala Thr Asn Glu Gln Pro Tyr Thr Asn Ser Leu Ile Leu Asn Asn Arg
290 295 300
Val Phe Val Pro Val Asn Gly Pro Ala Ser Val Asp Asn Asp Ala Leu
305 310 315 320
25 Asn Val Tyr Lys Thr Ala Met Pro Gly Tyr Glu Ile Ile Gly Val Lys
325 330 335
Gly Ala Ser Gly Thr Pro Trp Leu Gly Thr Asp Ala Leu His Cys Arg
340 345 350
30 Thr His Glu Val Ala Asp Lys Gly Tyr Leu Tyr Ile Lys His Tyr Pro
355 360 365
Ile Leu Gly Glu Gln Ala Gly Pro Asp Tyr Lys Ile Glu Ala Asp Val
370 375 380
Val Ser Cys Ala Asn Ala Thr Ile Ser Pro Val Gln Cys Tyr Tyr Arg
385 390 395 400
35 Ile Asn Gly Ser Gly Ser Phe Lys Ala Ala Asp Met Thr Met Glu Ser
405 410 415
Thr Gly His Tyr Thr Tyr Ser Phe Thr Gly Leu Asn Lys Asn Asp Lys
420 425 430
40 Val Glu Tyr Tyr Ile Ser Ala Ala Asp Asn Ser Gly Arg Lys Glu Thr
435 440 445
Tyr Pro Phe Ile Gly Glu Pro Asp Pro Phe Lys Phe Thr Cys Met Asn
450 455 460
Glu Thr Asn Thr Cys Thr Val Thr Gly Ala Ala Lys Ala Leu Arg Ala
465 470 475 480
45 Trp Phe Asn Ala Gly Arg Ser Glu Leu Ala Val Ser Val Ser Leu Asn
485 490 495
Ile Ala Gly Thr Tyr Arg Ile Lys Leu Tyr Asn Thr Ala Gly Glu Glu
500 505 510
50 Val Ala Ala Met Thr Lys Glu Leu Val Ala Gly Thr Ser Val Phe Ser
515 520 525
Met Asp Val Tyr Ser Gln Ala Pro Gly Thr Tyr Val Leu Val Val Glu
530 535 540
Gly Asn Gly Ile Arg Glu Thr Met Lys Ile Leu Lys
545 550 555

(2) INFORMATION FOR SEQ ID NO:526

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 428 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (iv) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION 1...428
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

WO 99/29870

PCT/AU98/01023

484/ 490

Met Lys Leu Ser Ser Lys Lys Ile Leu Ala Ile Ile Ala Leu Leu Thr
1 5 10 15
Met Gly His Ala Val Gln Ala Gln Phe Val Pro Ala Pro Thr Thr Gly
20 25 30
5 Ile Arg Met Ser Val Thr Thr Thr Lys Ala Val Gly Glu Lys Ile Glu
35 40 45
Leu Leu Val His Ser Ile Glu Lys Lys Gly Ile Trp Ile Asp Leu Asn
50 55 60
10 Gly Asp Ala Thr Tyr Gln Gln Gly Glu Glu Ile Thr Val Phe Asp Glu
65 70 75 80
Ala Tyr His Glu Tyr Thr Ile Gly Thr Gln Thr Leu Thr Ile Tyr Gly
85 90 95
Asn Thr Thr Arg Leu Gly Cys Arg Ser Thr Gly Ala Thr Ala Val Asp
100 105 110
15 Val Thr Lys Asn Pro Asn Leu Thr Tyr Leu Ala Cys Pro Lys Asn Asn
115 120 125
Leu Lys Ser Leu Asp Leu Thr Gln Asn Pro Lys Leu Leu Arg Val Trp
130 135 140
20 Cys Asp Ser Asn Glu Ile Glu Ser Leu Asp Leu Ser Gly Asn Pro Ala
145 150 155 160
Leu Ile Ile Leu Gly Cys Asp Arg Asn Lys Leu Thr Glu Leu Lys Thr
165 170 175
Asp Asn Asn Pro Lys Leu Ala Ser Leu Trp Cys Ser Asp Asn Asn Leu
180 185 190
25 Thr Glu Leu Glu Leu Ser Ala Asn Pro Arg Leu Asn Asp Leu Trp Cys
195 200 205
Phe Gly Asn Arg Ile Thr Lys Leu Asp Leu Ser Ala Asn Pro Leu Leu
210 215 220
30 Val Thr Leu Trp Cys Ser Asp Asn Glu Leu Ser Thr Leu Asp Leu Ser
225 230 235 240
Lys Asn Ser Asp Val Ala Tyr Leu Trp Cys Ser Ser Asn Lys Leu Thr
245 250 255
Ser Leu Asn Leu Ser Gly Val Lys Gly Leu Ser Val Leu Val Cys His
260 265 270
35 Ser Asn Gln Ile Ala Gly Glu Glu Met Thr Lys Val Val Ala Leu
275 280 285
Pro Thr Leu Ser Pro Gly Ala Gly Ala Gln Ser Lys Phe Val Val Val
290 295 300
40 Asp Leu Lys Asp Thr Asp Glu Lys Asn Ile Cys Thr Val Lys Asp Val
305 310 315 320
Glu Lys Ala Lys Ser Lys Asn Trp Arg Val Phe Asp Phe Asn Gly Asp
325 330 335
Ser Asp Asn Met Leu Pro Tyr Glu Gly Ser Pro Thr Ser Asn Leu Ala
340 345 350
45 Val Asp Ala Pro Thr Val Arg Ile Tyr Pro Asn Pro Val Gly Arg Tyr
355 360 365
Ala Leu Val Glu Ile Pro Glu Ser Leu Leu Gly Gln Glu Ala Ala Leu
370 375 380
50 Tyr Asp Met Asn Gly Val Lys Val Tyr Ser Phe Ala Val Glu Ser Leu
385 390 395 400
Arg Gln Asn Ile Asp Leu Thr His Leu Pro Asp Gly Thr Tyr Phe Phe
405 410 415
Arg Leu Asp Asn Tyr Thr Thr Lys Leu Ile Lys Gln
420 425

(2) INFORMATION FOR SEQ ID NO:527

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527

WO 99/29870

PCT/AU98/01023

487 / 490

5 GCAGTAGGGA AAATCGATGT GCATCTGGGC GCACAGGTCG ATTTTCTGAA AGAAATCGGC 840
 AAACCATATG AAGCCAAACG CTGTATGAG CGGGTCACGT ATGACTTGGG AATGATCCGT 900
 GAGTTGGGTT ATTGTTCCGG TATAGAGAAC TATTCGGGCT ACTTOGACGG CCSTGACGG 960
 GGGGAACGTC CTTCTGTCT GTTGGATTAT TTCCCGGAGG ATTTCTGTGT GSTCATAGAC 1020
 GAAAGCCATG TAACGATACC GCAGATACGT GCCATGTACG GAGGCGATCG TTCGCGCAAG 1080
 GAGAATCTGG TCGAATACGG ATTCGCGCTG CCTGCGGCTC TCGCAATCG GCCGCTTCGC 1140
 TTCGACGAGT TCGAAGCTCT CACCCCGCGG ACCCTTTATA TCAGTGCCAC GCCTGCCGAC 1200
 TATGAGCTGA ACAGAGCGCA AGGCGTGATC GTGAGGACG TGATCCGTCC GACCGGACTG 1260
 CTGGATCCCA TCATCGACGT CAAGCCGAGG GAAACCAAG TGGACGATCT GATGGAGGAG 1320
 10 ATAGCACCGT GCATCGAAAA GAAAGAGCGC GTACTGTGTA CCACCGTGAC CAAACGTATG 1380
 GCAGAGGAGT TTAGCGAATA CCTGCTACGC CACGSTATCA GCACCGGCTA CATAACAGC 1440
 GATGTGGACA CGCTGGAGCG TGTGCGTATC ATGGAAGACC TGCGCAAGGG GGTCTACGAT 1500
 GCACTCATCG GGTGTAATCT GCTCCGCGAA GGATTGSACT TGCGGAAAGT TTCGCTTGTG 1560
 GCTATTCTGG ATGCGSATAA GGAAGSATTC CTGCGCTCGC ATCGTTGCTC CACCGAGACT 1620
 15 GCAGGAGCTG CCGCCCGGCA CATTATGCG CGTGTCTCT TCTACGCGGA CAAGATCACC 1680
 GACAGTATGC AGCTCACCAT GGACGAGACT GCACGCGGAC GCGCAAGCA ACTGCGCTAC 1740
 AACGAAGCGC ACGGCATCAG CCCCCAACAG ATAGTGAAGA ACAGTGCTGC CATTGGGGGA 1800
 GAAGGCGATG TGTGCGGCTT GCAATCCGAT ACAGAATCGG GTGCGTACAT AGAAGAGAGC 1860
 AGCATGCTGG CTGCGGATCC TTGCGCGGAC TATCTGAGCA AACCCAAAGT GGAAGCACTC 1920
 20 ATTGCTTCCA CCAAGAAACA AATGCTGGCA GCAGCCAAAG AGCTGGACTT TCTGGAAGCG 1980
 GCACGACTTC GGGACGAAGC CGCAGGATTG GAAAGAAAC TGGAGCAACT CACAGCC 2037

25 (2) INFORMATION FOR SEQ ID NO:530
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2034 base pairs
 (B) TYPE: nucleic acid
 (C) STRAINDNESS: double
 30 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 35 (iii) HYPOTHETICAL: NO
 (iv) ALTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis
 40 (ix) FEATURE:
 (A) NAME/KEY: misc feature
 (B) LOCATION 1...2034
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

ATGGACTACA AACTCACTTC TCGATTCAAG CCCACGSGGC ACCAGCCGGA AGCCATTGCG 60
 CAATCTGTAC AGGCGATCAA CGAAGGGATG CCGGCTCAGA CGCTGCTCGG CGTAACGGGT 120
 TCGGGCAAAA CTTTACGGT GGCTAACGTG GTGGCGGCGG TCAATCGTCC GACCCTTGTC 180
 50 CTGAGTCACA ACAAGACCTT GGCAGCACAG CTATACGGAG AGTTCAAAGC CTTCTTCCCC 240
 GAGAATCGGG TGGAGTATTT CGTCAGCTAC TACGACTACT ATCAGCCCGA GGCCTACCTC 300
 CCGGTCACAG ACACCTATAT CGAAAAGGAC ATGGCCATCA ACACCGGAGT CGAAAAACTG 360
 CGATTGAGGG CCACGGGCTTC GCTCCTGTCA GGGCGGAAAG ATGTGCTTGT GGTCAGCTCC 420
 55 GTATCCTGTC TCTACGGTAT GGCCAATCCT GAAGCTTTT CCGAAAAGGT GATCAGCCTG 480
 CACACGGGAC AAAGGGCAGA CAGGGATCAT TTTATCCGCC TGCTGGTAGA GAGCTACTAC 540
 ACGAACATA AAGTAGAGTT CGAGAGCGGC AACTTCCGTG TCAAAGGCGA CAGCGTGGAC 600
 ATATTCCTCG CCGTAGAAGG TTATGACGGC GTGGCATACA GGGTGGAGTT TTGGGATGGA 660
 GAGTCTGAGC GGCTGAGTAC CTTGATCCCG CGAACGGGAC GGGAAATACG CCTGCTGTG 720
 60 GAGCTGAAGA TATATCGGGC CAATCTCTTC GTGACGACTA AGGAGCAGGT GGATCGGGCA 780
 GTAGGGAAAA TCGATGTGGA TCTGGGGCGA CAGGTCGATT TTCTGAAAGA AATCGGCAAA 840
 CCATATGAAG CCAACGCTT GTATGAGCGG GTACAGTATG ACTTGGAAAT GATCGGTGAG 900
 TTGGGTTATT GTTCCGGTAT AGAGAATCAT TCGGCTACT TCGACGGCCG TGACGCGGGC 960
 GAACGTCCTT TCTGTCTGTT GGATTATTTC CCGGAGGATT TCCTGTTGGT CATAGACGAA 1020
 65 AGCCATGTAA CGATACGGCA GATACGTGCC ATGTACGGAG GCGATCGTTC GCGCAAGGAG 1080
 AATCTGGTCC AATACGGATT CCGCCTGCGT GCGGCTCTCG ACAATCGGCC GCTTCGCTTC 1140
 CACGAGTTCC AAGCTCTCAC CCCCCGGACC CTTTATATCA GTGCCACGCC TGCCGACTAT 1200
 GAGCTGAACA GAAGCGAAGG CGTGATCGTC GAGCAGCTGA TCCGTCGAC CCGACTGCTG 1260
 GATCCCATCA TCGACGTCAA GCGGACGGCA AACCAAGTGG ACGATCTGAT GGAGGAGATA 1320
 70 GCACGCTGCA TCGAAAAGAA AGAGCGCGTA CTGGTAACGA CGCTGACCAA ACGTATGGCA 1380
 GAGGAGCTTA GCGAATACCT GCTACGCCAC GGTATCAGCA CCGGTACAT ACACAGCGAT 1440
 GTGGACAGCT TCGAGCGTGT GCGTATCATG GAAGACCTGC GCAAGGGGGT CTACGATGCA 1500
 CTGATCGGGG TGAATCTGCT CCGCGAAGGA TTGGACTTGC CGGAAGTTTC GCTTGTGGCT 1560
 ATTCTGGATG CGGATAAGGA AGGATTCCTG CGCTCGCATC GTTCGCTCAC GCAGACTGCA 1620
 75 GGACGTGCGG CCGCGCACAT TCATCGGCGT GTCATCTTCT ACGCGGACAA GATCACCGAC 1680
 AGTATGCAAC TCACCATGGA CGAGACTGCA CGCCGACGCG CAAAGCAACT GGCCTACAA 1740

WO 99/29870

PCT/AU98/01023

488 / 490

GAAGCGCACG GCATCACCCC CCAACAGATA GTGAAGAACA GTGCTGCCAT TTGGGGAGAA 1800
GGCGATGTGT CGGCCTTGCA ATCCGATACA GAATCCGGTG CGTACATAGA AGAGAGCAGC 1860
ATGGTGGCTG CGGATCCTTT GSCCGACTAT CTGAGCAAAC CCAAGCTGGA AGCACTCATT 1920
GCTTCGACCA AGAAGCAAT GCTGGCAGCA GCCAAGAGC TGGACTTTCT GGAAGCGGCA 1980
5 CGACTTCGGG ACGAAGCCGC ACGATTGGAA AAGAACTGG AGCAACTCAC AGCC 2034

(2) INFORMATION FOR SEQ ID NO:531

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 679 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- 20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...679
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531

Val Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln
1 5 10 15
30 Pro Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro
20 25 30
Ala Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val
35 40 45
Ala Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His
50 55 60
35 Asn Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe
65 70 75 80
Pro Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln
85 90 95
40 Pro Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met
100 105 110
Ala Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser
115 120 125
45 Leu Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Ser Val Ser Cys
130 135 140
Leu Tyr Gly Met Ala Asn Pro Glu Ala Phe Ser Glu Lys Val Ile Ser
145 150 155 160
Leu His Thr Gly Gln Arg Ala Asp Arg His Phe Ile Arg Leu Leu
165 170 175
50 Val Glu Ser Tyr Tyr Thr Asn Asn Lys Val Glu Phe Glu Ser Gly Asn
180 185 190
Phe Arg Val Lys Gly Asp Ser Val Asp Ile Phe Pro Ala Val Glu Gly
195 200 205
55 Tyr Asp Gly Val Ala Tyr Arg Val Glu Phe Trp Asp Gly Glu Val Glu
210 215 220
Arg Leu Ser Thr Phe Asp Pro Arg Thr Gly Arg Glu Tyr Gly Leu Leu
225 230 235 240
Ser Glu Leu Lys Ile Tyr Pro Ala Asn Leu Phe Val Thr Thr Lys Glu
245 250 255
60 Gln Val Asp Arg Ala Val Gly Lys Ile Asp Val Asp Leu Gly Ala Gln
260 265 270
Val Asp Phe Leu Lys Glu Ile Gly Lys Pro Tyr Glu Ala Lys Arg Leu
275 280 285
65 Tyr Glu Arg Val Thr Tyr Asp Leu Glu Met Ile Arg Glu Leu Gly Tyr
290 295 300
Cys Ser Gly Ile Glu Asn Tyr Ser Arg Tyr Phe Asp Gly Arg Asp Ala
305 310 315 320
Gly Glu Arg Pro Phe Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu
325 330 335
70 Leu Val Ile Asp Glu Ser His Val Thr Ile Pro Gln Ile Arg Ala Met
340 345 350
Tyr Gly Gly Asp Arg Ser Arg Lys Glu Asn Leu Val Glu Tyr Gly Phe
355 360 365
75 Arg Leu Pro Ala Ala Leu Asp Asn Arg Pro Leu Arg Phe Asp Glu Phe
370 375 380

WO 99/29870

PCT/AU98/01023

489/ 490

5 Glu Ala Leu Thr Pro Arg Thr Leu Tyr Ile Ser Ala Thr Pro Ala Asp
385 390 395 400
Tyr Glu Leu Asn Arg Ser Glu Gly Val Ile Val Glu Gln Leu Ile Arg
405 410 415
10 Pro Thr Gly Leu Leu Asp Pro Ile Ile Asp Val Lys Pro Thr Ala Asn
420 425 430
Gln Val Asp Asp Leu Met Glu Glu Ile Ala Arg Cys Ile Glu Lys Lys
435 440 445
15 Glu Arg Val Leu Val Thr Thr Leu Thr Lys Arg Met Ala Glu Glu Leu
450 455 460
Ser Glu Tyr Leu Leu Arg His Gly Ile Ser Thr Gly Tyr Ile His Ser
465 470 475 480
Asp Val Asp Thr Leu Glu Arg Val Arg Ile Met Glu Asp Leu Arg Lys
485 490 495
20 Gly Val Tyr Asp Ala Leu Ile Gly Val Acn Leu Leu Arg Glu Gly Leu
500 505 510
Asp Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu
515 520 525
25 Gly Phe Leu Arg Ser His Arg Ser Leu Thr Gln Thr Ala Gly Arg Ala
530 535 540
Ala Arg His Ile His Gly Arg Val Ile Phe Tyr Ala Asp Lys Ile Thr
545 550 555 560
Asp Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Arg Ala Lys
565 570 575
30 Gln Leu Ala Tyr Asn Glu Ala His Gly Ile Thr Pro Gln Gln Ile Val
580 585 590
Lys Asn Ser Ala Ala Ile Trp Gly Glu Gly Asp Val Ser Ala Leu Gln
595 600 605
35 Ser Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala
610 615 620
Ala Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu
625 630 635 640
Ile Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Ala Lys Glu Leu Asp
645 650 655
40 Phe Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys
660 665 670
Lys Leu Glu Gln Leu Thr Ala
675
40 (2) INFORMATION FOR SEQ ID NO:532
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 678 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
50 (iv) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...678
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532
60 Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln Pro
1 5 10 15
Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro Ala
20 25 30
65 Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val Ala
35 40 45
Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His Asn
50 55 60
Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe Pro
65 70 75 80
70 Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro
85 90 95
Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met Ala
100 105 110
75 Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser Leu
115 120 125

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU 98/01023

A. CLASSIFICATION OF SUBJECT MATTER		
Int Cl ⁶ : C12N 15/31; C07K 14/195; A61K 38/00, 38/16, 39/00		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) See Electronic Database box below		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched See Electronic Database box below		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)		
Medline	porphyromonas gingivalis, bacterial proteins, peptides, bacterial vaccines	
CA	porphyromonas gingivalis, genes microbial, antigens	
WPAT	porphoryomonas or porphyromonas gingivalis, C07K 07, 014/195: C12N 15/31 + *Seq IDS 265, 528, 340, 341	
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Derwent abstract 95-3513214/45 WO 95/26404 (MEITO SANGYO KK) 5 October 1995.	all
A	Derwent abstract 95-147309/19 WO 95/09181 (KYOWA HAKKO KOGYO KK) 6 April 1995.	all
<input type="checkbox"/> Further documents are listed in the continuation of Box C <input checked="" type="checkbox"/> See patent family annex		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search 11 January 1999		Date of mailing of the international search report 28 JAN 1999
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929		Authorized officer PHILIPPA WYRDEMAN Telephone No.: (02) 6283 2554

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU 98/01023

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 1 to 34 in part
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

The claims are directed to a very large number of polypeptides and nucleotides such that it is economically unfeasible to perform a full and comprehensive search on all the claimed sequences.
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6 4(a)

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
PCT/AU 98/01023

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report				Patent Family Member	
WO	95/26404	EP	753577		
WO	95/09181	EP	726276	JP	7097395